Atterney Doctot (LEZ)-5033-91W0 Thirmshillomologous Human Homologous Sequence Cluster (Ittle		proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, subunit, beta type, 6 macropain) subunit, beta type, 6	proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 6 macropain) subunit, beta type, 6
iumaniHomologous Roown GeneiName	proteasome (prosome, macropain) subunit, beta type 5, proteasome (prosome, macropain) subunit, beta type, 5	proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 6	proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 6
Model Gode	G, H, K, BB,		В, G, H, РРР, QQQ
Centenii Nee or Refeeg (D	D45247	660	B, G,
	72.0	6	25253
TABLES Segement Description	7867	3875	3875

Alternacy Docket (1921-5038-0100) Alternacy Document No. 1935323.1 Ani Homologous Human Homologous Sequence Custory III	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7), proteosome (prosome, macropain) ESTs, Highly similar to PRCY MOUSE PROTEASOME COMPONENT C13 subunit, beta type 8 (large multifunctional protease 7), proteosome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	type, 9
Homenikom Known Cono	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7), proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7)	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2), proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)
Model Gode	O, P,	X
Kee or Rassage	NM_080767	NM 012708 KKK
38 8 8 8 8 8 8	25252	4002
(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	3906	3123

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Michael Boeument Ne. 1935/22.1	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2), proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional			expressed sequence AW049591, protein kinase, AMP-activated, beta 1 non-catalytic subunit	similar to JN0723 phosphoprotein phosphatase [H.sapiens], protein phosphatase 1, catalytic subunit, alpha isoform	EST, Weakly similar to Arozaro prosphatase [H.sapiens], protein phosphatase 1, catalytic subunit, alpha isoform
Known Gene Nemo	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2), proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional	protease 2, protein C (inactivator of coagulation factors Va and VIIIa)	protein kinase C, beta protein kinase C, beta 1	protein kinase, AMP- activated, beta 1 non- catalytic subunit	protein phosphatase 1, catalytic subunit, alpha isoform	protein phosphatase 1, catalytic subunit, alpha isoform
Medell Godo		, J. KKK V, NN, OO	Q	K, U, X, Y, LLL, SSS	ш	RR, SS
## ## ## ## ## ## ## ##		NM_012708 X64336	2713	K, U, X, Y NM 031976 LLL, SSS	NM 031527	NM 031527
S S S S S S S S S S S S S S S S S S S		4003 556	24545	17601	9369	9370
TABLE Sequence of the sequence		3123 4246	3124	3716	3637	3637

Alterney Doekel 1227-5038-60000 Doeuman No. 1995228.1 The homeologous Sequence Clusterfills	protein phosphatase 1, catalytic subunit, beta isoform			protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform, protein phosphatase 2a, catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform, protein phosphatase 2a, catalytic subunit, alpha isoform	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600017J22:protein phosphatase 2a, catalytic subunit, beta isoform, full insert sequence, protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform
Human Homologous	protein phosphatase 1, catalytic subunit, beta isoform	protein phosphatase 2 (formerly 2A), catalytic subunit alpha	isoform, arpria phosphatase 2a,	catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform, protein phosphatase 2a, catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase Q, R, PP, QQ, 2a, catalytic subunit, SS, VV beta isoform
Model Gode	Z			Q, R, General Alternate	B, Q, R, WW, General Alternate	Q, R, PP, QQ, SS, W
	NM_013065			AI012595	NM_017039	Q, R, P
E3 GLGG GLGG	21287			3203	3202	24596
TABLESS Seq GL	3210		<u>-</u>	1424	3257	3258

						.= '		·= 1
Document No. 1995628.1 Human Homologous Known Cenel Name: Human Homologous Sequence Cluster Title	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600017J22:protein phosphatase 2a, catalytic subunit, beta isoform, full insert sequence, protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 22, catalytic subunit, beta isoform		alpha), protein phosphatase 3, catalytic suburit, arpire is	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase 4a3, protein tyrosine	phosphatase type IVA, member 1, protein syrosing processes (FC 3 1.3.48).	EST, Moderately similar to A34845 protein-tyrosine-priospriates (LO ST) HUMAN nonreceptor type 1B - rat [R.norvegicus], ESTs, Moderately similar to PTN1_HUMAN proTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 [H.sapiens], protein proTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 [H.sapiens], protein professional processions and protein protein professional protein professional protein professional protein professional protein professional prof	tyrosine phosphatase, non-teceptor 1972, tyrosine-phosphatase (EC 3.1.3.48), EST, Moderately similar to A34845 protein-tyrosine-phosphatase (EC 3.1.3.48),	nonreceptor type 1B - rat [R.norvegicus], ES IS, Moderatory Commerceptor 1 [H.sapiens], protein PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1 [H.sapiens], protein tyrosine phosphatase, non-receptor type 1
mani Homologous Innani Homologous Iown Gene Name	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha), protein phosphatase a catalytic subunit,	alpha isoform	B, I, J, DD, EE, protein tyrosine	IVA, member 1	protein tyrosine phosphatase, non-	receptor type 1	protein tyrosine phosphatase, non- receptor type 1
Medel Gode	B, =	<u> </u>	ZZ, AAA	B, I, J, DD, EE,	III, JJJ	0, P, Q, R, V, DD, NN, OO, PP, QQ, III,		DD, ZZ, AAA,
CENTENT TO RESERVE TO THE RESERVE TO	NM_017040_E		NM 017041		NM_031579	· · · · · · · · · · · · · · · · · · ·	A1113289	M33962
LIGGE No.	24597		21580		24219		1841	3 1843
7.000 B B B B B B B B B B B B B B B B B B	3258		3259		3652		1928	3016

	fyrosine phosphatase, north occupion 1975. ESTs, Moderately similar to JC5288 SHP substrate-1 protein, 509 - mouse [Killing of the control o	protein tyrosine ESTs, Weakly similar to 21032/44 receptor 1902 protein tyrosine phosphatase, receptor RIKEN cDNA 1600019004 gene, expressed sequence AU040377, protein tyrosine type, D phosphatase, receptor type, S phosphatase [M.musculus], 1906, D ESTS, Weakly similar to 2103274A receptor type protein Tyr phosphatase [M.musculus], 1906, 277, 2006, phosphatase [M.musculus], 1906, phosphat	protein tyrosine phosphatase, receptor RIKEN cDNA 1600019004 gene, expressed sequence AU040377, protein tyrosine phosphatase, receptor type, S type, D cotein tyrosine ESTs, Weakly similar to 2103274A receptor type protein Tyr phosphatase [M.musculus].	phosphatase, receptor RIKEN cDNA 1600019004 gene, expressed sequence AU040377, process of the phosphatase, receptor type, S type, D ESTS, Weakly similar to 2103274A receptor type protein Tyr phosphatase [M.musculus], protein tyrosine	eceptor RIKEN cDNA 16000 19004 gene, expressed con-	ESTs, Weakly similar to 2103274A receptor type protein 191 prospirates (M.musculus), ESTs, ESTs, ESTs, Weakly similar to S40282 protein-tyrosine-phosphatase [M.musculus], ESTs, Weakly similar to S46216 leukocyte antigen-related protein precursor - rat Weakly similar to S46216 leukocyte antigen-related protein cds, protein phosphatase, receptor [R.norvegicus], Mus musculus, clone IMAGE:5101040, mRNA, partial cds, protein tyrosine phosphatase, receptor type, F, protein tyrosine phosphatase, protein tyrosine phosphatase, receptor type, F, protein tyrosine phosphatase, protein tyrosine phosphatase, receptor type, F, protein tyrosine	receptor-type, i
HumaniHomologo KnowniGeneiNam protein tyrosine phosphatase, non-	receptor type 1 protein tyrosine phosphatase, non- receptor type	rotein tyrosine hosphatase, reci ype, D	onotein tyrosine shosphatase, rec ype, D	ohosphatase, reciype, D	phosphatase, rectype, D	protein tyrosine phosphatase, re type, F, protein tyrosine phosph	receptor-type, F
Model(Code)	LJ AM	JJ, KK		JJ, KK, General Alternate		I, J, Y, FF, KKK, LLL, OOO, RRR, SSS, General Core Tox Markers, General	Alternate
Centernia. Ace of Refiseq (D) Medel (Code)	M33962 A		NM_019140	NM_019140	NM 019140		M60103
8 GE		11904	14971	14973	14974		1973
TABLE 8		3197		3356	3356		3029

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Augument No. 198582.0 Church Homologous Human Homologous Sequence Queter III	bob goranylizansferase beta	geranylgeranyltransfer RAB geranylgeranyl transferase, b subunit, Rab geranylgeranylmansterase, postase, beta subunit subunit, expressed sequence AA409500		RAB3D, member RAS oncogene family	ESTs, Weakly similar to RAB7 MOUSE resorbered in Contract of Contr	_		Kal-interacting protein 1, rais billioning protein 1		Kal-interacting protein 1, lary billoung protein 188 oncodene family, clone MGC:18653	IMAGE:3600519, mRNA, complete cds, RAP1A, member of RAS oncogene family, RAP2A, member of RAS oncogene family, hypothetical protein DKFZp761C07121, RAP2A, member of RAS oncogene family, hypothetical protein DKFZp761C07121,	RAS oncogene family hypothetical protein similar to smail o proteins, especially results.	RAS-homolog enriched in brain, Ras ESTs, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus], homolog enriched in RAS-homolog enriched in RAS-RAS-RAS-RAS-RAS-RAS-RAS-RAS-RAS-RAS-	enriched in brain 2, ras-like protein viocococ
Human Homologous Known Geno Name	RAB geranylgeranyl transferase, b subunit, Rab	geranylgeranyltransfer ase, beta subunit	RAB11B, member RAS oncogene family	RAB3D, member RAS oncogene family	RAB7, member RAS	oncogene ranniy	Kal-interacting protein 1, ralA binding protein	-	Ral-interacting protein 1, ralA binding protein	_	RAP1A, member of	RAS oncogene family	RAS-homolog enriched in brain, Ras homolog enriched in	brain 2
Model Gode		Q, R, JJ, KK, MM, FFF, TTT	RR	D, V		^		ZZ, AAA		ZZ, AAA		LL		JJ, GGG
eemsemi Nee or Rafseq[D		NM_138708	AA891669	AA819333		NM_023950		NM_032067		NM 032067 ZZ, AAA		AA925664		NM_013216
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Tables Seq @ Define		3981			1	3532		3726		3726		794		3237

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TABLES	ଜ				Artomay Docket Krezn-Dusk-Vuwe Document No. 195523.1
		स्टिक्स हात्तर १८५५ हर		Homologous	
		GLEC AES MONO. RESSOND		Known Gene Name	Modeli Gode Known Genetivame Human Homologous Sequence Gluster mus
				ras-related C3	ESTs, Highly similar to Cdc42 From Human, Nmr, 20 Structures [n.sapiens], was
				ح (musculus DBC2 protein (Dbc2) michae, Camprete Co3, mas massages protein (Dbc2) michae Tc10, complete cds, RAC3, RIKEN cDNA 1700008H16 gene, ras homolog
				Substrate 1 (mo	gene family, member J, ras-like protein, ras-related C3 botulinum toxin substrate 1 (rho
1846	2069	A1103616	>	ng protein Rac1)	family, small GTP binding protein Rac1)
				receptor (calcitonin)	
				activity modifying	1 and the modified of the state
1415	2791	AI012429	ZZ, AAA	protein 1	receptor (calcitonin) activity illouilying protein
			H, I, J, FF,		
			FFF, 000,		
			SSS, UUU,		
			General Core		
			Tox Markers,	regucalcin, regucalcin	
			General	(senescence marker	
3645	28	NM 031546	Alternate	protein-30)	regucalcin, regucalcin (seriescence manya programa)
				regulator of G-protein	
				signaling 14, regulator	14. regulator of G-protein signaling 14. regulator of G-
				of G-protein signalling	of G-protein signalling regulator of G-protein signaling 12, regulator of G-protein signalling
3822	24621	NM 053764	Z, AA	14	protein signalling 14
				regulator of G-protein	
				signaling 5, regulator	
		-		of G-protein signalling	5 poilleanis distance of second and a second
2472	2088	A1229727	NN. 00	5	regulator of G-protein signaling 5, regulator of G-protein signalings
				retinoic acid receptor,	stad retacent bice of a situation of a
3638	12996	NM 031528 C, RR	C, RR	alpha	retinoic acid receptor, alpha, retirioic acid receptor, acid
	Т	ı		retinoid X receptor	
_			_	beta, retinoid X	
3043	25060	M81766	Ω	receptor, beta	

								_						٦ .
<u> </u>	Document No. 1645524.1	Human Homologous Sequence Ouster ittle	EST, Moderately similar to VAHU plasma retinol-binding protein precursor [H.sapiens], EST, Weakly similar to RETB_RAT Plasma retinol-binding protein precursor (PRBP) (RBP) (R.norvegicus], retinol binding protein 4, plasma	ESTs, Weakly similar to RNL4_RAT Ribonuclease 4 precursor (RNase 4) (RL3)	sequence Al385586, ribonuclease, RNase A family 4, ribonuclease, RNase A family, 4	EST, Moderately similar to KIBZ_HUMAN DOLICHTE-DIPHOSPHOOLIGOSACCHARIDEPROTEIN GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ESTs, Moderately similar to RIBZ_HUMAN CONTRANS CHARIDEPROTEIN	GLYCOSYLTRANSFERASE 63 KDA SUBUNIT PRECURSOR [H.sapiens], ribophorin	Z, related sequence 1, modifically		EST, Moderately similar to R10A MOUSE 60S RIBOSOIMAL PROTEIN LTUA [M.musculus], ribosomal protein L10A, ribosomal protein L10a	EST, Moderately similar to R10A MOUSE 60S RIBOSOMAL PROTEIN L10A	EST, Moderately similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], EST, Weakly similar to JC2368 ribosomal protein L13, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to ribosomal protein L13; 60S [validated] - rat [R.norvegicus], ESTs, Highly similar to ribosomal protein L13; breast basic conserved protein 1 [Homo sapiens] [H.sapiens],		RPL13-2 pseudogene mKNA, complete cus, ribosonia proteir E13
		Tuman Homologous (nown.Gene.Name =		ribonuclease, RNase A family 4,			:	ribophorin II	ribosomal protein	L10A, ribosomal protein L10a	ribosomal protein L10A, ribosomal			ribosomal protein L13
		Model Gode	SS HH	000	B, LLL, 555, UUU		1	V, FF	A, B, G, H, RR, EEE, MMM, UUU,	General Alternate	(p)	G, II, FFF, GGG, General	Alternate
		Genženik Aee or RefSeq (D	M10934		NM 020082			NM_031698		NM 031065		X40303		NM_031101
	9	अ <u>।</u> बिट । ।	17472		12087			21575		11849		000		23854
	1000 1000 1000 1000 1000 1000 1000 100		2080		3417			3670		3594		4053		3601

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		1000 - ECONI			
Se	9979	Ace or		Human Hamologous	Human Nomologous
<u></u>		RefSee D	Model Gode	Known.Gene⊾Name	Human Homologous Sequence Guester muse
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			G. H. EEE,		ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L18 [M.musculus], ribosomal
3602	20462	NM_031102		ribosomal protein L18 protein L18	protein L18
_					EST, Weakly similar to RL19 HUMAN 60S RIBOSOMAL PROTEIN L1 [M.musculus], ESTs, Weakly similar to RL19 HUMAN 60S RIBOSOMAL PROTEIN L1 [M.musculus],
					ESTs, Weakly similar to RL19_HUMAN 60S ribosomal protein L19 [K.norvegicus],
3603	16938	NM 031103	5 F, H, Ⅱ	ribosomal protein L19	ribosomal protein L19
		Т			EST, Moderately similar to 2113200B filosofitial process L2 (11.34prons); C3 (1)
					Moderately similar to RL21_RA1 605 RIBOSOMAL TRO Luit L21 [traing vegicas], ECT
					Weakly similar to 2113200B ribosomal protein LZ1 [n.sapiens], ES1, weakly similar to
					RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weany SHIMER OF
					RL21 HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ES1S, Hignly similar to
					2113200B ribosomal protein L21 [H.sapiens], ESTs, Highly similar to RLZ1 MOUSE bus
					RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to RL21 MOUSE
	7,00,	A147E20A	· 	Irihosomal protein L21	ribosomal protein L21 60S RIBOSOMAL PROTEIN L21 [M.musculus], ribosomal protein L21
2162	12014	1	-		EST Moderately similar to 2113200B ribosomal protein L21 [H.sapiens], ES1,
					Moderately similar to RL21 RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], EST,
		<u></u>			Weakly similar to 2113200B ribosomal protein L21 [H.sapiens], EST, Weakly similar to
-					RI 21 MOLISE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to
					RI 21 HIJMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to
					2113200B ribosomal protein L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE 60S
		· · · · · · · · · · · · · · · · · · ·	*		RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to KL21 MOUSE
2750	14025		NM 053330 K. Z. AA. KK	ribosomal protein L21	osomal protein L21 60S RIBOSOMAL PROTEIN L21 [M.musculus], ribosomal protein L21
2		- 1			

Document No. 1995328.1 [H.sapiens], EST, IN L21 [R.norvegicus], EST, rs], EST, Weakly similar to us], EST, Weakly similar to us], EST, Highly similar to	o RL21 MOUSE 60S ar to RL21 MOUSE 21 iens], EST, [R.norvegicus], EST,	Veakly similar to Veakly similar to lighly similar to RL21 MOUSE 60S to RL21 MOUSE SI, EST,	orvegicus], EST, eakly similar to eakly similar to ghly similar to 21 MOUSE 60% RL21 MOUSE	
A COLUMN TO A COLU			Moderately similar to RL21_RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], EST, Moderately similar to RL21_RAT 60S RIBOSOMAL PROTEIN L21 [H.sapiens], EST, Weakly similar to Weakly similar to 2113200B ribosomal protein L21 [M.musculus], EST, Weakly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Highly similar to RL21 MOUSE RIBOSOMAL PROTEIN L21 [M.musculus], ESTs, Moderately similar to RL21 MOUSE RIBOSOMAL PROTEIN L21 [M.musculus], ribosomal protein L21	
Humani Homologious Known Genel Name	ribosomal protein L21	ribosomal protein L21		ribosomai protein L
		>		0, P, W
Ensemi Referential	NM_053330 V, Z, AA	NM_053330		NM 053330 O, P, VV
	14926	14927		14929
	3750	3750		3750

TABLES	ଜ				Attionally Boeton (4:22) was some of the second of the sec
Se 36		General Age of Petse ID		Human Homologous Known Gene Name	Human Homologovs Sequence Giuster Müle
	S.		3, H, EEE,		
			MMM, General		
			Core Tox		
			Markers,		
			General		
4226	2667	X58200	Alternate	ribosomal protein L23	Mus Mac 37044 IMAGE 4793412 mRNA, complete cds, Mus
T	1				Homo sapiens, cione MCC.27044 INVOC.1700 Invocate MGC.6735 musculus, Similar to 60S ribosomal protein L30 isolog, clone MGC.6735
115	2696	AA817997	F. G. H. FFF	ribosomal protein L24	ribosomal protein L24 IMAGE:3590401, mRNA, complete cds, ribosomal protein L24
٦	Ţ	NM 022697	Π	ribosomal protein L28 r	ribosomal protein L28
					EST, Moderately similar to KL29—HUMAIN 603 KIBOSOMAL PROTEIN L29
					[H.sapiens], EST, Moderately similar to KLZ9_KST 1905 (KIDOSOMA) EST, Disply similar to S65784 ribosomal protein L29, cytosolic
			×, ∀,		(P23) [K.norvegicus], E31s, Figure C CCC C Communication of the communic
2429	18612	AI228624	포포	ribosomal protein LZ9	H. Sapiens), nibosonial process and process are process and process are process and proces
					EST, Moderately strings to N.L. 22. RAT 60S RIBOSOMAL PROTEIN L29. IH. Sapiens], EST, Moderately similar to RL29_RAT 60S RIBOSOMAL PROTEIN L29.
					(P23) [R.norvegicus], ESTs, Highly similar to S65784 ribosomal protein L29, cytosolic
3291	5351	NM 017150	KK, FFF, HHH	ribosomal protein L29	[H.sapiens], ribosomal protein L29
					EST Moderately similar to RL29 HUMAN 60S RIBOSOMAL PROTEIN L29
			BB, CC, II,		LS1, Modelately Similar to RL29 RAT 60S RIBOSOMAL PROTEIN L29
			WW, EEE,		(P23) [R.norvegicus], ESTs, Highly similar to S65784 ribosomal protein L29, cytosolic
-	10611	VE8200	Alternate	ribosomal protein L29	ribosomal protein L29 [H.sapiens], ribosomal protein L29
4770	200	\neg		ribosomal protein	
3421	15335	NM 021264	999	L35a	IR norvegicus].
		7	JJ. KK, FFF,		EST, Moderately similar to fibosomal protein Loo Indias its vegeed to mente 5
535	4259	AA892123	GGG	ribosomal protein L36	RIKEN cDNA 1110038G14 gene, ribosomal protein too
					ESIS, Highly Similar to 12A1_10M241111 CHIEFTON
3999	15380	NM 139083	3 F	ribosomal protein L41	ribosoniai pioteiri L4 i

TABLE 9	ଜ				With the process of t
899	(A)	CONTRACTOR AGE OF AGE	Wardal Gorda	Human Homologovs Known Gene Name	ran Homologous Human Homologous Sequence Guster Title Human Homologous Sequence Guster Title
<u>a</u>	900 900	National Park			EST, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [K.norvegicus], EST, Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly similar to R5RTL8 ribosomal protein L8, cytosolic [validated] - rat [R.norvegicus], ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], ESTs, Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus],
4237	15875	X62145	ш	\neg	expressed sequence AL024098, ribosomal protein Lo
1		X62145	G, H, JJ, ННН	ribosomal protein L8	EST Moderately similar to S65792 ribosomal protein L9, cytosolic [H.sapiens], EST,
4210	18250	X51706	F, V, EEE, MMM	ribosomal protein L9	Weakly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L9 [M.musculus], RIKEN cDNA 4930401B11 gene, ribosomal protein L9
			H, EEE, MMM, General		
4210	25687	X51706	Alternate	ribosomal protein L9	
4215	20427	X53378	FFF, HHH, General Alternate	ribosomal protein S13	ESTs, Moderately similar to RS13_HUMAN 40S RIBOSOMAL PROTEIN S13 [H.sapiens], ribosomal protein S13 [H.sapiens], ribosomal protein S13
		T			EST, Weakly similar to JEO 129 floosomal protein S14 - mouse [M.musculus], expressed Highly similar to JEO129 ribosomal protein S14
3503	17567	NM_022672	_	ribosomal protein 514	ribosomal protein S14 sequence ALV2301 0, incoming protein S16, cytosolic FST Al317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic
4206	15626	X17665	EEE, MMM	ribosomal protein S16	ribosomal protein S16 [H.sapiens], expressed sequence AA420385, ribosomal protein S16 [H.sapiens], ESTs. Weakly similar to RS17_HUMAN 40S RIBOSOMAL PROTEIN S1 [H.sapiens],
2272	26258	A1177501	n	ribosomal protein S17	ribosomal protein S17 ribosomal protein S17 ribosomal protein S17 HI IMAN 40S RIBOSOMAL PROTEIN S1 [H.sapiens],
3292		NM 017152	CC, II, EEE,	ribosomal protein S17	ribosomal protein S17 ribosomal protein S17
355	2				

FABILE S.	3.8				CARROLLO CONTROL OF THE CARROL
(S)	9979 1980	Ceneral	Model Gode Kno	HumaniRomotogous Known Gene Name	man Komologous
9			F, K, II, JJ, KK,		
			VV, EEE, FFF, GGG, MMM,		EST, Moderately similar to R3RT19 ribosomal protein S19, cytosolic [validated] - rat
4211	20872	X51707	General Alternate	ribosomal protein S19	[H.sapiens] [H.sapiens] [FGT_ Uichty similar to Ans RIROSOMAL PROTEIN S23 [H.sapiens], ESTs, Weakly
1					similar to ribosomal protein S23 [Rattus norvegicus] [R.norvegicus]. Mus musculus, similar to ribosomal protein S23 [Rattus norvegicus] (R.norvegicus). Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358,
3896	10498	NM 078617	L	ribosomal protein S23	mRNA, complete cds, mitochondrial ribosomal protein S12, ribosomal protein S23
					Weakly similar to RS24_HUMAN 40S RIBOSOMAL PROTEIN S24 [M.musculus], ESTs, Weakly similar to RS24_HUMAN 40S RIBOSOMAL PROTEIN S24 [M.musculus], ESTs,
			L L	S24	Highly similar to JH0213 fibosomal protein 324, cytosoma (moderna) 224, cytosoma (moderna) 224
3609	24615	NM 031112	JJ, KK, FFF	ribosofilai protein oza	ESTs. Highly similar to ribosomal protein S27a [Mus musculus] [M.musculus], ES1s,
					Highly similar to ubiquitin / ribosomal protein S27a [H.sapiens], ESTs, Weakly similar to
			F, II, FFF,		ribosomal protein S27a [Rattus norvegicus] [K.norvegicus], Mus Husschus, Chimical Complete des neural Complete cds, neural Complete cds
				ribosomal protein	upiquitin-like 4, civile in 2017 102 mm. 2017 in properties 8, ribosomal protein S27a
3610	20839	NM 031113	3 Alternate	9718	EST, Moderately similar to RS29_HUMAN 40S RIBOSOMAL PROTEIN S29
			EE. MM, YY,		
3161	17306	NM 012876	<u> </u>	ribosomal protein S29	
					EST, Moderately similar to RS3_MOUSE 403 incosoning process. ESTs, Highly Weakly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus], ESTs, Highly
					similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus], ESTs, Moderately
					similar to RS3_HUMAN 40S RIBOSOMAL PROTEIN S [H.saplens], ES 13, wearly
					similar to RS3 MOUSE 40S RIBOSOMAL PROTEIN SS [M.Indeculus), hypothetical protein FLJ23059, myo-inositol 1-phosphate synthase protein FLJ23059, myo-inositol 1-phosphate synthase
4208	10819	X51536	エ	ribosomal protein S3	A1, ribosomal protein S3
2		Э.			

		1							,
Aliomey Dockel (4921-5033-01W)	Human Homologous Seguence Cluster utile	EST, Weakly similar to JC4662 ribosomal protein S3a, cytosolic [H.sapiens], EST,	Weakly similar to RS3A MOUSE 40S RIBOSOMAL PROTEIN S3A [M.musculus], ESTS, Highly similar to RS3A_HUMAN 40S RIBOSOMAL PROTEIN S3 [H.sapiens], ribosomal protein S3A, ribosomal protein S3a		EST, Moderately similar to 2113200E ribosomal protein S5 [H.sapiens], EST, Weakly		EST, Moderately similar to 2113200E ribosomal protein S5 [H.sapiens], EST, Weakly similar to 2113200E ribosomal protein S5 [H.sapiens], ribosomal protein S5	EST, Moderately similar to R3HUO ribosolina protein 30, 33550. [1.32] Moderately similar to R36_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs, Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein	98
	firman Homologous (nowni Genei Name)	ribosomal protein S3	ribosomal protein S3A, ribosomal protein S3a	ribosomal protein S4, X-linked		ribosomai protein 55	ribosomal protein S5		ribosomal protein S6
	Model Code D		F, III, JJJ, General SAlternate	EEE, IMM	G, H, II, VV, DDD, EEE, FFF, GGG, III, JJJ, MIMM, General Core	Tox Markers X, Y, JJ, KK,	FFF, GGG, HHH, III, JJJ, General Core Tox Markers	G, H, II, JJ, KK, DDD, FFF, HHH, General	Alternate
	CONSTANT	X51536	M84716	X14210		X58465	X58465		NM_017160 Alternate
	elec. Dive	25686	1694	15652		10109	25702		17104
	Sec	4208	3047	T		4228	4228		3295

				CARROLL COCUMENT NO. 1995823.1
	cenetal. Lee or Rese ID	Nodel Gode	Human Homologous Known Gene Name	an Homologous nn Gene Name Human Homologous Sequence Gluster IIIIIo
				EST, Moderately similar to R3HU6 ribosomal protein Sb, cytosolic [n.sapiens], LST, Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Weakly similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], ESTs, Highly PROTEIN S6 [H.sapiens], ESTs, Weakly
		H, II, General		similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein
	NM_017160 Alternate		ribosomal protein S6	S6 EET Modorataly similar to R3H1/6 ribosomal protein S6, cytosolic [H.sapiens], EST,
				Moderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], EST, Woderately similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Highly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ESTs, Weakly similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein similar to RS6_HUMAN 40S RIBOSOMAL PROTEIN S6 [H.sapiens], ribosomal protein
17107	NM_017160	XX, YY	ribosomal protein S6	S6
			ribosomal protein S6 kinase polypeptide 1, ribosomal protein S6	(90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1) (RSK-1) (pp90RSK1) [R.norvegicus], Mus musculus, clone IMAGE:3156601, mRNA, ribonuclease P1, ribosomal protein S6 kinase polypeptide 1, ribosomal protein S6
17300	NM 031107	XX	kinase, 90kD, polypeptide 1	kinase, 90kD, polypeptide 1, ribosomal protein S6 kinase, 90kD, polypeptide 2, ribosomal protein S6 kinase, 90kD, polypeptide 3
				EST, Moderately similar to JC4388 ribosomal protein S7, Cyrosome It is appeared, EST, Weakly similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [M.musculus], EST, Weakly similar to RS7_HUMAN 40S ribosomal protein S7 (S8) [R.norvegicus], ESTs, Highly similar to JC4388 ribosomal protein S7, cytosolic [H.sapiens], ESTs, Highly
	. '	KK, FFF, HHH, General		similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.saplers], ES13, inducionally similar to RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.saplens], ribosomal protein
	NM 031570		ribosomal protein S7	S7

		Τ-	. 🕉	Γ.	<u> </u>		T^-		\neg
	EST, Moderately similar to JC4388 ribosonial process, 57, 57, 57, 57, 57, 57, 57, 57, 57, 57	S7	EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [M.musculus], ESTs, Highly similar to S25022 ribosomal protein S8, cytosolic [H.sapiens], ESTs, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], RIKEN cDNA 1110008P08	gene, ribosomal protein S8 Highly ESTS, Highly EST Weakly similar to 40S RIBOSOMAL PROTEIN S8 (M.musculus), ESTS, Highly EST Weakly similar to 40S RIBOSOMAL PROTEIN S8 (M.musculus), ESTS, Highly			Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene,	Homer, neuronal immediate early gene, 1B, homer, neuronal immediate early gene, 1 FSTs. Weakly similar to S10A MOUSE S-100 PROTEIN, ALPHA CHAIN [M.musculus], 2100	
HumaniHomologous KnowniGene Name		ribosomal protein S7		ribosomal protein S8		ribosomal protein S8	RuvB-like protein 1	RuvB-like 1 (E. coli), RuvB-like protein 1	S100 calcium binding protein A1
भूववा ७०वि भुववा ७०वि	-	B, 33, 00, HHH	JJ, KK, FFF, GGG, HHH, General Core Tox Markers, General	Alternate	v, z, KK, GGG, HHH, General	Alternate	ا .	uu, w	RR
3 		NM 031570 HHH		NM_031706 Alternate		NM 031706 Alternate	AA799735	AB002406	S68809
3) }	9621		16204		16205	18061		1471
77.ABLE 8 Seq. (C)		3649		3673		3673	85	1202	4069

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Miniman Homologous Sequence Guster Me	EST, Moderately similar to S110_RAT Calpactin I light chain (P10 protein) (P11) (Cellular ligand of annexin II) (Nerve growth factor induced protein 42C) [R.norvegicus], S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), S100 calcium binding protein A10 (calpactin)	S100 calcium binding protein A2, S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)			(yeast) Mus musculus, S-adenosylhomocysteine hydrolase-like 1, clone MGC:18748 adenosylhomocystein IMAGE:4007102, mRNA, complete cds, S-adenosylhomocysteine hydrolase, related sequence 3, expressed sequence AL024110	S-adenosylmethionine decarboxylase 1, S-adenosylmethionine decarboxylase 2
Ruman Homologous Model Godo Known Gene Name	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), S100 calcium binding protein A10 (calpactin)	S100 calcium binding protein A4, S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	\$100 calcium binding protein A6 (calcyclin)	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae), SAC1 suppressor of actin mutations 1-like	(yeast) S- adenosylhomocysteir e hydrolase	S-adenosylmethionine decarboxylase 1
	3		0, P		= '.	MM, TTT
Enternit III	4			1	A1171267 II NM_017201 [, J, HH	NM_031011 MM, TT
3. G.	OXO		\neg		8240	15683
TABLE Sequence	196				2083	3581

				Altomoy Doeltet (4.921-3038-611Wo Doeument No. 193522.1
C	THE RESERVE AND ADDRESS.		Human Homologous Known Gene Namer	H <u>túman Homològous Franciscous Komològous Human Homològous Sequence Gluster Müle</u> Model Gode Known Gene Name Human Homologous Sequence Gluster Müle
5	2		secreted acidic cysteine rich	
		glycoprotein, s G, H, M, EE, II, protein, acidic,	glycoprotein, secreted protein, acidic,	
NM 012656			cysteine-rich (osteonectin)	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich (osteonectin)
			secreted acidic	
			cysteine rich	
			glycoprotein, secreted	
			protein, acidic, cysteine-rich	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-rich
NM 012656	92	M, QQ	(osteonectin)	(osteonectin)
			secreted acidic	
			cysteine rich	
			glycoprotein, secreted	
			protein, acidic,	
			cysteine-rich	secreted acidic cysteine rich glycoprotein, secreted protein, acidic, cysteine-non
R47128		PP, QQ	(osteonectin)	(osteonectin)
			secreted	
			phosphoprotein 1,	
			secreted	
			phosphoprotein 1	
			(osteopontin, bone	
			sialoprotein I, early T-	
			lymphocyte activation	
23651 NM_012881	881	EEE, MMM	1)	
			secretoglobin, family 1A, member 1	
17654 AI012117	7	LL, XX	(uteroglobin)	secretoglobin, family 1A, member 1 (uteroglobin)
-1				

	88				Attorney Docket 4492/1-5083-41000 Document No. 1995223.1
	@ <u> </u> @@@	F CONSENTANT CONSENTANT CONTROL CONTRO		Human Homologous	Human Homologous Ring The Report of the Report of the Report of the Republic o
2	i ganga	an bereren			DIVEN ANNA 1700042018 gene. secretory carrier membrane protein 1, secretory
		000000		secretory carrier membrane protein 3	carrier membrane protein 2, secretory carrier membrane protein 3
1023	23919	AA930992		selenoprotein P,	
2485	4280	A1230247		plasma, 1	selenoprotein P, plasma, 1
	3			selenoprotein P,	
				plasma, 1,	
				sulfotransferase,	
				estrogen preferring,	and a state of the
			R, General	sulfotransferase,	selenoprotein P, plasma, 1, suitotransierase, estrogen pretorning, suitotransierase,
3165	4282	NM 012883	Alternate	estrogen-preferring	estrogen-preferring
		1	A, HHH, III, JJJ, General	selenoprotein W, 1, selenoprotein W,	ESTs, Weakly similar to SELW MOUSE SELENOPROTEIN W [M.musculus].
3199	17894	NM_013027	Alternate	muscle 1	selenoprotein W, 1, selenoprotein W, muscle 1
				(oriotorio ro) orino	
				serine (or cysterine) proteinase inhibitor.	
				clade A (alpha-1	
			F, S, EE, SS,	antiproteinase,	
1357	4213	AI010453	NNN	antitrypsin), member 1	
				(or cysteine)	
				proteinase inhibitor,	
			-	clade A (alpha-1	
				antiproteinase,	
3477	4212	NM_022519	NM 022519 M, HH, SS	antitrypsin), member 1	

	-022-	
Actionney Docket (4924-5038-01000) Document No. 1995828.1 Himfall Homologous Sequence Cluster ville	Homo sapiens CTCL tumor antigen se20-9 mRNA, complete cds, Ste20-related serine/threonine kinase, serine/threonine kinase 10 ESTs, Highly similar to SNK_RAT Serine/threonine-protein kinase SNK (Serum inducible kinase) [R.norvegicus], ESTs, Weakly similar to SNK MOUSE SERINE/THREONINE-PROTEIN KINASE SNK [M.musculus], ESTs, Weakly similar to SNK_RAT Serine/threonine-protein kinase SNK (Serum inducible kinase) [R.norvegicus], Homo sapiens cDNA FLJ30246 fis, clone BRACE2002202, weakly similar to SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1), NIMA (never in mitosis gene a)-related mitosis gene a)-related	kinase 4, serum-inducible kinase
Human Homologous		main
	SS O	F, DD, PP JJ, KK
CENTRUM AGE OF THE PARTY AGE OF THE PART	NM_019206	AA943886 A1100867
(a) (b) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	25681	2655 19647
	3477	855

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Attorney Doctot 44921-5038-01Wo Document No. 1995828-6 In Homelogous Human Homologous Sequence Cluster Wile	ESTs, Weakly similar to A54032 alpha-N-acetylneuraminate alpha-2,8-sialyltransferase	acetylneuraminate: [H.sapiens], ESTs, Weakly similar to alpha 2,8-sialyltransferase [M.musculus], acetylneuraminate: sialyltransferase 8 (alpha-2, 8-alpha-2,8-sialytransferase, GD3 synthase), sialyltransferase 8E (alpha-2, 8-polysialytransferase) sialytransferase, GD3 synthase).							
ra Miman Homologicus Known Gene Name	sialyltransferase 8 (alpha-2, 8- sialytransferase) A, sialyltransferase 8A	(apriente acetylneuraminate: alpha-2,8- sialytransferase, GD3 synthase)	sialyltransferase 8 (alpha-2, 8-	sialytransferase 8C (alpha2,3Galbeta1,4G	sialyltransferase)	complex (18kD)	complex (18kD)	signal peptidase	complex (18kD)
Model Code Know	w	v.			F, UU	J., J.	I, J, EEE, MMM	O, HH, XX, YY, PPP,	۵۵۵
# 1		200 Mil			U55938	A1058606	L11319		L11319
3 3 9 0 8 0 8		i co	000		1286	3550	3548		3549
TABLE See			3140		4145	1611	2949		2949

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män Romologous	EST, Moderately similar to SSRD_RAT TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT) (SSR-DELTA) [R.norvegicus], EST, Weakly similar to SSRD_HUMAN TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:4038523, mRNA, partial cds, signal sequence receptor, delta, signal sequence receptor, delta (translocon-associated	protein delta) EST Moderately similar to SSRD_RAT TRANSLOCON-ASSOCIATED PROTEIN,	DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT) (SSR-DELTA) [R.norvegicus], EST, Weakly similar to SSRD_HUMAN TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:4038523, mRNA, partial cds, signal sequence receptor, delta, signal sequence receptor, delta, signal sequence receptor, delta	protein delta) EST Moderately similar to SSRD RAT TRANSLOCON-ASSOCIATED PROTEIN,	DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT PRECURSOR (TRAP-DELTA), Weakly similar to DELTA SUBUNIT) (SSR-DELTA) [R.norvegicus], EST, Weakly similar to SSRD_HUMAN TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR [H.sapiens], Mus musculus, clone IMAGE:4038523, mRNA, partial cds, precure receptor, delta, signal sequence receptor, delta (translocon-associated	protein delta)	signal transducer and activator of transcription 5B, signal transducer and activator of transcription 6, interleukin 4 induced
Humen Homologous	nal sequence eptor, delta, signal luence receptor, ta (translocon- sociated protein		signal sequence receptor, delta, signal sequence receptor, delta (translocon- associated protein		nal .		signal transducer and activator of transcription 5B
Vestal Goda	XX	≯	00 NN O	XX, YY		Z, AA	M, Z, AA
Centenis		NM 017199		NM_017199		NM 017199	NM_022380 M, Z, AA
් න ම	20 N	9124		9125		9126	
(a)		3306		3306		3306	3462

frum-responsive protein JE precursor small inducible cytokine A2, small inducible cytokine A2, small tramily A (Cys-Cys), member 24 and inducible cytokine A2, small inducible cytokine A2, sm	ESTS, Wearly Strings Communications, Similar to Protein P3, clone MGC:38638 IMAGE:5355849, [M.musculus], Mus musculus, Similar to Protein P3, clone to carrier family 10 mRNA, complete cds, RIKEN cDNA 8430417G17 gene, solute carrier family 10 (sodium/bile acid cotransporter family), member 1	
	[M.musculus], Mus musculus, Similar to Protein P. [M.musculus], Mus musculus, Similar to Protein P. mRNA, complete cds, RIKEN cDNA 8430417G17 (sodium/bile acid cotransporter family), member 1	
Small inducible cytokine A2, small inducible	GGG, HHH, solute carrier family MMM, General 10 (sodium/bile acid cotransporter family),	member 1
	GGG, HHH, MMM, Genera Core Tox	Markers
M_031530		NM 017047
20448 20448 2329		0 24771
3639 20 3639 20 3639 20		3260

Raissayllo Modelleede King Raissayllo Modelleede King 12 (poti tran 4, so 12, 4, so 12, 12, 12, 12, 14, mer grou fam trar NM 019346 Z, AA, SS 1 14 NM 019347 RR me solu agrou fam trar trar trar tran tra	man Homologous) Own Gene Name Inte carrier family otassium/chloride insporters), member 4 member 4	Known Genel Name Rumaniflo Mologous Sequence Cluster Title EST, Moderately similar to T31429 K-Cl cotransport protein KCC1, furosemide-sensitive solute carrier family - rat [R.norvegicus], EST, Weakly similar to T31429 K-Cl cotransport protein KCC1, -rat [R.norvegicus], EST, Weakly similar to T31429 K-Cl cotransport protein KCC1, -rat [R.norvegicus], EST, Weakly similar to T31429 K-Cl cotransport protein KCC1, -rat [R.norvegicus], cation-chloride cotransporter-interacting furosemide-sensitive - rat [R.norvegicus], cation-chloride transporters, member 4, solute carrier family 12 (potassium/chloride transporters), member 6, solute carrier family 12, member 4, solute
16 Z, AA, SS 16 Z, AA, SS 16 CC, BBB, CCC	tute carrier family otassium/chloride Insporters), member solute carrier family , member 4	EST, Moderately similar to T31429 K-Cl cotransport protein KCC1, 1010sering-Scripture and IRC
JJ, KK Z, AA, SS RR CC. BBB. CCC	tute carrier family stassium/chloride insporters), member 4 in member 4	rat [R.norvegicus], ES1, weakly similar to 15172010 corrections furosemide-sensitive - rat [R.norvegicus], cation-chloride cotransporter-interacting protein, solute carrier family 12 (potassium/chloride transporters), member 6, solute carrier family 12 carrier family 12 (potassium/chloride transporters), member 6, solute carrier family 12, member 4, solute (potassium/chloride transporters), member 8, solute carrier family 12, member 4, solute
JJ, KK Z, AA, SS CC. BBB. CCC	otassium/chloride Insporters), member 4, member 4	protein, solute carrier family 12 (potassium/chloride transporters), member 4, solute carrier family 12 carrier family 12 carrier family 12 carrier family 12, member 6, solute carrier family 12, member 4, solute (potassium/chloride transporters), member 8, solute carrier family 12, member 4, solute
Z, AA, SS RR CC. BBB. CCC	solute carrier family member 4	carrier family 12 (potassium/chloride transporters), member o, solute carrier family 12, member 4, solute (potassium/chloride transporters), member 8, solute carrier family 12, member 4, solute
JJ, KK Z, AA, SS RR CC. BBB. CCC	solute carrier family member 4	(potassium/chloride transporters), irielliber o, source commit, 42 member 6
Z, AA, SS RR CC. BBB. CCC	member 4	District town 1.7 married 0
Solution	Vinto corrier family	
me group garo garo garo sol sol sol sol sol sol sol sol sol so	ומנפ כשווניו ומוווויא	
grogen fan fan fan fan fan fan fan fan fan fa	t (urea transporter),	
fan fan fan fan fan fan fan fan fan fan	ember 1 (Kidd blood	
tran tran tran tran tran tran tran tran	oup), solute carrier	
trai	family 14 (urea	
2 Sol	ansprorter), member	
sol me sol 16 16 16 16 CCC me		
RR me so 16 16 ac CC BBB. CCC me	olute carrier family	
RR CC. BBB. CCC	4 (urea transporter),	member 2
CC. BBB. CCC	member 2	solute carrier family 14 (urea transporter), montage
CC. BBB. CCC	olute carrier family	
CC. BBB.	 (monocarboxylic acid transporters), 	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier family
	CCC member 1	16 (monocarboxylic acid transporters), member 1
los	olute carrier family	
16 BB, CC, LL, ao	 (monocarboxylic acid transporters), 	RIKEN cDNA 1110004H10 gene, RIKEN cDNA 1200003C15 gene, solute carrier family
NM 012716 TT m	member 1	וס (monocarboxy) ב מכום המוכל ביים ביים ביים ביים ביים ביים ביים ביי

P.S.	<u>ē</u>	J. J.	ja	
Document No. 1959 250	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 2, solute carrier family 19 (thiamine transporter), member 2, solute carrier family 19, member 3 carrier family 19 (thiamine transproter), member 2, solute carrier family 19, member 3	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen (sodium/hydrogen), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 2, solute exchanger), member 3, solute carrier family 19 (thiamine transporter), member 3 carrier family 19 (thiamine transproter), member 2, solute carrier family 19, member 3	ESTs, Weakly similar to solute carrier family 2 (facilitated glucose transporter), member 2; liver-type glucose transporter [Mus musculus] [M.musculus], solute carrier family 2 (facilitated glucose transporter), member 2	solute carrier family (20 (phosphate transporter), member 1, solute carrier family 20 transporter), member solute carrier family (phosphate transporter), member 2, solute carrier family (phosphate transporter), member 2, solute carrier family 20, member 2
Human Homologous Known Gene Name	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member ex	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 6	solute carrier family 2 (facilitated glucose transporter), member 2	solute carrier family 20 (phosphate transporter), member 8 2, solute carrier family (20, member 2
Model Gode	KK, EEE,	D, Z, AA	U, FF, MM, NN, OO, EEE, LLL, MMM, RRR, SSS,	
eomsemi Nee or ResSeq (D	NM_017299	NM 017299		NM_017223 Z, AA
9 3 9 8 9 8	23825	23826		15872
745(E9	3333	3333		3312

Humani Homologousi Sequence (Gluster IIII)	ESTs, Weakly similar to solute carrier larning 22 (urganic carrier and the large large large). Lath-like [Mus musculus] [M.musculus], ESTs, Weakly similar to OCN2 MOUSE ORGANIC CATION/CARNITINE TRANSPORTER 2 [M.musculus], Homo sapiens OAT4L mRNA for organic anion transpoter 4 like protein, complete cds, Mus musculus, Similar to solute carrier family 22 (organic cation transporter)-like 2, clone MGC:25980 IMAGE:4242162, mRNA, complete cds, RIKEN cDNA 4921504E14 gene, expressed sequence Al987855, solute carrier family 22 (organic anion/cation transporter), member 11, solute carrier family 22 (organic cation transporter), member 5, solute carrier family 22 (organic cation transporter), member 9	RIKEN cDNA 3632410G24 gene, RIKEN cDNA 5730438N18 gene, expressed sequence W51672, solute carrier family 25 (mitochondrial carrier, brain), member solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3, solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11, solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	EST, Weakly similar to VLCS_HUMAN VEKY-LONG-CHAIN ACT L-CONG SYNTHETASE [H.sapiens], ESTs, Weakly similar to solute carrier family 27 (fatty acid transporter), member 2 [Rattus norvegicus] [R.norvegicus], Homo sapiens cDNA FLJ23784 fis, clone HEP21238, VLCS-H1 protein, fatty-acid-Coenzyme A ligase, very long-chain 1, hypothetical protein MGC4365, solute carrier family 27 (fatty acid transporter), member 2, solute carrier family 27 (fatty acid transporter), member 3
inman Hömölöggous	solute carrier family 22 (organic cation transporter), member 5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3, solute carrier family 25 (mitochondrial carrier; phosphate	solute carrier family 27 (fatty acid transporter), member 2
100 (100 (100 (100 (100 (100 (100 (100	BBB, CCC	G, H, WW, FFF, GGG, HHH, General	
Semental Sem	NM_019269	130100	111
9 6 2 6 2 6 2 6 2 6 6 2 6 6 6 6 6 6 6 6	23625	047	
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මුල් 11	(원) (원) (1)	Ace of RafSee D	Model Gode	de Kaowa cene Neme	Human Homologous Sequence Guster IIIIo.
				solute carrier family	
				rucleoside	
			General	transporter), member	corrier family 28 (sodium-coupled nucleoside transporter), member 2
911	211	AA945453	Alternate	2	Solute Callier lating to (comment to be provided to
				solute carrier family	nember 1
			i, J, KKK,	29 (nucleoside	(nucleoside ESTS, Weakly Similar to Source Carrier Concleoside ESTS, Weakly Similar to Source Carrier Concleoside
				transporters), member	[Kattus norvegicus] [n.:iov vegicus], r.s.s.s.
3668	20743	NM 031684	Alternate		ramily 28 (independent indispense)
3		7		solute carrier family	
		.,.		29 (nucleoside	
	. :			transporters), member	
3681	18074	NM 031738	RR, UU	2	
3		_	_	solute carrier family 3	
				(activators of dibasic	
			QQQ, General	and neutral amino	
			Core Tox	acid transport),	2 (member 2
3386	20734	NM 019283		member 2	solute carrier family 3 (activators of discuss are
		Т-	G, H, L, R, II,	solute carrier family 3	
			JUU, KKK,	(activators of dibasic	
			OOO, General	and neutral amino	
			Core Tox	acid transport),	member 2
2286	20735	NM 019283		member 2	solute carrier family 3 (activators of dipasic and for complete cds, Rattus
8		_	1	solute carrier family	Rattus norvegicus mKNA idi Na7/Filositat isperiori 3/Filositat idi. 17
<u>.</u>				34 (sodium	Inorvegicus mixina for inaring aring, compressed sequence Al649385, solute carrier (seed) in my hydrogen exchanger), member 2, expressed sequence Al649385, solute carrier
_				phosphate), inelliber	family 34 (sodium phosphate), member 1
3200	18078	3 NM 013030	0 IRK		

Aitemay Doeket 44921-5033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6033-60180-6	ESTs, Moderately similar to B3AT MOUSE BAND 3 ANION EXCHANGE PROTEIN [M.musculus], expressed sequence Al503023, solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	Mus musculus, Similar to solute carrier family 5 (sodium/glucose corransporter), member 1, clone MGC:29197 IMAGE:5012356, mRNA, complete cds, RIKEN cDNA 2010013B02 gene, RIKEN cDNA 2010104G07 gene, low affinity sodium-dependent glucose cotransporter, solute carrier family 5 (sodium/glucose cotransporter), member 1, solute carrier family 5, member 3, solute carrier family 5, member 4a	(neurotransmitter transporter, dopamine), member 3 solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	ESTs, Weakly similar to cationic amino acid transporter-2A [Rattus norvegicus] [R. norvegicus], solute carrier family 7 (cationic amino acid transporter, y+ system), member 2		
fuman Homologous	solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood	solute carrier family 5 (sodium/glucose cotransporter), member 1, solute carrier family 5, member 1	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	solute carrier family r (cationic amino acid transporter, y+ system), member 2	solute carrier ramily o (sodium/calcium exchanger), member	-
Wedel Code	· · · · · · · · · · · · · · · · · · ·		ss, uu	MM, SS, TTT		Z
Sansemi Ge of Geogle	7		NM_012694	U53927		X68812
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TABLES SERVE SERVE BOLD NO.		4089	3118	4143		4251

Altomay Dockrat Americano Colored Americano Colored Co	Ceneanik Accor- Researin Model Code Known Genetiname Human Homologous Sequence Cluster, Title	EST, Moderately similar to GTK1_RAT Glutathione S-transferase, mitocrioridia (GST 13-13) (Glutathione S-transferase subunit 13) (GST class-kappa) [R.norvegicus], EST, Weakly similar to GTK1_HUMAN GLUTATHIONE S-TRANSFERASE SUBUNIT 13) MITOCHONDRIAL (GST 13-13) (GLUTATHIONE S-TRANSFERASE SUBUNIT 13)	(GST CLASS-KAPPA) (HDCMD47P) [H.sapiens], Kirken CDNA 0010020110 gold, glutathione S-transferase subunit 13 homolog, somatostatin	ESTs, Highly similar to A54674 L-iditol 2-dehydrogenase [H.sapiens], sorbitol	enydrogenase, sorbitor denydrogenese		ESTs, Highly similar to A54674 L-iditol 2-dehydrogenase [H.sapiens], sorbitol	dehydrogenase, sorbitol dehydrogenase 1	ESTS, Weakly Similar to Strict MOOSE of ESTS, MAGE:4945988, mRNA, complete 5 [M.musculus], Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA, complete 5 [M.musculus], Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA, complete 5 [M.musculus], Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA, complete 5 [M.musculus], Musculus, Co	arginine/serine-rich 1 (splicing factor 2, alternate splicing factor), splicing factor,	arginine/serine-rich 5 (SRp40, HRS)	40mo sapiens cDNA FLJ30/30 lis, divide i LDI 0450/15 1 345			
	fuman Hor snown Ger		somatostatin	sorbitol dehydrogenase, sorbitol	dehydrogenase 1	sorbitol	dehydrogenase, sorbitol	dehydrogenase 1	splicing factor, arginine/serine-rich 5,	splicing factor,	arginine/serine-rich 5 (SRp40, HRS)	squalene epoxidase	stem cell growth factor, stem cell	growth factor; lymphocyte secreted	C-type lectin
			M, V, JJ, KK	. '		W, DD, EE, SS, WW, XX,						A, B			99
	<u>රතෙන්නේදී ැ</u> දුරුණු		AI105137 N		AI030175 /			X74593			NM 019257	NM 017136	+		AB009246
အ		anti Gil	17171		1876			1877	7			16681			25149
RETURNE S	Sed		1887		1507			4260			3384	3284			1207

						
Human Homologous Human Homologous Sequence Cluster (118)	d 5 alpha- reductase, polypeptide 1 (3- i alpha-steroid 4- drogenase alpha RIKEN cDNA 4930435F02 gene, steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-			ESTS, Highly similar to 137186 arylsulfatase D [H.Saplens], ESTS, Weakly Similar to MOUSE STERYL-SULFATASE PRECURSOR [M.musculus], ESTS, Weakly similar to STS_RAT STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) [R.norvegicus], arylsulfatase E (chondrodysplasia punctata 1), arylsulfatase F, steroid sulfatase, steroid sulfatase, microsomal), arylsulfatase (L. isozyme S)	EST, Weakly similar to NLTP_HUMAN NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR [H.sapiens], sterol carrier protein 2, sterol carrier protein 2, liver	sterol regulatory element binding factor 1, sterol regulatory element binding factor 2, sterol regulatory element binding transcription factor 2
Human Homologous	steroid 5 alpha- reductase 1, steroid-5- alpha-reductase, alpha polypeptide 1 (3- oxo-5 alpha-steroid delta 4- dehydrogenase alpha	steroid 5 alpha- reductase 1, steroid-5- alpha-reductase, alpha polypeptide 1 (3-	oxo-5 alpira-steroto delta 4- dehydrogenase alpha 1)	steroid sulfatase, steroid sulfatase (microsomal), arylsulfatase C, isozyme S	sterol carrier protein 2, sterol carrier protein 2, liver	sterol regulatory element binding transcription factor 2
Model Gode	F, T, GG,		F, T, GG, GGG, General Alternate	H H	r, LL, DDD	FFF, General Alternate
Central According Robert Rober		concor	J05035	NM 012661	NM 138508 L, LL, DDD	AI170663
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Tables Seq Que Id Id		7830	2930	3107	3973	2062

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Model Gode Known Gene Name Homologous Sequence Gluster Title	cholesterol 25-hydroxylase, chromosome 5 open reading frame 4, sterol-C4-methyl oxidase-like						succipate dehydrogenase complex, subunit A. flavoprotein (Fp)					succinate dehydrogenase complex, subunit A, flavoprotein (rp)			succinate-CoA ligase, ADP-forming, beta subunit					
Humani Homologows Knjown Gene Name	sterol-C4-methyl oxidase-like		stromal cell derived factor 1, stromal cell-	derived factor 1	succinate	dehydrogenase	complex, subunit A,	ilavopi otelii (i p.)	succinate	dehydrogenase	complex, subunit A,	flavoprotein (Fp)	succinate-CoA ligase,	ADP-forming, beta	subunit	succinate-CoA ligase,	GDP-forming, alpha	subunit	succinate-CoA ligase,	subunit
Modal Gode	Sterol-C4-mi NM 080886 II, J, II, XX, FFF oxidase-like	G, J, S, WW, 000, PPP,	QQQ, General Core Tox	Markers			W, General	Alleriare			S, General	Alternate			BBB, CCC			BBB, CCC	II BAB	CCC, RRR
Kensank Ase or Refseq ID	NM 080886			NM_022177			A 3 3 3 5 4 4	AA920004				NM_130428 Alternate			AA923982			NM 053752		NM_053752 CCC, RRR
33 @L@@ @Ko.	21842			24321			77077	1/514				17512			22847			18174		18175
TABLES Reg G DO D	3909	1		3444			2	(31				3921			727			3819		3819

WO 35, 30 112		-634-		
Atterney Document No. 1925820.1 NYomologous Sequence Guster IIII le	Aryl sulfotransferase cytosolic, 1A, phenol-preferring, member 3, RIKEN cDNA 1110030E23 gene, sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	Aryl sulfotransferase cytosolic, 1A, phenol-preferring, member 3, RIKEN cDNA 1110030E23 gene, sulfotransferase family 1A, phenol-preferring, member 1, sulfotransferase sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	Homo sapiens cDNA FLJ32344 fis, clone PROST2006450, moderately similar to N-HYDROXYARYLAMINE SULFOTRANSFERASE (EC 2.8.2), sulfotransferase family 1A, phenol-preferring, member 2, sulfotransferase family, cytosolic, 1C, member 2	Homo sapiens cDNA FLJ32344 fis, clone PROST2006450, moderately similar to N-HYDROXYARYLAMINE SULFOTRANSFERASE (EC 2.8.2), sulfotransferase family 1A, phenol-preferring, member 2, sulfotransferase family, cytosolic, 1C, member 2
umaniHomologous hown(GeneiName	sulfotransferase family 1A, phenol- preferring, member 1, sulfotransferase family, cytosolic, 1A, 1 phenol-preferring, s member 1	erase phenol- member 1, erase osolic, 1A,	ferase phenol- , member 2, ferase tosolic, 1A, eferring,	sulfotransferase family 1A, phenol- preferring, member 2, sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
	8 25 Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q		A, G, II, GGG, PPP, QQQ, General Atternate	A, B, G, S, W, GGG, PPP, QQQ, General Core Tox Markers, General Alternate
SONE NATIONAL SONE SONE SONE SONE SONE SONE SONE SONE		102.00	NM 031732	
		4748	4749	24811
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) 	CONSENT NGC OT PASSON ID	Model Gode	Human Homologous Known GeneiName	Human Homologous Human Homologous Model Gode Mnown Gene Name Human Homologous Sequence Gluster Miles
-11	3 3 3 3			superoxide dismutase	
			= = = = = = = = = = = = = = = = = = = =		EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus], superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
	20876	DCD/10 MN	200 2	3Se	
				1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral	EST, Weakly similar to SODC MOUSE SUPEROXIDE DISMUTASE [M.musculus].
	77806	NM 017050	Σ	sclerosis 1 (adult))	superoxide dismutase 1, soluble (alliyon opino accounts)
Т					
	2703 21414	AI235842	W. NN	2, mitochondrial	
		1114 04 70E4	u u u w W	Superoxide districtions 2. mitochondrial	
3262	789	CO LO MINI	7	superoxide dismutase	reli llegestore
_	701	NM 012880		3, extracellular	superoxide dismutase 3, extracellulari
3103	404	NINI O ININI			EST, Weakly similar to Assess syndromin of the second similar to
					Similar to Ascent 1 symptom in the second of the second in
					IRXZ_HOWAN INCOCOCIO TO TO TO TO THE MANAGERIA I [M.musculus], Mus musculus, IESTs Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus], Mus musculus,
					clone IMAGE:3992752, mRNA, partial cds, PRO0149 protein, RINEIN CLIVA
					1810026J23 gene, RIKEN cDNA 4933428P19 gene, RIKEN cDNA 393041 St. 30 gene, RIKEN cDNA 393041 St. 30 gene, RIKEN cDNA 4933428P19 gene, RIKEN cDNA 393041 St. 30 gene, RIKEN CDNA 39304 ST. 30 gene, RIKEN 39304 ST. 30
					guanine nucleotide binding protein (G protein), beta polypeptide 1-mc, marm., guanine nucleotide binding protein (G protein), beta protein BC011833, synapsin I
3354	24785	NM 019133	s ss	synapsin I	hypothetical protein BC00/540, nypothetical protein
1 9			T II III SSS syndecan 1	SS syndecan 1	syndecan 1
3198	1588	NM 0130Z	0 11, 0, 11, 0	(5) 50	

Alterney Deckel 4/924-5035-501000 Deckel 4/9254-5035-501000 Decument No. 1995523.1 Decument No. 199553.2 Decument No. 199	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	n syndecan 4, syndecan 4 (amphiglycan, ryudocan) Homo sapiens cDNA FLJ31164 fis, clone KIDNE1000104, weakly similar to SYNTAXIN T, expressed sequence Al317144, expressed sequence AU041521, syntaxin 12,	syntaxin 7	T-cell death associated			[H.sapiens], ESTs, Weakly similar to JOUSED 1-complex process.] (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta).	protein 1 EST Moderately similar to S10486 t-complex-type molecular chaperone TCP1	[H.sapiens], ESTs, Weakly similar to JQ0866 1-complex process 1 tomplex chaperonin containing TCP1, subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), t-complex chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 7 (eta), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 8 (eta), chaperonin s	protein 1
The state of the s	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	syntaxin 7	T-cell death	associated gene, pleckstrin homology-like domain family A,	member 1	-t -t wolow	complex protein 1	t-complex 1, t-	complex protein 1
M	J, L, U, W, EE, NNN, DOO, General Alternate	Ċ	Z	¥		a, R		L, FF		<u> </u>
	NM 012649	C, L, W, DI NM_012649 WW, NNN		NM 031656	·	NM_017180 Q, R		AA859980		H34047
න නම්	9423	9424		9428		19031		18578		26368
TABLE 3	3103	3103	3442	3665		3301		408		2917

F-complex testis expressed 1, 1- complex associated- expressed 1, 1- complex associated- testis-expressed 1-like testis expressed 1-like testis-expressed 1-like testis-expressed 1-like testis expressed 1, 1- testis-expressed 1-like testis expressed 1, 1- testis-expressed 1-like testis expressed 1, 1- testis-expressed 1-like testis expressed 1-like 1 testis-expressed 1-like 1 testis enhanced gene transcript (BAX inhibitor 1) thioredoxin reductase thioredoxin reductase 1, thioredoxin reductase 2 thioredoxin reductase 2 thioredoxin reductase 2 thioredoxin-like 3 thioredoxin-like 2 thioredoxin-like 3 thioredoxin-like 3 thioredoxin-like 3 thioredoxin-like 3 thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase, mitochondrial thiosulfate sulfurtransferase thiosulfate sulfurtransferase, mitochondrial	職職 311 1933	eemsemi		Keinsenk Kas or Reksen ID (Neds) Gode (Ka	Human Homologous Known Gene Name	Man Hörrölögöus Human Homologous Sequence Cluster III le.
script, testis script, testis anced gene script, testis anced gene script (BAX socipt (BAX sociption society soc	t-cx ext cor tes	t-cx ext cor cor	t-cx ext cor tes	S Z X Y	t-complex testis expressed 1, t- complex-associated- Il testis-expressed 1-like t	omo sapiens, Similar to RIKEN cDNA 0610012D17 gene, clone MGC:33212 IAGE:4830500, mRNA, complete cds, RIKEN cDNA 2310075M16 gene, t-comple: stis expressed 1, t-complex-associated-testis-expressed 1-like, t-complex-associa
9		NM 031318 P, ZZ, AAA		_		istis-expressed 1-like i
98 88	te		te	يز ور	testis enhanced gene transcript, testis	
38 88 8e	<u>. 0</u>	; 	<u> </u>	: <u>a</u>		BIKEN CONA 4930500J03 gene, RIKEN CDNA
ISe t t t t t t t t t t t t t t t t t t t	ppp,	HHH, PPP, tra	ppp,	크랙	transcript (BAX inhibitor 1)	031406P05 gene, testis enhanced gene transcript (BAX inhibitor 1)
88 88 1				三	thioredoxin reductase	2 - Section of the se
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	G, H, Q, 11	NM 031614 G, H, Q, II	0, 11	-	-T	nioredoxin reductase 1, unoredoxin redecase
886	O, HH, ZZ, thi	-	-	[₹]	oredoxin reductase	hioredoxin reductase 1, thioredoxin reductase 2
υ v		NM 031614 AAA, HHH		-1	_	
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	<u>=</u>	<u>=</u>	<u>=</u>	<u>트</u>	nodanese),	
	<u>=</u>	=	<u>=</u>	<u>=</u>	iosulfate	thiosulfactuate sulfurtransferase, thiosulfate sulfurtransferase (rhodanese),
	R, DDD, PPP, Is	R, DDD, PPP, IS	s אסס, ססר (s ר	S	sulfurtransferase, mitochondrial	mercaptopyi uvate suiturationeres, mitochondrial thiosulfate sulfurtransferase, mitochondrial

TABLE S				Altomay Docket Christian and Colonial Christian and
@ @L@@ @R@@ @R@@	Mis M. 6 or - 1800 (D	censenk Vec of Refse ID Model Gode	Human Homologous Known Gene Name	man Homologous Jynn Gene Name Human Homologous Sequence Cluster Title
4		<u></u>	thiosulfate sulfurtransferase	
		Q, R, SS, DDD, PPP,		(rhodanese),
	X56228	eral		mercapiopyi uyaco saila saila mitochondrial thiosulfate sulfurtransferase, mitochondrial
	A30250		Thy-1 cell surface	
	0 0004330	> ×	antigen, thymus cell antigen 1, theta	Thy-1 cell surface antigen, thymus cell antigen 1, theta
0	M324000		Thy-1 cell surface	
47447	NM 012673	¥	antigen, thymus cell antigen 1, theta	Thy-1 cell surface antigen, thymus cell antigen 1, theta
1		T, EE, KKK,	thymopoietin	cDNA 5630400D24 gene, thymopoietin
16871	NIM UTZOO MININ	OO NN d O	thymosin, beta 10	
01.807	$\neg \Gamma$		thyroid stimulating	
			hormone receptor, thyroid stimulating	instinct hormone receptor, thyroid stimulating hormone, receptor
24857	NM_012888	RR, SS	hormone, receptor	thyrold stiffludaring from the DLG2_RAT Channel associated protein of synapse-110
1				(Chapsyn-110) (Synaptic density protein PSD-93) (Discs, large normory 27) (Chapsyn-110) (Synaptic density protein PSD-93) (Discs, large homolog [R.norvegicus], ESTs, Highly similar to DLG2_RAT Channel associated protein of
			tight junction protein 2. tight junction	synapse-110 (Chapsyn-110) (Synapus Carley) Promise PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTs, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PRESYNAPTIC PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.norvegicus], ESTS, Weakly similar to SP02 MOUSE PROTEIN 2) [R.n
			protein 2 (zona	SAP102 [M.musculus], discs, lalye normong 2 (2000). SAP102 [M.musculus], tight junction protein 2 chapsyn-110 (Drosophila), tight junction protein 2
1279	U75916	¥	tice to inhibitor of	Homo sapiens mRNA; cDNA DKFZp/61A061/ (noin concess)
243	NM 021989	9	metalloproteinase 2	inhibitor of metalloproteinase 2
ı		٦.		

				·	$\overline{}$		
Attorney Document No. 199522.1 Kuman Homologous Human Homologous Sequence Gluster Title	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)		deficiency) topoisomerase (DNA) ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Weakly II alpha, II alpha [Rattus norvegicus] [R.norvegicus], similar to topoisomerase (DNA) II alpha [Rattus norvegicus] [R.norvegicus], similar to topoisomerase (DNA) II alpha [Rattus norvegicus]	topoisomerase (DNA) (170kD) (1	topoisomerase (DNA) II alpha, topoisomerase (DNA) II beta	Homo sapiens, Similar to hypothetical protein FLJ21616, clone MGC:14941 IMAGE:3947903, mRNA, complete cds, Mus musculus, clone IMAGE:3490304, mRNA, partial cds, hypothetical protein FLJ21616, transcription factor 1, transcription factor 1, hensity 15-B1, hepatic nuclear factor (HNF1), albumin proximal factor	
Human Homologous Known Gene Name	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tocopherol (alpha) transfer protein, tocopherol (alpha) transfer protein (ataxia (Friedreich- like) with vitamin E	deficiency) topoisomerase (DNA) II alpha,	II alpha (170kD) topoisomerase (DNA) III alpha,	II alpha (170kD)	transcription factor 1, transcription factor 1, hepatic; LF-B1, hepatic nuclear factor II (HNF1), albumin	proximal factor
Model Gode Kno	α	F, T, LL, RR, EEE, MMM, General	Alternate	ס	WW		m
Constant Reformed Reformed	A CONT	A10274	NM_013048	AA899854	NM_022183		NM 012669
98		17234	2667	23778	23782		24427
TABLES See GU		1814	3203	669	3446		3110

Altomay Docket (45227-5033-91WG) Document No. 1935328.1	Human Homologousi Sequence Cluster Title Human Homologousi Sequence Cluster Title ESTs, Weakly similar to TRFL MOUSE LACTOTRANSFERRIN PRECURSOR	[M.musculus], RIKEN CDINA 13000 1302 93.0.7 Transferrin ESTs, Weakly similar to TRFL MOUSE LACTOTRANSFERRIN PRECURSOR [ESTs, Weakly similar to TRFL MOUSE LACTOTRANSFERRIN PRECURSOR [M.musculus], RIKEN cDNA 1300017J02 gene, Rattus norvegicus Ncione10 mRNA, [M.musculus], RIKEN cDNA 1300017J02 gene, Rattus norvegicus Ncione10	transferrin ESTs, Weakly similar to TRFL MOUSE LACTOTRANSFERRIN PRECURSOR [M.musculus], RIKEN cDNA 1300017J02 gene, Rattus norvegicus Nclone10 mRNA, Transferrin, transferrin		transformation related protein 73, tumor protein p53 (Li-Fraumeni syndrome)	expressed sequence AA408768, transthyretin, transthyretin (prealbumin, amyloidosis type I)	expressed sequence AA408768, transthyretin, transthyretin (prealbumin, amyloidosis type I)	EST, Highly similar to TPIS MOOSE TRIOSEPHOSPHATE ISOMERASE [H.sapiens], ESTs, Highly similar to TPIS_HUMAN TRIOSEPHOSPHATE ISOMERASE [H.sapiens], Rattus norvegicus resection-induced TPI (rs11) mRNA, complete cds, triosephosphate isomerase 1	tropomyosin 1 (alpha), Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence tropomyosin 1, alpha Al854628, expressed sequence C76867, tropomyosin 1, alpha Al854628, expressed sequence C76867, tropomyosin 1, alpha
	timen Homologous Mown, Genel Name	transferrin	transferrin	transferrin transformation related protein 53, tumor	protein p53 (Li- Fraumeni syndrome)	transthyretin (prealbumin, amyloidosis type I)	transthyretin transthyretin (prealbumin, amyloidosis type I)	triosephosphate isomerase, triosephosphate isomerase 1	tropomyosin 1 (alph tropomyosin 1, alph
	1000 Gode	S, V, NNN	NNN.	s, i	CC, NN, OO	V, EE, HH, TT	上 王	THH.	3
	conseni Nee or Refer ID	NM_017055	055	U31866	NM_030989	AA945169	0.0045169		
	MEGG /	14533	14534	14535	17377	4185	001	18277	457
		3263	3263	4117	3576	903		903 1870	3031

TABLE 8	88				Comment No. 1935323.1
Sea	9919	<u>ें</u> एकास्त्राप्त शब्द वर	10.00	Humani Romologous	Ruman (Romologous)
35.2°°50		RESEQ 10	Model Geograph	tropomyosin 1 (alpha), It	tropomyosin 1 (alpha), Homo sapiens cDNA FLJ30635 fis, clone CTONG2002520, expressed sequence tropomyosin 1, alpha Al854628, expressed sequence C76867, tropomyosin 1, alpha
3332	20850	1 .		troponin I, cardiac	
903 903 903	402	AA945143	C, E, DD, SS, WW, KKK, NNN	tryptophan 2,3- dioxygenase	tryptophan 2,3-dioxygenase
3414	20776	NM 012680	XX, YY	tuberous sclerosis 2	DKFZpood 133 protein, 201, most of the Manimal 1002250, KIAA1272 [H.sapiens], Homo sapiens cDNA FLJ12339 fis, clone MAMMA1002250, KIAA1272 protein, tuberous sclerosis 2 protein, tuberous sclerosis 2
5			· · · · · · · · · · · · · · · · · · ·	tumor necrosis factor	ESTS, Weakly Sithilian to STS 2000 and the superfamily, member 14 lymphotoxin B receptor, tumor necrosis factor receptor superfamily, member 19, (herpesvirus entry mediator), tumor necrosis factor receptor superfamily, member 4, tumor necrosis factor receptor superfamily, member 4, tumor necrosis factor receptor
3204	20535	NM_013049) l, J	member 4	superfamily, member 7
	1				[H.sapiens], EST, Weakly similar to TCTP MOUSE TRANSLATIONALLY [H.sapiens], EST, Weakly similar to TCTP MOUSE TRANSLATIONALLY CONTROLLED TUMOR PROTEIN [M.musculus], ESTs, Highly similar to factor [H.sapiens], ESTs, Moderately similar to
				tumor protein, translationally-	dependent nistatrime-releasing foods (2007) (2008) (21 kDa TCTP MOUSE Translationally controlled tumor protein (TCTP) (p23) (21 kDa polypeptide) (p21) (Lens epithelial protein) [R.norvegicus], Homo sapiens mRNA full polypeptide) (p21) (Lens epithelial protein) [R.norvegicus], Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 926491, apoptosis inhibitor, tumor protein,
3845	5 17728	NM_053867	7 FF	controlled 1	translationally-controlled 1

					7
Attornay Doctor (4454) every produce of the control	ESTs, Highly similar to 138947 14-3-3 protein epsilon isoform [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	ESTs, Highly similar to 143F MOUSE 14-3-3 PROTEIN ETA [M.musculus], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma		polypeptide polypeptide tyrosine 3- monooxygenase/trypt eSTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX monooxygenase activation	la [H.saplens], tyrosine office of the protein, zeta polypeptide
The state of the s	tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, epsilon polypeptide	tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, eta	polypeptide tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase activation protein, eta	polypeptide tyrosine 3- monooxygenase/trypt ophan 5- monooxygenase	activation protein, zet polypeptide
Model Code	£		W, SS, HHH W, JJ, GGG,	HH	A
Constint	NM 031603	1	NM_013052 W, SS, HHH	NM_013052	AA926328
(%) (%) (%) (%)	19340		16683	16684	3817
TABLES SESSES OF THE SESSES OF	3656 3656		3205	3205	818

FABLES	ଙ				Doeument No. 1935328.1
() () () ()		GLEG AE OT.	MUNA BI Gorde	Human Homologous Nown Gene Name	nan Hömölögöus nan Hömölögöus win Gene Name RumaniHomologous Sequence Cluster Mile
<u></u>	% ଜୁନା			sine 3- ooxygenase/trypt	
				ophan 5- monooxygenase activation protein, zeta	ophan 5- ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX monooxygenase CESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX monooxygenase activation protein, zeta [H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation
3195	3404	NM_013011	A, B, P, W	polypeptide	protein, zeta polypeptide
				tyrosine 3- monooxygenase/trypt	
				ophan 5- monooxygenase activation orotein, zeta	ophan 5- ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX monooxygenase ESTs, Highly similar to A Chain A, 14-3-3 ZetaPHOSPHOPEPTIDE COMPLEX monooxygenase activation crotein, zeta[H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta[H.sapiens], tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
3195	25279	NM_013011	0, P, R, W	polypeptide	protein, zeta polypeptide FSTs Highly similar to S60718 tat protein [H.sapiens], Homo sapiens, Similar to
				tyrosine	tyrosine aminotransferase, clone MGC:22474 IMAGE:4710626, mrNA, compress cyclesine aminotransferase, clone MGC:37790 Mus musculus, Similar to Tyrosine aminotransferase
3109	24825		3 C, D, I, J, NNN	NM_012668 C, D, I, J, NNN aminotransferase	IMAGE:509/591, Illing A. Company of the interacting protein, A1U protein, FSTs. Highly similar to ataxin-1 ubiquitin-like interacting protein, DIVEN COMP
			- - - -	inbiauilin 1	chromosome 1 open reading frame 6 [Homo sapiens] [H.saplens], Kincin Control chromosome 1 open reading frame 6 [Homo sapiens] (1110046H03 gene, ataxin-1 ubiquitin-like interacting protein, ubiquilin 1, ubiquilin 2
3818	15376	NM 033747		hinininol-cytochrome	
				c reductase hinge	uhiminol-cytochrome c reductase hinge protein
1266	22056	A1008066	<u>"</u>	protein	

PCT/US03/03194

Adtorney Doctes (AVS21-6038-60100) The protein CEP52 - rat (fragment) The protein CEP52 - rat (fragment) The protein (Mus musculus) (M.musculus), The protein (Mus musculus) (M.musculus), Sculus) (M.musculus), ESTs, Weakly CEP52 (H.sapiens), Neural precursor cell developmentally down-regulated gene 8, product 1 A6, UDP glycosyltransferase 1 family,	l, J, K, L, M, N, family, polypeptide U, X, Y, GG, A6, UDP- HH, LLL, SSS, glucuronosyltransfera DDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransfera 1 polypeptide A8
EST, Highly similar to S66575 ubiquitin / ribosoi EST, Highly similar to S66575 ubiquitin / ribosoi usion product 1; ubiquitin/60S ribosomal fusion protein [Mus musiquitin/60S ribosomal fusion protein fusion similar to UQHUR ubiquitin / ribosomal protein similar to UQHUR ubiquitin / ribosomal protein fusion ubiquitin A-52 residue ribosomal protein fusion ubiquitin A-52 residue ribosomal protein fusion ubiquitie A-8	UDP glycosyltransferase 1 family, polypeptide A8
ubiquitin A-52 residue eribosomal protein fusion product 1 tamily, polypeptide A cluster, UDP glycosyltransferase 1 family, polypeptide A cluster, UDP glycosyltransferase 1 family, polypeptide A cluster, UDP glycosyltransferase 1 family, member 1 tamily, member 1 tamily, polypeptide A cluster, UDP glycosyltransferase 1 family, member 1 cluster, UDP glycosyltransferase 1 family, polypeptide A cluster, UDP clusterse 1	J. K, L, M, N, family, polypeptide U, X, Y, GG, A6, UDP- HH, LLL, SSS, glucuronosyltransfera se 1 family, member 1
J. K. L. N. S. U. FF, GG, HH, TT, LLL, UUU	
83. (CEMBERNIX.) [CEMBERNIX.) [D) NO. (RESSEQ [DD.) 19727 NM_031687 [15124 NM_057105]	NM_057105
3 GLGG ID No. 1 19727	15126
3879 118	3879

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Attennel Docket (4.924-5033-041W) Document No. 1025223.1	v-erb-b2 erythroblastic ESTs, Weakly similar to A53183 epidermal growth factor receptor precursor - mouse leukemia viral [M.musculus], Homo sapiens clone R2 ErbB-3 R2 (c-erbB-3) mRNA, partial cds, Mus (M.musculus, clone MGC:38648 IMAGE:5356166, mRNA, complete cds, v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	d Signary Cristons	vesicle-associated membrane protein 1, vesicle-associated membrane protein 2, vesicle-associated membrane protein 4			
Human Homologous	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3	vesicle-associated membrane protein 1, vesicle-associated membrane protein 1 (synaptobrevin 1), vesicle-associated membrane protein 2,	membrane protein 2 (synaptobrevin 2)	vesicie-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)	vesicle-associated membrane protein 2, vesicle-associated membrane protein 2	(synaptobrevin 2)
	3		z	SS CC		Z, AA
Semeseral Residence of the second sec		7	AI229196	NIM 012663		NM_012663
	ONO.	317	16203	16108	08101	16199
	V-07-1	5 115	2452	9	3108	3108

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Alionaly Document No. 195522.1	Human Homologous Sequence Cluster Wilo	ESTs, Weakly similar to vesicle-associated membrane protein 3 [Rattus norvegicus] [R. norvegicus], vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin), vesicle-associated membrane protein 4					complete cds, RIKEN cDNA 4921513O20 gene, v-raf murine sarcoma viral oncogene complete cds, RIKEN cDNA 4921513O20 gene, v-raf-1 murine leukemia viral oncogene homolog B1, v-raf-1 leukemia viral oncogene	homolog 1 FSTs. Highly similar to B-raf oncogene [M.musculus], Mouse B-raf oncogene mRNA,		homolog 1	Mingless-related Mingless-related MMTV integration site 3, wingless-related MMTV integration site 7B, wingless-type wingless-related MMTV integration site 4, wingless-type MMTV integration site family, member 3A, wingless-type MMTV integration site wingless-type MMTV integration site wingless-type MMTV integration site wingless-type MMTV.	integration site ramily, meriber 15
	Human Homologous Model Godo Known Genel Name	vesicle-associated membrane protein 3, vesicle-associated membrane protein 3 (cellubrevin)	vitronectin, vitronectin (serum spreading factor, somatomedin	protein)	von Hippel-Lindau syndrome, von Hippel-	Lindau syndrome homolog	v-raf-1 leukemia viral oncogene 1, v-raf-1 murine leukemia viral	oncogene homolog 1	oncogene 1, v-raf-1 murine leukemia viral	oncogene homolog 1	wingless-related MMTV integration site 4, wingless-type MMTV integration site	family, member 4
	Andel Gode K	× × × × × × × × × × × × × × × × × × ×		M, N, SS		W		۷, x, ٧		_		NM_053402 O, P, PP, QQ
		7007		NM_019156		U14746		NM_012639 V, X, Y		NM_012639		
ଡ		<u> </u>	73230	24362		1424		20798		20799	·. :	17252
FABLE 8			3874	3361		4101		3100		3100		3760

1970 1970												
3279 Al103224 SSS, UUU 20919 NM 017172 L 20919 NM 017172 L 20919 NM 017172 L 3279 Al103224 SSS, UUU 3279 Al103224 SSS, UUU 3279 Al103224 SSS, UUU U, LL, RRR, GGG, HHH, LLL, PPP, GGG, HHH, LLL, PPP, CORE TOX CORE TOX 20299 NM 022220 Markers CORE TOX 20299 NM 022220 Markers V, X, Y, HH, JJ, SS, ZZ,	Altonney Doeltel 4482/1-9026-91100-9 Doeument No. 1835323.1	Human Homologous Sequence Giveter Wille	FSTs Weakly similar to S10471 cMG1 protein - rat [R.norvegicus], zinc finger protein			2-4-dienoyl-Coenzyme A reductase 2, peroxisorina, parallel 2, putative peroxisomal 2,4-dienoyl-CoA reductase putative peroxisomal 2,4-dienoyl-CoA reductase 20, alaba-hydroxysteroid dehydrogenase, ESTs, Weakly similar to DHBX MOUSE	ESTRADIOL 17 BETA-DEHYDROGENASE, A-SPECIFIC [M.musculus], aldo-keto ESTRADIOL 17 BETA-DEHYDROGENASE, A-SPECIFIC [M.musculus], aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase), aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, typedhydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, typedhydrogenase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4), expressed	sequence AW14604/	24 debydrocholesterol reductase, Mus musculus, clone MGC:29968 IMAGE:5123684,	mRNA, complete cds mRNA, complete cds mRNA, complete cds mRNA, complete cds mRNA, complete cds	13(2), 3-bispinspinate indicates 1-PHOSPHATASE [M.musculus], bisphosphate 3-INOSITOL POLYPHOSPHATE 1-PHOSPHATASE [M.musculus], bisphosphate 3-Inositol polyphosphate-1-phosphatase nucleotidase 1, hypothetical protein FLJ20421, inositol polyphosphate-1-phosphatase	
3279 Al103224 SSS, UUU 20919 NM 017172 L 20919 NM 017172 L 20919 NM 017172 L 3279 Al103224 SSS, UUU 3279 Al103224 SSS, UUU Coneral 4462 AA866264 Alternate A, B, Y, FFF, GGG, HHH, LLL, PPP, Core Tox 20299 NM 022220 Markers Core Tox 20299 NM 022220 Markers V, X, Y, HH, JJ, SS, ZZ, ZJ, SS, ZJ, ZJ, SS, ZJ, ZJ, ZJ, ZJ, ZJ, ZJ, ZJ, ZJ, ZJ, ZJ		Human Homologous Known Gene Namo	kanthene dehydrogenase, kanthine dehydrogenase	zinc finger protein 30 C3H type-like 1	C3H type-like 1							
3279 AI103224 20920 AI136891 20919 NM_017172 20919 NM_017172 20919 NM_017172 20919 NM_017172 20919 NM_02222 20299 NM_02222		ලානු ලාන	, FF, LLL, RR, SSS, IUU, General			J, LL, RRR, SSS, UUU	Genera	Alternate	A, B, Y, FFF, GGG, HHH, LLL, PPP, QQQ, Genera	Core Tox Markers	V, X, Y, HH, JJ, SS, ZZ, AAA, HHH	
3279 20920 20919 3279 3279 20299 20299		Semiseruk Nee er Refesea ID IM	E R U U NM_017154_A		NM 017172 L		·				A 1000347	AUCOUCT
3300 3300 3450 3450 3450	3	@ @ 						4462			00000	73220
	FABLE	889	74	т-		1830		414		3450		2833

Filter annion of the control of the	PHOSPHOGLYCERATE DEHYDROGENASE [M.musculus], what independence testis cDNA, RIKEN full-length enriched library, clone:4930404C15:3-phosphoglycerate dehydrogenase, full insert sequence, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
nologous in the furnant Homologous 3-hydroxy-3-methylglu Coenzyme A synthase 3-hydroxy-3-methylglu Coenzyme A synthase Shydroxybutyrate dely BDH_RAT D-beta-hychydroxybutyrate dely BDH_RAT D-beta-hychydroxyisobutyrate dely Coenzyme A synthase Coenzyme Coenzyme A synthase Coenzyme A synt	PHOSPHOGLYCERATE DEHYDRC testis cDNA, RIKEN full-length enrict dehydrogenase, full insert sequence phosphoglycerate dehydrogenase
Madelicode V, FF, PP, QQ Y, FF, RRR, SSS U, FF G, General Alternate S S	αα, xx, ΥΥ
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1950 1950 1950 1950	22542
3014 15 3014 15 3014 15 3014 15 3014 15 592 2	2557 22

Antiolines) Document No. 1995626.1 Secure Human Homologous Sequence Cluster IIII D	4-aminobutyrate aminotransferase, RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, ornithine aminotransferase	2900006B13 gene, ornithine aminotransferase 2900006B4, mRNA, partial	cds, Homo sapiens, similar to unnamed protein product, clone MGC:34672 cds, Homo sapiens, similar to unnamed protein, hypothetical protein BC009881 IMAGE:5199154, mRNA, complete cds, PAN2 protein, hypothetical protein BC009881 5-oxoprolinase (ATP-hydrolysing), RIKEN cDNA 1700010G02 gene	7-dehydrocholesterol reductase, expressed sequence AI505894	7-dehydrocholesterol reductase, expressed sequence AI505894	domain 17 (tumor necrosis factor, alpha, converting enzyme) A kinase (PRKA) anchor protein 1, Mus musculus, clone IMAGE:4512174, mRNA,	partial cds, tudor and KH domain-containing protein, tudor domain containing 1, tudor partial cds, tudor and KH domain-containing protein, tudor repeat associator with PCTAIRE 2 repeat associator with PCTAIRE 2 A kinase (PRKA) anchor protein 8, ESTs, Weakly similar to A53414 A-kinase anchor	protein 95, AKAP95 - rat [R.norvegicus], Mus musculus 10 days embryo whole body protein 95, AKAP95 - rat [R.norvegicus], Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610301A12:neighbor of A-kinase anchoring protein 95, full insert sequence, expressed sequence Al467606, neighbor of anchoring protein 95, zinc finger protein 326	A-Killabe aliciola process
S. Nodel Gode. Known Gene Name	A, B, III, JJJ, OOO, General Core Tox Markers	B, J, OO, RRR	SS, TT	KKK, NNN, General Alternate	KKK, NNN, General Alternate	О,Р	DD, EE		Q, WW
(1997年) 1997年 19			AI104245 S	NM 053904 WW Kind 022380 G	<u> </u>		NM_138871_[U01914
138	737		3259	15934	12082	13486	5719		347
	2877	\top	T	3848	3465	3419	3985		4086

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7 9		الافهوا		Kaown ල්බෙම් Name	Human Homologous Seguence (1985) 1
					Leucine-rich acidic nuclear protein [R.norvegicus], acidic (leucine-rich) nuclear
					phosphoprotein 32 family, member A, acidic nuclear prosprioprocess 22, concerning
1279	4098	A1008642	}		ataxia 3, hypotnetical gene moo rooc
1	17304	4	99		מכום הווספהושנים כי ימי המכי כי
	47646		T, LL, YY, RRR, SSS		aconitase 1, aconitase 1, soluble
1678	22684		M		actin related protein 2/3 complex, subdim 2 (37 %)
2			XX, YY, ZZ,		
-	204	NIM 021753	AAA, LLL, RRR SSS		activated leucocyte cell adhesion molecule, activated leukocyte cell adhesion molecule
3682	47/07	Т	_		Acyl-Coa dehydrogenase, Very long citality Edition and acyleration in the skilv
<u></u>					DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC [M.musculus], Lot., Water,
					Similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, micconscients
					precursor (VLCAD) [R.norvegicus], EST, Weakly Similar to 334 to 334 to 35.
					dehydrogenase [H.sapiens], RIKEN CUIVA 20000 I.T. 13 gc.13; 23.
77.7	3069	01178764	RR. SS		dehydrogenase, very long chain
2 2	\neg	X05180	M XX YY		acyl-Coenzyme A oxidase 2, prancing chair
4280	3	V30103	100 LAIN		
- 203	4636	A A 899491	MMM (C. L.		adaptor-related protein complex 1, mu 1 subunit
00	200		0		adenylyl cyclase-associated CAI protein cyclase-associated protein Cyclase-associated protein ADP-
277	23981	A4630040			ADP-ribosylation factor 1, ADP-ribosylation lactor 1, ADP-ribosylation factor 1, ADP-ribosylation fact
	· 				ribosylation factor-like 5 [Rattus norvegicus] [K.norvegicus], Loris, World ADP-ADP-RIBOSYLATION FACTOR 1 [M.musculus], Homo sapiens, similar to ADP-ADP-ADP-ADP-ADP-ADP-ADP-ADP-ADP-ADP-
					ribosylation factor-like 5, clone MGC:22841 IMAGE:3931093, IIINAC, Compression
3861	15324	4 NM 053979	я 8		expressed sequence T25534
		T			RIBOSYLATION FACTOR 1 [M.musculus], expressed sequence T25534
2950	4144	L12380	PP, QQ, 11		

Alterney Decket (Algertelas)	Imman Homologous (Anown Gene Name) Human Homologous Sequence (Cluster fift) (Anown Gene Name) Human Homologous Sequence (Cluster fift) (Anown Gene Name) ADP-ribosylation factor 4 (ADP-ribosylation factor 5, ESTs, Moderately similar to ADP-RIBOSYLATION FACTOR	5 [M.musculus], ESTs, Weakly similar to A54022 ADP-ribosylation lactors] R.norvegicus] ADP-ribosylation factor 6, ESTs, Moderately similar to S39543 GTP-binding protein -	mouse [M.musculus], ESTs, Weakly similar to ARF6_HUMAN ADP-ribosylation ractor of mouse [M.musculus], GTP-binding protein Sara, RIKEN cDNA 2310075M17 gene, SAR1 protein, SAR1a gene homolog (S. cerevisiae), hypothetical protein FLJ22595	ADP-fibosylation factor of ESTs, weakly similar to ARF6_HUMAN RIBOSYLATION FACTOR 6 [M.musculus], ESTs, Weakly similar to ARF6_HUMAN ADP-ribosylation factor 6 [R.norvegicus], RIKEN cDNA 1110033P22 gene, RIKEN cDNA 9130014L17 gene, SAR1 protein, SAR1a gene cDNA 2310075M17 gene, RIKEN cDNA 9130014L17 gene, SAR1 protein, SAR1a gene	ADP-ribosylation factor-like 1, ESTs, Weakly similar to A54022 ADP-ribosylation factor-like 1 - rat fR.norvegicus], RIKEN cDNA 2310008D22 gene	ADP-ribosylation factor-like 1, ESTs, Weakly similar to A54022 ADP-ribosylation factor-like 1 actor-like 1 - rat [R.norvegicus], RIKEN cDNA 2310008D22 gene	AFG3 ATPase ramily gene 3-like 1 (yeast), 200 miles (yeast), PRS4 HUMAN 26S protease regulatory subunit 4 (P26S4) [M.musculus], ESTs, Highly PRS4 HUMAN 26S protease regulatory subunit 4 (P26S4) [H.sapiens], Homo similar to PRS4 HUMAN 26S protease regulatory subunit 4 (P26S4) [H.sapiens], Homo sapiens cDNA FLJ31926 fis, clone NT2RP7005502, moderately similar to Homo sapiens cDNA FLJ31926 fis, clone NT2RP7005502, moderately similar to Homo	Sapiens mRNA for paraplegin-like protein, protease (prosonie, macropain) 26S subunit, ATPase, 1 ATPase 1, proteasome (prosome, macropain) 26S subunit, ATPase, 1	member B2, aldehyde dehydrogenase 3 family, memberA1, aldehyde dehydrogenase family 3, subfamily A1
	ලකු (ලකු '' nn	×, ×				μ. ⊢		Y, CCC, PPP, QQQ	99
SETTLY SE	Aee © RefSeq ID M NM_024151 LI	NM 024149 X	A1105294 L		2	AA875253 P	l	D50696	NM_031972
	@L@@ [6] [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	15367	02221			15933 15931		727	24644
8 ENE	Seq ලා ලා ලා 3539 17	3538 15	893			448 1 3464 1	T	2870	3714
		35	7		<u>_ਲ </u>	<u>4 4</u>	01	~~~~	

OLGG According No. Refrequence	9	जन्दा ©न्दे	RumaniHomologousi Known GeneiName HumaniHomologousi Seguence (Cluster/Ilittle) Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb Pstl fragment, probably the Aldehyde reductase (H.sapiens), ESTs, functional gene), EST, Weakly similar to A39763 aldehyde reductase (H.sapiens), ESTs, Moderately similar to ALDR_RAT Aldose reductase (AR) (Aldehyde reductase (AR) (Aldehy
233	Al233740	X	[R.norvegicus], ES18, Weakly Silming to ALDI 17, 12000 R.norvegicus], RIKEN cDNA 2310005E10 gene, aldo-keto reductase family reductase) [R.norvegicus], RIKEN cDNA 2310005E10 gene, aldo-keto reductase family 1, member B3 (aldose reductase), aldo-keto reductase family 1, member B3 (aldose reductase), fibroblast growth factor regulated protein reductase), fibroblast growth factor regulated protein
8	AA943149	A, B	KIAA0512 [H.sapiens], armadillo repeat protein ALEX2, hypothetical protein MGC3195
8 8 8	AA998619 AI045802	D G, General Alternate	alpha 7A integrin, alpha 6, integrin, alpha 7 6, integrin alpha 7, integrin, alpha 6, integrin, alpha 7
			Alpha-2-macroglobulin, CCR4 carbon catabolite repression 1 mm (CCC) Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], Homo sapiens, clone MGC:1119 IMAGE:3598248, mRNA, complete cds, Mus Mus musculus, clone MGC:29037 IMAGE:3598248, mRNA, complete cds, alpha-2-musculus, clone MGC:29167 IMAGE:5052974, mRNA, complete cds, alpha-2-musculus, clone MGC:59167 IMAGE:5052974, mRNA, complete cds, alpha-2-musculus, clone MGC:59167 IMAGE:5052974, mRNA
A9(AA900290	Z, MM, TTT	macroglobulin, carbon catabolite repression 4 normolgy (2: 20: 20: 20: 20: 20: 20: 20: 20: 20: 2
≥	NM_023103_N, SS,	N, SS, TT	1 1 21-h-2-macroalobulin murinoalobulin 1, murinoglobulin 2, murinoglobulin, pseudogene
₹	NM_023103	General Alternate	1 alpha-2-macroalobulin, murinoglobulin 1, murinoglobulin 2, murinoglobulin, pseudogene
≦	NM_023103	RR, WW	
AA8	AA891914	O. R. NNN	aminoacylase

Allomely wearst tractions of the control of the con	nan Hemelegeus Waleso Name	AMP-activated protein kinase, ESTs, Weakly similar to MAP/microtubule affinity- regulating kinase 3; ELKL motif kinase 2 long form [Mus musculus] [M.musculus], ESTs,	Weakly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMA Weakly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMA WEAKLY SIMILAR S	IMAGE:4947563, mRNA, partial cds, maternal entitiyonic recentor zippor marenal kinase. AMP-activated, alpha 2 catalytic subunit	amyloid beta (A4) precursor-like protein 2	Amyloid protein precursor-like protein 2, ESTS, Weakly Silling to Line (2017)	precursor [M.musculus], amyloid beta (A4) precursor-like protein 1, annyloid beta	precursor-like protein 2	angiotensin receptor 1	annexin Ab	APC11 anaphase promoting complex successions of the state	protein 1 [H.sapiens], ring finger protein 7, ring-box 1	andinoprofein A-II	analinontratein C-II. apolipoprotein CII	apolipoprotein C-IV. apolipoprotein CIV	apolipoprofein M	
		Here Here		3	ر ار ج	20		တ	F, LL, FFF	W.0			111	<u> </u>	×, ××	۵	PPP, QQQ
	<u> </u>	ୁଆ ଜୁଞ୍ଚାଥ			NM 144755 Q, W	M31322		AA894130		1		1	AA850733	X03468	AA819259	AA945171	3405 15066 NM 019373 PPP, QQQ
ଫୁ	9979	D No.			11494	4225		18419	24648	18850			22797	428	6329	16635	15066
RABLE 3	Sed	<u> </u>			4021	3011		999	2573	3000	3223		588	4187	506	904	3405

			1		<u> </u>	
Document No. 1985828.1 Train Homologous Human Homologous Sequence Cluster Title Swin Gene Name. Human Homologous Sequence Cluster Title	ARP2 actin-related protein 2 from the protein of th	sapiens cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN, sapiens cDNA FLJ31247 fis, clone KIDNE2005296, weakly similar to ACTIN CYTOPLASMIC 1, Homo sapiens CDNA similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA DKFZp434B2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15 gene, actin, beta, cytoplasmic, calcitonin gene-related peptide-receptor component	protein, expressed sequence AV259599 ARP2 actin-related protein 2 homolog (yeast), ARP3 actin-related protein 3 homolog (yeast), EST, Weakly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) (yeast), EST, Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1	[K.norvegicus], ESTs, Highly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [M.musculus], ESTs, Highly similar to A29861 actin gamma [H.sapiens], ESTs, [R.norvegicus], ESTs, Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [M.musculus], Homo Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [M.musculus], Homo	sapiens cDNA FLJ31247 fis, clone KIDINEZUCISCO, WCC., J. Cons. PEBLM1000068, highly CYTOPLASMIC 1, Homo sapiens cDNA FLJ32120 fis, clone PEBLM1000068, highly similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA similar to ACTIN, CYTOPLASMIC TYPE 5, Homo sapiens mRNA; cDNA 1700052K15 gene, page 727434R2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15	actin, beta, actin, beta, cytoplasmic, calcitonin gene-related peptide-receptor component protein, expressed sequence AV259599
GENERALIA GENERALIA GENERALIA NO REFERENTIAL MEGAL COSE KNOWN CENE NAME			21624 NM 031144 VV			21625 NM_031144 II
TABLE 3 See @			3619			3619

Company Comp
5 18830 AA964496 T, W 67 18831 Al104357 S, T, W 67 18831 NM_012780 RR
5 18830 AA964496 T, W 67 18831 AI104357 S, T, W 67 18831 NM_012780 RR
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5 18830 67 18831 38 721
38 22 29 29 38

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CONSENT CONSENT CC			Human Homologous F. Scone Sequence (Fig.	mile
Refer ID		Model Gode	Known Gene Name III human houseseed the mischardrial F0 complete	ingitial nonicoccio (subunit e) isoform interpolation mitochondrial F0 complex, subunit c (subunit 9) isoform
	1		ATP synthase, H+ transporting, mitochondrial F0 3, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 3, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 3, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 4, EST, Moderately similar to ATP synthase, H+ transporting, ESTs, Synthase, H+ transporting, mitochondrial F0 4, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 5, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to Similar to ATP synthase, H+ transporting, mitochondrial F0 6, EST, Moderately similar to Similar to Mitochondrial F0 6, EST, Moderately similar to Similar to Mitochondrial F0 7, EST, Moderately simila	se, H+ transporting, mitochondrial F0 tattus norvegicus] [R.norvegicus], ESTs, eattus norvegicus] [R.norvegicus], ESTs, extra norvegicus], ESTs, extra norvegicus], e
, ,	ر ا		Moderately similar to AT93 MOUSE ATP SYNTHASE LIPID-BINDING TO THE SYNTHASE LIPID-BINDING THE SYNTHASE LIPID-BINDING TO THE SYNTHASE LIPID-BINDING TO THE SY	SYNTHASE LIPID-BINDING LICE STATES
0075CU MN	8			List to sempley enthunit d. EST. Weakly
MM 040383	0383	Ü	ATP synthase, H+ transporting, mitochondrial FU Complex, Subunit 5, EU. Sapien similar to ATPQ_HUMAN ATP SYNTHASE D CHAIN, MITOCHONDRIAL [H.sapien similar to ATPQ_RAT ATP synthase D chain, mitochondrial [R.norveg EST, Weakly similar to ATPQ_RAT ATP synthase D chain, mitochondrial [R.norveg EST, Weakly Similar to ATPQ_RAT ATP Synthase D chain, mitochondrial [R.norveg EST], Weakly	ATP synthase, H+ transporting, mitochondrial FO complex, subdimed, L. T. Sapiens], similar to ATPQ_HUMAN ATP SYNTHASE D CHAIN, MITOCHONDRIAL [H.sapiens], EST, Weakly similar to ATPQ_RAT ATP synthase D chain, mitochondrial [R.norvegicus]
	3		ATP synthase, H+ transporting, minochion	TO CHAIN MITOCHONDRIAL [H.sapiens],
			similar to ATPQ_HUMAN ATP SYN I HASE D CHAIN, WILLOW SIMILAR ATPQ RAT ATP Synthase D chain, mitochondrial	similar to ATPQ_HUMAN ATP SYN I HASE D Chair, with Construction of the synthase D chain, mitochondrial
	0000	× × × × × × × × × × × × × × × × × × ×	[R.norvegicus], myo-inositol 1-phosphate synthase A1	synthase A1
18141 NIM 0	320	١, ٥٥	ATP synthase, H+ transporting, mitocholidia ro complex, contractions is some	urial FO complex, security is isoform 1
AI103097	097	KKK	ATD synthase H+ transporting, mitochon	ATD synthase H+ transporting, mitochondrial F1 complex, alpha subunit, isolaring,
		·	ATP synthase, H+ transporting, mitochon cardiac muscle, EST, Moderately similar	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoloring, ATP synthase (EC cardiac muscle, EST, Moderately similar to A35730 H+-transporting ATP synthase (EC
	20426	000	3.6.1.34) alpha chain precursor - rat (fragment) [R.norvegicus]	ment) [R.norvegicus] वस्ता E1 complex delta subunit. EST,
18810 NIM 130430	5045		Moderately similar to ATPD_HUMAN ATP SYNTHASE DELTA CHAIN, Moderately similar to ATPD_HUMAN ATP SYNTHASE DELTA CHAIN, Moderately Similar to ATPD_HUMAN ATP SYNTHASE DELTA CHAIN, MATCHONDRIAL PRECURSO [H.sapiens], RIKEN cDNA 0610008F14 gene	ATP synthase, H+ transporting, mitochondral F1 Compos, Society Chain, Moderately similar to ATPD_HUMAN ATP SYNTHASE DELTA CHAIN, MODERAL PRECURSO [H.sapiens], RIKEN cDNA 0610008F14 gene, RIKEN
	12010	NIM 130106 III CCC RRR		lence Al467246
18420 ININI 1	2	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		

	clone MGC:6568 IMAGE:2812497, mRNA, complete cds	000	NM_130823_000
	Iysosomal 16kD, V0 subunit c, ATPase, H+ transporting, lysosomal 21kD, V0 subunit c, Iysosomal 16kD, V0 subunit B, ESTs, Weakly similar to ATPase, H+ transporting, lysosomal 21kDa, V0 subunit B, ESTs, Weakly similar to VATI MOUSE Vacuolar ATP synthase 16 kDa proteolipid subunit [R.norvegicus], Mus		
	clone MGC:6568 IMAGE:2812497, IIINAY, COmpose General H+ transporting, lysosomal 16kD, V0 subunit C, ATPase, Lysosomal V, V0 subunit C, V0 subun	=	NM 130823
	WAIL_MOUSE vacuotal ATT Symmoso Income (vacuolar proton pump) 21kD, musculus, Similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD, musculus, Similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD,		
	ATPase, H+ transporting, lysosomal 21kDa, Vo subulin D, ED1s, VOC., MOLISE Vacuolar ATP synthase 16 kDa proteolipid subunit [R.norvegicus], Mus		
	lysosomal 16kD, V0 subunit c, ATPase, H+ transporting, lysosomal 21kD, V0 subunit c,		
	ATPase, H+ transporting lysosomal 16kD, V0 subunit C, ATPase, H+ transporting lysosomal C, ATPase, H+ transporting lysosomal C, ATPase, H+ transporting lyso	FFF	NM 053884
	VI [Mus musculus] [M.musculus], KINEN CDIAN 1100 ST. 3	Z, AA	AI228004
	type 8A, member 1, ATPase, class VI, type 11A, AtPase, class VI, type 11A, ptype, ATPase 11A, class Weakly similar to ATPase, class 1, member h; ATPase 11A, ptype, ATPase 11A, class		
	ATPase, Class VI, type 11C, ATPase, annihopinospinospinospinospinospinospinospino		COCCI ININI
	Moderately similar to ATPO_HOWAY ATL_STATE (H.sapiens] CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL [H.sapiens]	ממט	NIM 138883
	CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL [H.sapiens], ESTs,		
	SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL [H.sapiens],		
•	transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conterting transporting) with the sensitivity of the		
	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit, ATP synthase, H+	Model Gode	RefSeq 🗈 ्
	Human Homologous Known Gene Name II Human Homologous/Sequences Cluster III II 6	AND DESCRIPTIONS	(
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TABLE	VINES				Amender Comment No. 1998509.
	7 SETECT 1	/tee or 1: Teksee [0 *	Model Gode :	-	mee Gusterfillde
	8				ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit b, Isoloini 1 (Nema tubulation ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, acidosis with deafness), ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, acidosis with deafness), ATPase, H+ transporting, ISOSOMAL 56/58kD, V1 subunit B, acidoma 1 EST
				isoform 2, ATPase, H+ transl Moderately similar to VAB2_	isoform 2, ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isolorin 1, EC1, Moderately similar to VAB2_MOUSE Vacuolar ATP synthase subunit B, brain isoform (V
				ATPase B2 subunit) (Vacuoli 58 kDa subunit) fR.norvegica	ATPase B2 subunit) (Vacuolar proton pump B isoform 2) (Endomembrane proton pump 58 kDa subunit) [R.norvegicus], ESTs, Highly similar to VAB2_MOUSE VACUOLAR
			O, P, Q, II,	ATP SYNTHASE SUBUNIT	ATP SYNTHASE SUBUNIT B, BRAIN ISOFORM (V-ATPASE B2 SUBUNIT) A17 SYNTHASE SUBUNIT B, BRAIN ISOFORM (V-ATPASE B2 SUBUNIT) A17 SYNTHASE SUBUNIT B, BRAIN ISOFORM (V-ATPASE B2 SUBUNIT)
	2021	710635	MM, VV, PPP,	KDA SUBUNIT) [M.musculus]	S] ST Weakly similar to 154197
4700	200	20071		ATPase, H+ transporting, lys	ATPase, H+ transporting, lysosomal interacting protein 1, ES1, wearly summer the byzochetical protein [H.sapiens], ESTs, Weakly similar to VAS1_RAT Vacuolar ATP
				synthase subunit S1 precurs	synthase subunit S1 precursor (V-ATPase S1 subunit) (V-ATPase S1 accessory
				protein) (V-ATPase Ac45 su	protein) (V-ATPase Ac45 subunit) (C7-1 protein) [K.norvegicus], notific sapieris C27.1 protein [K.norve
3680	16178	NM 031785 T. V. JJ, KK	T V JJ KK	SUBUNIT AC45 PRECURS	SUBUNIT AC45 PRECURSOR (EC 3.6.1.34), expressed sequence AW108110
8		00200	I, M, MM, TT,	ATPase, Na+/K+ transporting, beta 1 polypeptide	ig, beta 1 polypeptide
3223	23710	23710 NM 013113	I, M, MM, TTT	ATPase, Na+/K+ transporting, beta 1 polypeptide	ig, beta 1 polypeptide
	22744	NIM 013113			ng, beta 1 polypeptide
2775	11/67		+	ATP-binding cassette, sub-f	ATP-binding cassette, sub-family A (ABC1), member o, ES1s, wearly similar to the binding CASSETTE TRANSPORTER 2 [M.musculus], hypothetical
1314	12071	A1009456	U, X, Y, LLL, UUU	protein FLJ14297	protein FLJ14297
2		\neg	G, L, BB, II,	ATP-binding cassette, sub-far family F (GCN20), member 2	family b (MDN IA), manager 1,171.
3685	4314	NM_031760 VV, DDD	W, DDD	/// (muo)	

1906 1906		PABLE 3				Automiey Boewer - Free Comment No. 199323.1
3650 AI235738 S 24146 AI169668 R 9176 NM_153303 HH 4193 AI172274 PPP 3504 AI104659 QQ CGeneral 15703 NM_144750 Alternate) Sed		ALS TO	30000	an Homell	us Sequence Guster Mus
3650 Al235738 S 24146 Al169668 R 9176 NM_153303 HH 4193 Al172274 PPP 3504 Al104659 QQ General 15703 NM_144750 Alternate	<u>a</u>	പ്ര				ATP-binding cassette, sub-family C (CFTR/MRP), member 4, ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 9, enfondures-hinding protein 2; sulfondures receptor 2
3650 AI235738 S 24146 AI169668 R 9176 NM_153303 HH 4193 AI172274 PPP 3504 AI104659 QQ General 15703 NM_144750 Alternate	···-				family C, meriber 9, [Mus musculus] [M.r.	musculus), Homo sapiens cDNA FLJ31957 fis, clone
3650 Al235738 S 24146 Al169668 R 9176 NM_153303 HH 4193 Al172274 PPP 3504 Al104659 QQ E, FFF, General 15703 NM_144750 Alternate					NIZKP/00/381, nic pituitary gland cDNA	N12KP/00/381, nigniy similar to Sulloriyludga receptor 27, mas medana pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding
24146 Al169668 R 9176 NM_153303 HH 4193 Al172274 PPP 3504 Al104659 QQ E, FFF, General 15703 NM_144750 Alternate	2701	3650	AI235738	S	Cassette, sub-tailing	to cut family E (GCN20) member 2
9176 NM_153303 HH 4193 AI172274 PPP 3504 AI104659 QQ E, FFF, General 15703 NM_144750 Alternate	2026	24146	AI169668	2	ATP-binding cassed	te, sub-fallilly r (control), member 2
9176 NM_153303 HH 4193 Al172274 PPP 3504 Al104659 QQ E, FFF, General 15703 NM_144750 Alternate					ATP-dependant intellibration (ATP-dependant intellibration)	sculus, clone MGC:18883 IMAGE:4238480, mRNA, complete cds,
9176 NM_153303 HH 4193 AI172274 PPP 3504 AI104659 QQ E, FFF, General 15703 NM_144750 Alternate					dystonia 1, torsion (autosomal dominant; torsin A), torsin family 2, member A, torsin
4193 Al172274 PPP BB, CC, PP, 3504 Al104659 QQ C E, FFF, General 15703 NM_144750 Alternate	4043	9176	NM_153303	壬	family 3, member A	
4193 AI172274 PPP BB, CC, PP, 3504 AI104659 QQ QQ E, FFF, General 15703 NM_144750 Alternate					AU RNA binding pro	otein/enoyl-Coenzyme A hydratase, ESTs, Weakly similar to 137195
4193 A1172274 PPP 3504 A1104659 QQ E, FFF, General 15703 NM_144750 Alternate					AU-specific RNA-bii	nding protein / enoyl-CoA hydratase homolog [H.sapiens], enoyl
3504 Al104659 QQ ΔQ E, FFF, General 15703 NM_144750 Alternate	2138	4193	AI172274	ЬРР	coenzyme A hydrat	ase 1, peroxisomal, uncharacterized hypothalamus protein HCDASE
E, FFF, General 15703 NM_144750 Alternate	1879	3504	A1104659	BB, CC, PP, QQ	B-cell CLL/lymphor	na 10, B-cell leukemia/lymphoma 10
E, FFF, General 15703 NM_144750 Alternate					B-cell CLL/lymphon ESTs, Weakly simil sapiens cDNA FLJ1	B-cell CLL/lymphoma 3, B-cell leukemia/lymphoma 3, DNA segment, EST 1000 104, ESTs, Weakly similar to T42713 ankyrin 3, splice form 1 - mouse [M.musculus], Homo sapiens cDNA FLJ11375 fis, clone HEMBA1000411, weakly similar to ANKYRIN, Homo
E, FFF, General 15703 NM_144750 Alternate					sapiens clone 2464 1700007B22, clone	sapiens clone 24649 mRNA sequence, Homo sapiens, similar to RIKEN cDNA 1700007B22, clone MGC:26734 IMAGE:4826296, mRNA, complete cds, KIAA1223
15703 NM_144750 Alternate				E, FFF, General	protein, hypothetics nuclear factor of ka	protein, hypothetical protein DKFZp564O043, nuclear factor kappa B p105 suburiu, nuclear factor of kappa light chain gene enhancer in B-cells 1, p105, nuclear factor of
	4020		NM_144750	Alternate	kappa light polypep	otide gene ennancer in b-ceils 2, p43/p100

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<u> </u>	- W.O.	යිස්පිලේ මි	Model Gode	Known Geno Name Humani Homologeus Seguenes Greek, 1995 1885 1886	lymphoma 3, ESTs, Weakly similar to
L				NUCLEAR FACTOR NF-KAPPA-B P105	NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT [M.musculus], ESTs, Weakly similar
				to T42713 ankyrin 3, splice form 1 - mouse [M.musculus], Mus musculus, clone	se [M.musculus], Mus musculus, clone
			O.P.O.R.W,	MGC:7734 IMAGE:3498403, mRNA, cor	MGC:7734 IMAGE:3498403, mRNA, complete cds, nuclear lactor of happenight criminal
			NN, 00, PP.	gene enhancer in B-cells 1, p105, nuclear factor of Kappa light propried gone	ar racioi oi kappa iigiii polypopiido gotto
2967	13499	126267	g	enhancer in B-cells 2, p49/p100	enhancer in B-cells 2, p49/p100
				B-cell linker, DKFZP564J01Z3 protein, r	
3716	18702	NM 020080	T. MM. TTT	gene supported by BC007071	Tr. Vishinging to SA6996 B-cell recentor-
5				B-cell receptor-associated protein 37, E	B-cell receptor-associated protein 37, ESTS, mignify Sulling to
				associated protein BAP37 - mouse [M.musculus], E313, Wedany 3111111111111111111111111111111111111	IUSCUIUS], EO 19, Wedaniy Silling to
				PHB HUMAN PROHIBITI [H.sapiens], Homo sapiens, clone MICC. 20074	Homo sapiens, clone MGC.2007
-		1175302	IIII BBB CCC		hypothetical protein MGC13071
60	0220	073332	20, 200		B-cell translocation gene 1, anti-proliferative, ES1s, Highly similar to 10b1 nowhile
				TOB1 PROTEIN [H.sapiens], transduce	TOB1 PROTEIN [H.sapiens], transducer of ERBB2, 1, transducer of ERBB2, 2,
-			TTT WW	transducer of ErbB-2.1	COLINATION
1328	22240	A1003747	1, 0, 141141, 1 1 1	BCL 2/adenovirus E1B 19 kDa-interactin	BCI 2/adenovirus E1B 19 kDa-interacting protein 1, NIP2, ESTs, Weakly Similar to INIT 2
				MOUSE BCL2/ADENOVIRUS E1B 19-1	MOUSE BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2
				IM musculus]. KIAA0367 protein, KIAA1	IM musculus], KIAA0367 protein, KIAA1872 protein, Mus musculus, Similar to Kno
				GTPase activating protein 1, clone MG(GTPase activating protein 1, clone MGC:7050 IMAGE:3156467, mRNA, complete cas,
		1,000,14		RIKEN cDNA 3110043J09 gene, hypothetical protein MGC8103	netical protein MGC8103
7380	3821	A1180114	2, 1, 1, 2	BCL2/adenovirus E1B 19 kDa-interactir	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like, BCL2/adenovirus E1B 19kD
2011	13700	NM OROSSS	2 T Z	interacting protein 3-like	10 10 10 10 10 10 10 10 10 10 10 10 10 1
60	Т	_		BCL2/adenovirus E1B 19 kDa-interactir	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like, BCL2/adei10vii us E1B 19 kDa-interacting protein 3-like,
204	10605	NM 080888 II. J. L. Z	3 L. J. L. Z	interacting protein 3-like	19kD BCI Stadenovinie E1B 19kD
8	十	Т		BCL2/adenovirus E1B 19 kDa-Interactii	BCL2/adenovirus E18 19 kDa-interacting protein 3-iike, bCL2/adenovirus E15 1515
2011	23033	NM 080888		interacting protein 3-like	in a death promoter
2 2		_	×	BCL2-antagonist of cell death, BCl-associated death promoter	Scialed dealth promoter
<u></u>		7	- 1	BCL2-antagonist/killer 1, Mus musculu:	BCL2-antagonist/killer 1, Mus musculus N-BAK1 (Bak1) mKNA, comprete cus,
2831	4361	NM 053812	2 0. P	alternatively spliced, RIKEN cDNA 0610031G08 gene	0031G08 gene
5	- 1				

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CLCC Accor Divo Refect Model Code	 Model Gode		Human Homologous) Kniown Gene Name i H <mark>uma</mark> n Homologous Sequence Gluster IIIIe	
AA859362 XX YY	×			ed athanogene 5, Bcl2-associated
	. δ \		BCL2-associated athanogene 3, BCL2-associated athanogene 5, Bcl2-associated athanogene 3, RIKEN cDNA 1700081D05 gene	ed athanogene 5, Bcl2-associated
AA942718 C, F, W, HH,	C, F, W, HH,	=	BCL2-related ovarian killer, Bcl2-like	
NM_031535 I, J	1		BCL2-related ovarian killer, Bcl2-like, ilvB (bacterial acetolactate synthase)-like	erial acetolactate synthase)-like
AA819362 LL	רר		beta-site APP-cleaving enzyme, hypothetical protein MGC/4/4	otein MGC/4/4
			BH3 interacting (with BCL2 family) domain, apoptosis agonist, ES 15, weakly similar to HRK MOUSE ACTIVATOR OF APOPTOSIS HARAKIRI [M.musculus], harakiri, BCL2	ptosis agonist, ESTS, weakiy sirtiliar to ARAKIRI [M.musculus], harakiri, BCL2
E13573 F, X, Y, LLL	F, X, Y, LLL		interacting protein (contains only BH3 domain)	TOTEGRADO OTTOT
		T .	Bmp2-induced gene, ESTs, Weakly similar to T2D4_HUMAN I KANSCRIP I ION INTERPRESENT INTERP	2D4_HUMAN TRANSCRIP HON [H.sapiens], Mus musculus F-box-
			WD40 repeat protein 6 (Fbxw6) mRNA, complete cds, Mus musculus, clone MGC:7934	te cds, Mus musculus, clone MGC:7934
			IMAGE:3583848, mRNA, complete cds, RIKEN cunA 15000098001 gene, RINEN cunA	CDINA 1500009KOI gene, Kinein CDINA
-			2310009C03 gene, KIKEN CDNA 4933429D11 gene, 1Ar 3-line 14th poymersor, p300/CBP-associated factor (PCAF)-associated factor (PCAF)	gerie, 12t J-line 13th Polymerase 1., I factor, 65 kD, WD repeat domain 18,
			guanine nucleotide binding protein (G protein), beta polypeptide 1, guanine nucleotide	oeta polypeptide 1, guanine nucleotide
			binding protein beta subunit 4, guanine nucleotide binding protein, beta 1, guanine	de binding protein, beta 1, guanine
			nucleotide binding protein, beta 4, hypothetical protein FLJ00012, nuclear matrix protein	protein FLJ00012, nuclear matrix proteir
NM 139333 GG			NIMPZOU related to splicing factor in the 19	subfamily B member 6 Dual (Hsn40)
			Bmp2-inducible Kinase, UnaJ (HSp40) homolog, subjeting b, Tiletinger o, Dijas (198740)	, subjecting b, illefilled of bridge (chapter)
			homolog, subfamily C, member 6, ES1S, Weakly Similar to P1EN MOUSE PROTEIN-	y similar to PTEN MOOSE PROTEINS
-			TYROSINE PHOSPHATASE PTEN [W.:musculus], Mus Indeculus, Olimia to cyclin Grassociated	Als, Ivius Illusculus, Sillingi (C. cyclin) C
			associated Kinase, Gone IMAGE, 3407831, HINNA, parkar day, dyoning daysociated	לא, למו ומו כנס, כלכווון כן מספסומים
D38560 DD, EE, NNN	DD, EE, NNN	_ '	kinase	
NM 030851 I, J	٦, ا	ı	bradykinin receptor B1, bradykinin receptor, beta	8
MM, DDD,	 -	1	branched chain ketoacid dehydrogenase E1, beta polypeptide, pyruvate denydrogenase	eta polypeptide, pyruvate denydrogenase
AA892828 TTT	111	- 1	(iipoamide) pera	

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Seq.	<u>er.ec</u>			Human Homologous Human Homologous Y
<u>.</u>	~ W @	RefSeq D -	ැන්නෙ ලක්ක	Known generalide principal of the control of the control of the control of the control of the dehydrogenase
				branched chain Ketoacid denydrogenase E1, beta polypopudo, Pyrorem 2
594	11998	AA892828	MM, TTT	(lipoamide) beta
				branched chain Ketoacid derlydrogeriase E., Sold polypopulari P. C.
1028	12000	AA957319	MM, TTT	(lipoarrille) Deta
2487	5876	A1176117	nn	(lipoamide) beta
7017	3			BRCA1 associated RING domain 1, BRCA1-associated RING dollian processing the second se
				cDNA 5830466J11 gene, SH3 domain protein 3, ankyrin repeat and SUCS box-
4039	8278	NM 148892	о В	containing 12, expressed sequence C78236, osteoclast surriuraling ractor.
			_	Breakpoint cluster region protein, uterine leionilyonia, 1, valuel to accompany and accompany accompany and accompany accompany and accompany and accompany accompany and accompany accompany accompany and accompany accompan
3808	9055	NM 053631	x, Y, UUU	breakpoint cluster region protein 1, expressed sequence of one
				BRF1 homolog, subunit of KNA polymerase in dailson programment in the control in close MGC 6859
				(S.cerevisiae), Mus musculus, general transculution factor III.
000	00000		NM 031041 TT 77 AAA	IMAGE:2650779, mRNA, complete cds, general transcription lactor incomplete cds, general transcription in the complete cds, general transcription in the cds, g
2000	50077			BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast), E315, Wedny Silling
				to quanine nucleotide-binding protein, beta-1# subunit [Rattus norvegicus]
				IR norvegicus], Mus musculus, clone MGC:7934 IMAGE:3583848, mRNA, complete
		-		cds hudding uninhibited by benzimidazoles 3 homolog (S. cerevisiae), guanine
				nucleotide binding protein, beta 1, neural precursor cell expressed, developmentally
1		AAA 77 70000 4814	77 444	down-regulated gene 1
32/3	71801	Т	25. 7 7	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast), ES Is, Weakly Similar
		-		to guanine nucleotide-binding protein, beta-1# subunit [Kattus norvegicus]
				[R.norvegicus], Mus musculus, clone MGC:7934 IMAGE:3583848, mKNA, complete
				cds, budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae), guarnine
				nucleotide binding protein, beta 1, neural precursor cell expressed, developinement
2575	21802		NM 030987 O. P. VV. AAA	
2	1201	_		

					-004-								_	_	_	1
Altorney Docket (KEZ1-5133-611W0	n Homologous n Gene Name Human Homologous Sequence Cluster Mile	C1q related factor, ESTs, Highly similar to 1917150A collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to CA18 MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus], Homo sapiens, clone MGC:15203 IMAGE:3163767, mRNA, complete cds, collagen, type VIII, alpha 1, extracellular glycoprotein EMILIN-2 precursor,	procollagen, type VIII, alpha 1	expressed sequence Al849185, expressed sequence R75232, muscleblind-like (Drosophila)	C3H-type zinc finger protein; similar to D. melallogaster musclebilind-like expressed sequence R75232, muscleblind-like (Drosophila)	Ca++/calmodulin-dependent protein kinase II, delta subunit, EK to nucieus signaliing 1,	MAP kinase-activated protein kinase 2, Mus musculus, clone MGC:18731 IMAGE:3980838, mRNA, complete cds, calcium/calmodulin-dependent protein kinase II, delta, expressed sequence AI874665	Ca++/calmodulin-dependent protein kinase II, delta suburiit, EN to ructeus signalining ii. MAP kinase-activated protein kinase 2, Mus musculus, clone MGC:18731	IMAGE:3980838, mRNA, complete cds, calcium/calmodulii ruependen processioner and delta, expressed sequence Al874665	cadherin 13, cadherin 2, cadherin 2, type 1, N-cadherin (neurona), desmocollin 1,	cadherin 13, cadherin 2, cadherin 2, type 1, N-cadherin (neuronal), desmocollin 1,	desmoglein 2	calcium binding protein Cap45 precuisor, suoma cen democratica neces	calmegin, calnexin	calmegin, carrexiii	CAMP inducible gene 1, solute carrier rathing 10 (Camp in the carrier in the carr
	uman Homologous nown Gene Name	0 6 2 5 6	a													
	Merstall Georgia		E, NN, 00	MM	SS	23 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	MW.		L WW	: .	L, LLL, 555	GGG, LLL	天	LL		노
	<u>eensenz</u> Ae or Posson ID	The Republic	AI170516	AA818999	A1236907	AIK 20301	AA799814		A1237813	20010	NM_031333	NM 031333	AA997861		NM 053404	NM_139341
	91.66 8.06	92	13361	22175	20178	0/177	21042		24042	2017	6672	6673	3458	11935	6962	6735
	Seq. (6		2055 /	197	T		02		2706		3629	3629	1154	634	3761	4018

TABLE 3	3.8 3.8				Afformay Docket 44524-5055-501WC
Seq.		(<u>centank</u> Ace or ### Be(See 10	Model Gode	Humani Homologous Known Gene Name Human Homologous Sequence (Guster IIII)	in the second of
1025	22251				candidate tumor suppressor OVCA2, diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1
2838	14882	D00362	O, P, NN, OO, XX, YY, BBB, DDD	carboxylesterase 3 (brain), esterase 1), esterase 1
3000	14881	M20629	0, P, NN, 00, XX, YY, CCC	carboxylesterase 3 (brain), esterase 1), esterase 1
				CARD only protein, ESTs, enzyme [H.sapiens], EST enzyme beta isozyme [H.sapiens], p. 1900.	CARD only protein, ESTs, Moderately similar to A5/511 interleukin-1 beta converting enzyme [H.sapiens], ESTs, Weakly similar to A56084 interleukin-1beta converting enzyme beta isozyme [H.sapiens], Homo sapiens mRNA; cDNA DKFZp586A181 (from enzyme beta isozyme [H.sapiens], Homo sapiens mRNA; cDNA DKFZp586A181).
3136	18068	NM 012762 P, VV	γ, ≪	1, apoptosis-related cyste	1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
2486	1480	AI230260	RR	casein kinase 2, beta poly	casein kinase 2, beta polypeptide, casein kinase II, beta subunit
2957	1481	L15619	N, V, ZZ, AAA, PPP, QQQ	casein kinase 2, beta poly	casein kinase 2, beta polypeptide, casein kinase II, beta subunit
				cathepsin G, granzyme B serine esterase 1), granzy	cathepsin G, granzyme B, granzyme B (granzyme Z, cytotoxic I-lymphocyte-associated serine esterase 1), granzyme C, similar to granzyme B (granzyme 2, cytotoxic T-
3975	24672	NM 138517	SS	lymphocyte-associated se	lymphocyte-associated serine esterase 1) (H. sapiens)
2945	1894	L03201	DOD	cathepsin S	f rigatory worker dail and M. 10 th.
				Cbp/p300-interacting tran Cbp/p300-interacting tran Cbp/p300-interacting tran Cbp/p300-interacting tran	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain transaction transactivator, with Glu/Asp-rich carboxy-terminal domain transaction transactivator transaction transactivator
2242	16124	AI176963	ດດດ	Cbp/p300-interacting tran	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
				Cbp/p300-interacting tran (Cbp/p300-interacting tran (Cbp/p300-interacting tran (Cbp/p300-interacting tran	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2,
3813	16123	NM_053698 F, DD, EE	F, DD, EE	Cbp/p300-interacting tran	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4

14736 NM 053899 July KK COCTC-binding factor (zinc finger protein), EST, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Transcription and the ZF3 MOUSE ZINC FINGER PROTEIN 28 Transcription and the ZF3 MOUSE ZINC FINGER PROTEIN 28 Transcription and the ZF3 MOUSE ZINC FINGER PROTEIN 28 Transcription and the ZF3 MOUSE ZINC FINGER PROTEIN 28 Transcription and the ZF3 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to ZF28 MOUSE ZINC FINGER PROTEIN 28 Manacoulus], EST3, Weakly similar to CD81 FAT CD81 similar to CD8		ଜୁ				Doeument No. 1935223
14795 NM_053699 JJ, KK 24518 L19927 GG 24518 L19927 GG 24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 N, GG) (Sec.)	elec Salva	<u> </u>	9.50 KI S	Human Homologous Koown GenelName	HumaniHomologous Sequence GusternIIII)
14795 NM U3039 U3, NA 24518 L19927 GG 24518 L19927 GG 8898 NM 013087 G, H, J G, H, J G, H, J S, UUU G, H, J G, H, I, J, S, G, UUU G, H, J, S, J, J, S, J,	2	9000				Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
24518 L19927 GG 24518 L19927 GG 8898 NM 013087 G, H, J 8899 NM 013087 SS, UUU 8900 NM 013087 PPP, QQQ 19710 NM 021744 II, KKK 19711 NM 021744 II, KKK 19711 NM 021744 II, KKK	3814	14/80	GEOCCO MINI	99, NY		CCCTC-binding factor (zinc finger protein), EST, Weakly similar to ZF37_RAT Zinc
7775 AI071481 D 24518 L19927 GG 24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 II, KKK 19711 NM_021744 II, KKK 19711 NM_021744 II, KKK						finger protein 37 (Zfp-37) [R.norvegicus], ESTs, Highly similar to ∠F∠8 MOUSE ∠INC
7775 AI071481 D 24518 L19927 GG 24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG						FINGER PROTEIN 28 [M.musculus], ESTs, Weakly similar to ZF93_MOUSE ZINC
24518 L19927 GG 24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 SPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG						FINGER PROTEIN 93 (ZFP-93) [M.musculus], Mus musculus, clone MGC:31575
24518 L19927 GG 24518 L19927 GG 8898 NM_013087 G, H, J, S, G, H, J, S, G, H, J, S, SS, UUU 8899 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG 17854 NM 139103 O, P						IMAGE:4504776, mRNA, complete cds, zinc finger protein 28, zinc finger protein 37,
24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG	1704	7775	A1071481	٥		zinc finger protein 37 homolog (mouse)
24518 L19927 GG 8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 II, KKK 19711 NM_021744 II, KKK						CCR4-NOT transcription complex, subunit /, EST, Figling Similar to C Criain C, Nat
8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG	2960		_	99		Liver F1-Atpase [R.norvegicus], expressed sequence Cou404
8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 II, KKK						CD 81 antigen, CD81 antigen (target of antiprometative atmoody 1), Ed. 3, 1553, 1553, CD81 antigen (target of antiprometation)
8898 NM_013087 G, H, J 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 II, KKK						similar to CD81 ANTIGEN [M.musculus], ES1S, Weanly Simila
8899 NM_013087 G, H, J, S, 8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG						antigen (26 kDa cell surface protein TAPA-1) (Target of the antiprolinerative altitloody T
8999 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG	3215	808	NM 013087			[R.norvegicus]
8999 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG	2	3		_		CD 81 antigen, CD81 antigen (target of antiproliferative antibody 1), E313, weakly
8899 NM_013087 SSS, UUU 8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 II, CG						similar to CD81 ANTIGEN [M.musculus], ESTs, Weakly similar to CD81 RATIONAL
8999 NM 013087 SSS, UUU 8900 NM 013087 PPP, QQQ 19710 NM 021744 II, KKK 19711 NM 021744 N, GG				G. H. I. J. S.		antigen (26 kDa cell surface protein TAPA-1) (Target of the antiproliferative antipoody 1)
8900 NM 013087 PPP, QQQ 19710 NM 021744 II, KKK 19711 NM 021744 N, GG 17854 NM 139103 O, P	3215		NM 013087			[R.norvegicus]
8900 NM_013087 PPP, QQQ 19710 NM_021744 II, KKK 19711 NM_021744 N, GG		Т		7		CD 81 antigen, CD81 antigen (target of antiproliferative antibody 1), E313, ***Can't
8900 NM 013087 PPP, QQQ 19710 NM 021744 II, KKK 19711 NM 021744 N, GG						similar to CD81 ANTIGEN [M.musculus], ES1S, Weakly Simila
8900 NM 013087 PPP, QQQ 19710 NM 021744 II, KKK 19711 NM 021744 N, GG						antigen (26 kDa cell surface protein TAPA-1) (Target of the anuprolinerative annipouy T
19710 NM 021744 II, KKK 19711 NM 021744 N, GG 17854 NM 139103 O, P	3215		NM 013087			[R.norvegicus]
19711 NM_021744 N, GG 17854 NM 139103 O, P	3432	_	T	1 II, KKK		CD14 antigen
17854 NM 139103 O, P	3/32	-	Т	1 N GG		CD14 antigen
17854 NM 139103 O, P	7107	Т	T			CD2 antigen family, member 10, CD48 antigen, CD48 antigen (B-cell member 10, CD48)
17854 NM 139103 O, P						protein), CD84 antigen, ESTs, Weakly similar to CD48_RA1 MRC UX-43 sunace
17854 NM 139103 O, P				-	-	antigen precursor (BCM1 surface antigen) (BLAS1-1) (CD46) [R.IIIGI Vegicus], MINELA
	4005					cDNA 5830408F06 gene, expressed sequence Aittazat

				т-	-		T		T^-		Т				T	-			П		<u>s</u> _	7
AMEGINES DECEMBER 100 (1989) DECEMBER 100 (198	Win Gene Name Numan Homologous/Sequence/Gluster Ifftle Act A	fragment of IgE, high affinity I, receptor for; gamma polypeptide, Fc receptor, IgE, high affinity I, receptor for; gamma polypeptide, Fc receptor, IgE, high affinity learned polypeptide. Home sapiens, Similar to Fc fragment of IgE, high affinity and the polypeptide.	It, receptor for; gamma polypeptide, clone MGC:22620 IMAGE:4704425, mRNA,	complete cds, T-cell receptor CD3, subunit zeta	CD36 antigen (collagen type I receptor, unombospondin receptor)-like 2 (lysosomal integral membrane) (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane)	protein II), EST, Moderately similar to LYII_HUMAN LYSOSOME MEMBRANE	PROTEIN II [H.sapiens]	CD63 antigen (melanoma 1 antigen), Cdo3 altigen, L31, Wcdn) Similar (Mouse CD63 ANTIGEN [M.musculus], expressed sequence C75951, tetraspan 3,	transmembrane 4 superfamily member 8	CDA02 protein, ESTs, Weakly similar to IF39_HUMAN EUKARYOTIC TRANSLATION	INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]			CDA02 protein, ESTs, Weakly similar to IF39_HUMAN EUKARYOTIC TRANSLATION	INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]			CDC28 protein kinase 1. ESTs, Highly similar to A36670 cell division control protein	CKS1 fH saniens!	CRV related protein kinase PNOI ARE cyclin-dependent kinase 7 (MO15 homolog,	Xenopus laevis, cdk-activating kinase), cyclin-dependent kinase 7 (homolog of Xenopus	MO15 cdk-activating kinase)
										, L		-	Sore	ers,		in in						000
	ගිමේවූ ලිලේම			P, W	C	General	Alternate		N, O, P	N, MM, T	Alternate	A, B, FFF	General Core	Tox Markers	Alternate	L, Genera	Core Tox	Markers,	General	Alternate		S, PPP, QQQ
्रा । । इस्तान्त्रकार	Ace or RefSeq (D			AA957422			NM 054001		AA892498		AA875205				AA875205				1	AI103556		X83579
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A SECTION OF THE SECT	CDP-diacylglycerolinositol 3-phosphatidyltransferase (phosphatidylinositol synthase), DNA segment, Chr 7, Brigham & Women's Genetics 0575 expressed	cell division cycle 25 homolog B (S. cerevisiae), cell division cycle 25B, cell division cycle 25C cerevisiae), cell division cycle 25B, cell division cycle 25 homolog C (S.	cell division cycle 25 homolog B (S. cerevisiae), cell division cycle 25C cerevisiae), cell division cycle 25B, cell division cycle 25 homolog C (S. cerevisiae), cell division cycle 25 homolog C (S.	cerevisiae), cell division cycle 25B, cell division cycle 25C	cell division cycle 25 nominally by the carefusion cycle 25C cerevisiae), cell division cycle 25B, cell division cycle 25C	Centaurin-alpha2 protein, EST, Weakly similar to T42627 ADP-ribosylation factor-directed GTPase activating protein, isoform a - mouse [M.musculus], ESTs, Weakly similar to Centaurin-alpha2 protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to T42627 ADP-ribosylation factor-directed GTPase activating protein, isoform mouse [M.musculus], RIKEN cDNA 1700030C10 gene, centaurin, beta 2, centaurin, beta 5, development and differentiation enhancing, hypothetical protein AL133206	Centaurin directed G	similar to mouse [N	ceroid-lip	sednence	CGI-10 protein	CGI-10 protein
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Decument No. 199523.4	Rumanikomologóus Rumanikomologóus Ramanikomologous kartinanikomologous Seguence (Gluster Titulo	CGI-109 protein, ESTs, Weakly similar to P24_MOUSE COP-COATED VESICLE	MEMBRANE PROTEIN P24 PRECURSOR (P24A) [M.musculus], KINEN CDINA	1110014C03 gene, Nincia Colar 12002C010 33777 Pp. Sene, coated vesicle RIKEN cDNA 4432412D15 gene, coated vesicle	membrane protein, integral type I protein	CGI-110 protein	CGI-115 protein, RIKEN cDNA 2810430M08 gene	CGI-116 protein	CGI-127 protein	CGI-141 protein, ES1s, Weakly Similar to 140900 hypometical process.	DKFZp/6162423.1 [n.sapiens]	CGI-143 protein	CGI-19 protein, ESTs, Weakly similar to JC5026 UDP-galactose transporter related	protein 1 - rat [R.norvegicus], Mus musculus, clone MGC:31031 IMAGE:3137.003,	mRNA, complete cds, UDP-galactose translocator 2, UDP-galactose transporter refered,	YEA4 protein, expressed sequence Al428460, hypometical protein, mixed	CGI-20 protein	CGI-69 protein, EST, Moderately similar to 143493 riybutretical protein, 25	DKFZp434C119.1 [H.sapiens], ES1s, Weakly similar to soluce carrier range and partial proventions].	(carnitine/acylcarnitine translocase), member 20 [Natura ho. 70] (carnitine/acylcarnitine translocase), member 20 [Natura ho. 70]	Mus musculus, similar to costass gene product, some massed sequence	MRNA, complete cds, Kinery conva 130000000 gotto, cyfrod of the converse family 25	Awy 43 1445, Illicondition translocase), member 20, solute carrier family 25 (mitochondrial	carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial	carrier), member 18, solute carrier family 25 (mitochondrial carrier, Araiar), member carrier), member	solute carrier tamily 25 (mitochordial carrier, agening response a service tamily 25)	13
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		Homologous Sene Name		CGI-74-like SR-rich, DNA segment, Chr 17, human D6S45, ES1, Weakly similar to SR4 HUMAN CTD-BINDING SR-LIKE PROTEIN RA4 [H.sapiens], ESTs, Highly	similar to T31420 C-terminal domain-binding protein rA8 - rat [R.norvegicus], ESTs,	PROTEIN [M.musculus], ESTs, Weakly similar to T31420 C-terminal domain-binding	protein rA8 - rat [R.norvegicus], KIAA1116 protein, expressed sequence A1447044,	protein rA4		CGI-83 protein	GGI-97 protein, EST, Weakly similar to YC37_HOWAN HTPOTHETICALT TO ENGLY STEEL	checkpoint with forkhead and ring finger domains	chemokine (C-C motif) receptor-like 1	cholinergic receptor, muscarinic 3, cardiac, cholinergic receptor, muscarinic o	chromosome 11 onen reading frame 17. predicted gene ICRFP703B1614Q5.6	Citioniosonie 11 open reading frame 17 predicted gene ICRFP703B1614Q5.6	chomosome 14 open reading frame 1	chromosome 14 open reading frame 1	chromosome 20 open reading frame 36, protein-L-isoaspartate (D-aspartate) O-	methyltransferase, protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	chromosome 20 open reading frame 36, protein-L-isoaspartate (U-aspartate) U-	methyltransferase, protein-L-isoaspartate (D-aspartate) O-illeti ytiralisidase i	methyltransferase, protein-L-isoasparlate (D-asparlate) O-methyltransferase 1
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Human Homologous Human Homologous Sequence Guster fills	chromosome 20 open reading frame 36, protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	chymase 1, mast cell, mast cell protease 1	clathrin, light polypeptide (Lca), clathrin, light polypeptide (Lcb), expressed sequence	AV026556	Sequence	AV02656	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	CLLL7 protein, DKFZP586C1619 protein, ESTs, Weakly similar to T31081 cca3 protein	rat [R.norvegicus], Homo sapiens cDNA FLJ25141 fis, clone CBR0/151, KIKEN CDNA	4933432B13 gene, RIKEN cDNA 6330404E16 gene, chromosome condensation 1-tike,	expressed sequence AW539457, gene trap artikytiit repeat	CLLL8 protein, EST, Highly similar to S30385 G9a protein (n.Sapiens), ESTS, weday	Similar to 117453 ERG-associated protein ESE1 - Induse [W.:indsculus], OE1 domain, high protein ESE1 domain, oE1 domain, high protein ESE1 domain ESE1 domain, high protein ESE1 domain, high protein ESE1 domain ESE1 domain, high protein ESE1 domain E	(Drosophila) homolog 2; hypothetical protein FLJ23414	CipP caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli),	caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli), expressed	sequence AU019820	ClpX caseinolytic protease X homolog (E. coli)	CLST 11240 protein, DKFZP564K247 protein, ESTs, Highly similar to T14766 hypoxia hypoxidal protein DKFZP564K247.1 [H.sapiens]. ESTs, Weakly similar to hypoxia	induced gene 1 [Rattus norvegicus] [R.norvegicus], Homo sapiens mRNA; cDNA	DKFZp434A1627 (from clone DKFZp434A1627), RIKEN cDNA 2010110M21 gene,	RIKEN cDNA 2310056K19 gene, hypothetical protein MGC2198, hypoxia induced gene	
	77 AAA		K, Q, R, BBB,	RRR, SSS	H, LLL, UUU,	General				General	Alternate						F, S, RRR					C, General	Alternate
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	ramHomologous	CMP-NeuAC:(beta)-N-acetylgalactosaminide (alpha)2,6-sialyltransferase member VI, ESTs, Weakly similar to CAG7_RAT ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-	2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY) [R.norvegicus], sialyltransferase	7.0 ((alpria-N-acetyliteurariii)1-2,5-beta-galactosyi-1,3/-14-acetyr galactosariiiinde alpria- 2,6-sialyltransferase), similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-	betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) E	CMRF35 leukocyte immunoglobulin-like receptor, EST, Weakly similar to PIGR_RAT	Polymeric-immunoglobulin receptor precursor (Poly-IG receptor) (PIGR) [Contains:	Secretory component] [R.norvegicus], Fc receptor, IgA, IgM, high affinity, Homo	sapiens, similar to CMRF35 ANTIGEN PRECURSOR, clone MGC:26887	IMAGE:4827737, mRNA, complete cds, Mus musculus polymeric immunoglobulin	receptor 3 precursor (Pigr3) mRNA, complete cds, RIKEN cDNA 1810037B05 gene,	RIKEN cDNA 2310016B05 gene, immunoglobulin superfamily, member 7, polymeric	immunoglobulin receptor, regulator of Fas-induced apoptosis	CMRF35 leukocyte immunoglobulin-like receptor, EST, Weakly similar to PIGR_RAT	Polymeric-immunoglobulin receptor precursor (Poly-IG receptor) (PIGR) [Contains:	Secretory component] [R.norvegicus], Fc receptor, IgA, IgM, high affinity, Homo	sapiens, similar to CMRF35 ANTIGEN PRECURSOR, clone MGC:26887	IMAGE:4827737, mRNA, complete cds, Mus musculus polymeric immunoglobulin	receptor 3 precursor (Pigr3) mRNA, complete cds, RIKEN cDNA 1810037B05 gene,	RIKEN cDNA 2310016B05 gene, immunoglobulin superfamily, member 7, polymeric	immunoglobulin receptor, regulator of Fas-induced apoptosis
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109 L14004 TT, DDD 110 U01145 D, F 22851 AA925204 FF 22851 AA925204 FF 22853 AA819749 PPP, QQQ 20668 AA819749 PPP, QQQ 20669 AI177590 GG 20669 AI177590 GG	AMOUNE) BOCKEL FEED OF THE STATE OF THE STAT	Philipping to the second secon	nemon in the recent RST Weakly similar to PIGR RAT	CMRF35 leukocyte Immunoglobulii Filike receptor, Edit, modify [Contains: Polymeric-immunoglobulin receptor precursor (Poly-IG receptor) (PIGR) [Contains:	Secretory component [R.norvegicus], Fc receptor, IgA, IgM, high affinity, Homo	sapiens, similar to CMRF35 ANTIGEN PRECURSOR, clone MGC:26887	IMAGE:4827737, mRNA, complete cds, Mus musculus polymeric immunoglobulin	receptor 3 precursor (Pigr3) mRNA, complete cds, RIKEN cDNA 1810037B05 gene,	RIKEN cDNA 2310016B05 gene, immunoglobulin superfamily, member 7, polymeric	immunoglobulin receptor, regulator of Fas-induced apoptosis	CMRF35 leukocyte immunoglobulin-like receptor, EST, Weakly similar to PIGR_RAT	Polymeric-immunoglobulin receptor precursor (Poly-IG receptor) (PIGK) [Contains.	Secretory component R.norvegicus), Fc receptor, IgA, IgM, high affinity, Homo	saniens similar to CMRF35 ANTIGEN PRECURSOR, clone MGC:26887	IMAGE-4827737 mRNA, complete cds, Mus musculus polymeric immunoglobulin	Increator 3 precursor (Pigr3) mRNA, complete cds, RIKEN cDNA 1810037B05 gene,	RIKEN cDNA 2310016B05 gene, immunoglobulin superfamily, member 7, polymeric	imminoalobulin receptor, regulator of Fas-induced apoptosis	CMRF35 leukocyte immunoglobulin-like receptor, EST, Weakly similar to PIGR_RAT	Polymeric-immunoglobulin receptor precursor (Poly-IG receptor) (PIGR) [Contains:	Secretory component [R.norvegicus], Fc receptor, IgA, IgM, high affinity, Homo	saniens similar to CMRF35 ANTIGEN PRECURSOR, clone MGC:26887	IMAGE-4827737, mRNA, complete cds, Mus musculus polymeric immunoglobulin	receptor 3 precursor (Pigr3) mRNA, complete cds, RIKEN cDNA 1810037B05 gene,	RIKEN CONA 2310016B05 gene, immunoglobulin superfamily, member 7, polymeric	imminopholilin receptor, regulator of Fas-induced apoptosis	Section of BDC 4	Colacion of the component of the compone	Complement of olicomeric order complex 4	Component of olicomeric color complex 4	componential fiscular growth factor	
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Seq.	(A)	(<u>consents</u> Xee or Prism Prism		Human Homologous The Company Homologous Sequence @ US(er IIII)
		800		COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana), eukaryotic translation initiation factor 3, subunit 5 (epsilon), eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD), expressed sequence AW107203, initiation factor 3, subunit 5 (epsilon, 47kD), expressed sequence AW107203, proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
148	2845	AA816020	A, G, BB, CC,	
			GGG, HHH, General Core	corticosteroid binding globulin, serine (or cysteine) proteinase inhibitor, clade A (alpha-1
639	13088	AA893495	Tox Markers	antiproteinase, artuti ypsiri), rieniber o
4102	53	U16253	<u>¥</u>	
3784	8358	NM 053540	>- 	COX17 homolog, cytochrome c oxidase assembly protein (yeast), cytochrome c oxidase, subunit XVII assembly protein homolog (yeast), expressed sequence Al037035
2419	22915	AI228299		craniofacial development protein 1
2265	15251	AI177363	Z	c-src tyrosine kinase
2307	15252	AI178605	GG, HH	C-src tyrosine kinase
				EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11) [H.sapiens], ESTs, Weakly similar to
				MEA6_HUMAN MENINGIOMA-EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11) I'H sapiens]. KIAA0268 protein, meningioma expressed antigen 6 (coiled-coil proline-
1882	22957	AI104897	a R	rich)
				CTAGE-1 protein, ES1s, Moderately Similar to MEAU_TOWNEY MENTIONS. EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11) [H.sapiens], ESTs, Weakly similar to MEA6_HUMAN MENINGIOMA-EXPRESSED ANTIGEN 6/11 (MEA6) (MEA11) MEA6_HUMAN MENINGIOMA-EXPRESSED ANTIGEN 6/11 (MEA6) (MIT (MEA11))
			<u>.</u>	[H.sapiens], KIAA0268 protein, meningiorna expressed arriger o (concer com promoter) rich)
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TABLE 3.	(S)			Attorney Doctret 24.8241-2028-201000 Document No. 1925523.1
Sag	GLEGE TINNS	Generals	Modell Gode	Human Homologous Human Homologous Sequence Guster IIIIe
		F		
			х, Ү, ЕЕЕ,	receptor [K.norvegicus], Langernans cell specific c-type fecult, must misser a construction (C type lectin (langerin gene), RIKEN cDNA 1810046124 gene, RIKEN cDNA
3820	24728	NM_053753 MMM	MMM	STIDOS/N.1 gene Chang (raing dependent carbohydrate recognition domain) lectin, superfamily
				member 13, ESTs, Weakly similar to KUCR_RAT Kupffer cell receptor [R.norvegicus],
2481	1650	AI230142	0, P	Kupffer cell receptor, Langerhans cell specific c-type lectin
			NN, OO, PP,	
3137	17257	NM_012766 QQ, ZZ	QQ, ZZ	cyclin D3
3137	17258		NM 012766 NN, ZZ, AAA	cyclin D3
651	19171	AA893699	ပ	cyclin D-type binding-protein 1, maternal innibition of dillerentiation
3545	20770	NM 024160	Μ	cytochrome b-245, alpha polypeptide
4029	1448	NM_145783	Ω	cytochrome c oxidase subunit Va, cytochrome c oxidase, subunit Va
3795	21424	NM_053586	XX, YY	cytochrome c oxidase subunit vb, cytochilone c oxidase, subunit vb
3650	15024	NM 031572	99	cytochrome P450, 2c40, cytochrome P450, sublaininy ii.c. (iiiepiieiiytoiii +1iyalooyaaco), polypeptide 19, expressed sequence Al662255
			T	cytochrome P450, 3a25, cytochrome P450, subfamily IIIA (niphedipine oxidase),
4028		16278 NM_145782 X	×	polypeptide 5
				D-amino acid oxidase, D-amino-acid oxidase, D-asparate oxidase, must missered. Similar to D-aspartate oxidase, clone MGC:6692 IMAGE:3582980, mRNA, complete
3807	1127	NM_053626 III, JJJ) III, JJJ	cds, RIKEN cDNA 5730402C02 gene

					
## 4 4 A 4 A 4 A 4 A 4 A 4 A 4 A 4 A 4 A	DAZ associated protein 1, ESTs, Highly similar to 152962 FBRNP [H.saplens], ESTS, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1) (HDP) destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 [M.musculus], Homo sapiens cDNA: FLJ22720 fis, RIBONUCLEOPROTEINS A2/B1 [M.musculus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, similar to heterogeneous nuclear ribonucleoprotein A3 (10025E17 gene, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A2/B1 (Asp-Glu-ribonucleoprotein A2/B1)	DEAD (asparate-gludalitate-grafting Coperate) similar to A57514 RNA Ala-Asp/His) box polypeptide 17 (72kD), ESTs, Moderately similar to PROBABLE RNA-helicase HEL117 - rat [R.norvegicus], ESTs, Weakly similar to PROBABLE RNA-helicase HEL117 - rat [R.norvegicus], Homo sapiens cDNA FLJ25329 fis, clone DEPENDENT HELICASE P68 [M.musculus], Homo sapiens clone MGC:31579 IMAGE:4505095, mRNA, DKFZp586K2322), Mus musculus, clone MGC:31579 IMAGE:4505095, mRNA, complete cds, RIKEN cDNA 2310061004 gene, RIKEN cDNA 4921506D17 gene, RNA complete cds, RIKEN cDNA 2310061004 gene, RIKEN cDNA 4921506D17 gene, RNA complete cds, RIKEN cDNA 4921506D17 gene, RNA complete cds, RIKEN cDNA 2310061004 gene, RIKEN cDNA 4921506D17 gene, RNA	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 20, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 20, 103kD, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 39, DEAD/H polypeptide 20, 103kD, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD), DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase, 52kD), EST, Moderately similar to HLA-Baspy/His) box polypeptide 7 (RNA helicase, 52kD), EST, Moderately similar to HLA-Baspociated transcript 1A, DNA segment, Chr 17, human D6S81E 1; nuclear RNA helicase Rat1 (Mus musculus) [M.musculus], HLA-B-associated transcript 1A	וופווכמסט חמנו לאינס ווייבים וויבים
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()		0	Medal ලබෙන 	Khown (Gene Name) Humanitlomologous School (September 1988) MOUSE PROBABLE RNA-DEAD-box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTs, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTS, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTS, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTS, Weakly similar to DDX5 MOUSE PROBABLE RNA-DEAD-Box protein, ESTS, Weakly similar protein, ESTS, Weakl
				DEPENDENT HELICASE P68 [M.musculus], Homo sapiens cuiva redessaria, como representativo de la compacta del compacta del compacta de la compacta del compacta de la compacta del compacta de la compacta del compacta de la compacta de la compacta de la compacta del compacta del compacta del compacta de la compacta de la compacta del compacta
				MGC:21583 IMAGE:4479998, mRNA, complete cds, Mus musculus, clone MGC:315/9 MGC:21583 IMAGE:4479998, mRNA, complete cds, Mus musculus, clone MGC:315/9 MGC:31
		000	-	IMAGE:4505095, mrink, complete cus, remember 25, complete cus, remember 25, complete cus, remember 25, complete cus, complete cu
325	13772	AA851920	3	DEAD-box protein, ESTs, Weakly similar to DDX5 MOUSE PROPAGLE 1000
				DEPENDENT HELICASE P68 [M.musculus], norito saperis convolus.
		· ·		MGC:21583 IMAGE:4479998, mRNA, complete cds, Mus musculus, clone MGC:31579
				IMAGE:4505095, mRNA, complete cds, RIKEN cDNA 9130430L19 gene, RNA Heilcase,
7464	22058	A1229450	K.	expressed sequence Al325430
5	2000	CO. C. T.		death-associated kinase 3, death-associated kinase 17a (anoptosis-
			H, T, DD, EE,	kinase 3, expressed sequence Al120141, serine/unredimite kinase 1.5 (specification)
3489	12422	NM 022546		inducing), serine differentiated in the sering of the seri
	T -	1		death-associated will account to the serine/threonine kinase 17a (apoptosis-kinase 3, expressed sequence Al120141, serine/threonine kinase 17a (apoptosis-kinase 17a (
2400	12423	NM 022546	χ. ζ. 	inducing), serine/threonine kinase 17b (apoptosis-inducing) inducing), serine/threonine kinase 2,
000	Т	1		death-associated Kinase 3, expressed sequences
3894	24459	UM 057209 UN	nn	skeletal muscle
	+-		S, W, PPP,	dendritic cell protein
7	16950	\neg	200	dentatorubral-pallidoluysian atrophy (atrophin-1)
1177	23770	AA998488	SS	(asilom) C solomod
1418	12766	AI012505	SSS	diacylglycerol O-acyltransferase 2, diacylglycerol O-acyltransferase fromoug 2 (modacy)
		T		[H.sapiens], NAD(P)H dehydrogenase, quinone 1, NAD(P)H dehydrogenase, quinone 2,
920	22612	2 AA945624	000	NAD(P)H menadione oxioored oxiooxiooxiooxiooxiooxiooxiooxiooxiooxi

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<u>.</u> <u>@</u>	(D) No.	RefSeq [D]	Model Gode	Known Genel Namer, Human Indiagous School State Component of The Component	mide dehydrogenase (E3 component of
1579	5607	A1045119	MM	dihydrolipoamide denydrogeriase, uiriyarolipoamide denydrogenase complex, branched chain keto acid pyruvate dehydrogenase complex), expressed sequence Al746344, thioredoxin reductase 1 dehydrogenase complex), expressed sequence Al746344, thioredoxin reductase 1	ate complex, branched chain keto acid AI746344, thioredoxin reductase 1
0/61		1		DIPB protein, ESTs, Weakly similar to 143483 translation latter in 2 from 52 graphs in	translation initiation ractor in 2 normals stein DKFZp761F2014, translation
931	21974	AA945769	Ω, R	initiation factor IF2	olog 2 (Drosophila), disabled homolog 2,
3544	4504	NM 024159	ЬЬ	disabled nomolog 1 (Diosophila), disabled mitogen-responsive phosphoprotein (Drosophila)	a)
2037	8794	A1170002	ပ္ပ	discs, large homolog 2 (Drosophila), discs, large homolog 2, chapsyn-110 (Drosophila)	le homolog 2, chapsyn-110 (Drosophila)
202	5			dishevelled 2, dsh homolog (Drosophila), dishevelled, dsh homolog 1 (Drosophila), dishevelled, dsh homolog 1 (Drosophila),	elled, dsh homolog 1 (Drosophila),
1782	3537	AI101690	SS	dishevelled, dsn nomolog s (Urosoprina)	
1148	2354	AA997763	C, L, Z, GG, HH	DKFZP434B027 protein	
2496	7881	AI230528	z	DKFZP434B0335 protein EXTERN 224 154 protein FSTs Moderately similar to T12539 hypothetical protein	nilar to T12539 hypothetical protein
				DKFZP4343134 plotein, LOTS, modernory CDNA FLJ13282 fis, clone DKFZp4343154.1 [H.sapiens], Homo sapiens cDNA FLJ13282 fis, clone OVARC1001092, highly similar to Homo sapiens mRNA for JM5 protein, hypothetical contein FLJ10055	cDNA FLJ13282 fis, clone ns mRNA for JM5 protein, hypothetical
1448	$\neg r$	AI013442	R O	DKFZp434J1813 protein	
2723	73422	A11.2034		DKFZp434P106.1 [H.sapiens], hypothetical protein FLJ14906, hypothetical protein from	r to 11/23/ nypometical protein otein FLJ14906, hypothetical protein from
755	5009	AA924737	×	EUROIMAGE 588495 DKFZP564B167 protein, RIKEN cDNA 2010002107 gene, RIKEN cDNA 2610205H19	02107 gene, RIKEN cDNA 2610205H19
1385	14267	A1011738	U, FF	gene	ar to T08675 hypothetical protein
2115			FFF, General Alternate	DKFZp564F0522.1 [H.sapiens], Homo sapiens cDNA FLJ25180 fis, clone CBR09247	s cDNA FLJ25180 fis, clone CBR09247
2					

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Antolines) Bocurrent No. 1995828.1		Win Gene Name I fluman notified by Section 1131 and 1157 protein, EST, Weakly similar to B24264 proline-rich protein MP3	mouse [M.musculus], EST, Weakly similar to B36298 proline-rich protein PKB39 mouse [M.musculus], EST, Weakly similar to CGHU3B collagen alpha 3(IV) chain precursor, long [H.sapiens], EST, Weakly similar to CGHU3B collagen alpha action protein PRB1/2S	splice form [H.sapiens], EST, Weakly similar to D407.30 profine-rich protein precursor IH.sapiens], EST, Weakly similar to PIHUB6 salivary profine-rich protein precursor IH.sapiens], EST, Weakly similar to PIHUB6.	PRB1 [H.sapiens], EST, Weakly similar to PRP1_HUMAN SALIVARY FINCE TO PRB1 [H.sapiens], EST, Weakly similar to T34520 hypothetical	protein DKFZp564J157.1 [H.sapiens], ESTs, Highly similar to 134320 riypounement	protein DKFZp564J157.1 [n.sapletts], CO13, WORK jumilar to T34520 hypothetical protein MP3 - mouse [M.musculus], ESTs, Weakly similar to T34520 hypothetical	protein DKFZp564J157.1 [H.sapiens]	DKFZP564K1964 protein, E313, modelacy comments	DKFZp564K1954.1 [n.saple18]	DK FZP566C0424 protein		DKFZP586B1621 protein	DKFZP586D0623 protein, hypothetical protein MGC1203	DKFZP586F1524 protein	DKFZP586F1918 protein, EST, Weakly Silling to 1007 10 10 10 10 10 10 10 10 10 10 10 10 10	DKFZp586F1918.1 [H.saplens], mucin o, gasuro	DKFZF2000011 procein, E013, morvegicus], ESTS, Weakly similar to 161730 polypeptide 1C short splice form - rat [R.norvegicus], ESTS, Weakly	lamina associated polypeptide 1C short splice joint 1 at 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2	similar to 108707 produce lamina cooperation in Mus musculus, clone MGC:6357 Homo sapiens, clone IMAGE:4651703, mRNA, Mus musculus, clone IMAGE:4651703, mRNA, mas musculus, clone IMAGE:4651703, mRNA, clone IMAGE:4651703, mRNA, clone IMAGE:4651703, mRNA, clone IMAGE:4651703, clone	IMAGE:3493883, mRNA, complete cds	
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122																						

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Cantonical Coormant No. 1995826.1	an Hömölögövs Merken Kemplogovs Sequence Glüster Wille	DKFZP586G011 protein, ESTs, Weakly similar to T08767 probable lamina-associated protein DKFZp586G011.1 [H.sapiens], Mus musculus, clone MGC:6357	IMAGE:3493883, mRNA, complete cas DKEZP586G1517 protein, EST, Moderately similar to A Chain A, Human	Tetrahydrofolate Dehydrogenase [H.sapiens], ESTs, Highly similar to T17244 Tetrahydrofolate Dehydrogenase [H.sapiens], ESTs, Weakly similar to hypothetical protein DKFZp586G1517.1 [H.sapiens], ESTs, Weakly similar to hypothetical protein DKFZp586G1517.1 [H.sapiens], ESTs, Weakly similar to C1TC_RAT C-1-tetrahydrofolate synthase, Methenyltetrahydrofolate dehydrogenase; Methenyltetrahydrofolate synthetase] [R.norvegicus], expressed sequence Al647056, Formyltetrahydrofolate synthetase] [R.norvegicus],	hypothetical protein FLJ13105 hypothetical protein FLJ13105 hypothetical protein MAD homolog 1 (Drosophila), MAD, mothers against	decapentaplegic homolog 1 (Drosophila)	UKFZF30000120 protein	DNA polymerase epsilon, subunit 3, ESTs, Moderately similar to CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A [M.musculus], ESTs, Weakly similar to A23692 transcription factor, CCAAT-binding, chain A1 - rat [R.norvegicus], RIKEN a23692 transcription factor, CCAAT-binding, chain A1 - rat [R.norvegicus], RIKEN cDNA 1810034K18 gene, down-regulator of transcription 1, down-regulator of transcription 1, TBP-binding (negative cofactor 2), nuclear transcription factor Y, beta, polymerase (DNA directed), epsilon 3 (p17 subunit) nuclear transcription factor-Y beta, polymerase (DNA directed), epsilon 3 (p17 subunit) DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed, EST, Weakly Similar to suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 1700010124 gene, RIKEN cDNA 2310040B03 gene, expressed sequence AW538196, sperm associated antigen 1, suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
	(Library	1000N						
		Model (Coco			x, Y, UUU	PP, QQ		LLL, UUU X, Y, BB, CC, DD, EE, KKK,
	उन्ताहरात्ता । शब्द वर्ग	ැමැපිලේ [D	U19614		AI235935	U66478	AA892310	AA817843 LLL, t X, Y, DD, E
ଙ) Series] • • • • • • • • • • • • • • • • • • •	1948		7307		_	1822
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3 3 3 3 3	<u>ම</u> ම්ම			tumani Homologous	
<u> </u>		RefSeq 10	Model Gode Land	Mn Generiame	DNA segment, Chr 11, Wayne State University 99, expressed, hypothetical protein FLJ14775, low density lipoprotein B, low density lipoprotein receptor defect B
94	18442	AA800258	ZZ. AAA	Complementing	complementing Noderately similar to
				hypothetical protein FLJ10416 simil IH. Sapiens], ESTs, Weakly similar t	hypothetical protein FLJ10416 similar to constitutive photomorph [Homo sapiens] H.sapiens], ESTs, Weakly similar to retinoblastoma binding protein 7 [Rattus
				norvegicus] [R.norvegicus], Mus mi	Dorvegicus] [R.norvegicus], Mus musculus, Similar to glutamate rich WD repeat protein provegicus] [R.norvegicus], Mace: 3408842, mRNA, partial cds, RIKEN cDNA 2610016K01 gene,
				RIKEN CDNA 2610529112 gene, co	RIKEN cDNA 2610529112 gene, constitutive photomorphogenic protein 1 (Arabidopsis),
3606	17535	NM 031816	۵	retinoblastoma binding protein 4, retinoblastoma binding protein 4	400 Signoblastoma billuling protein i
				DNA segment, Chr 14, ERAIO Do	DNA segment, Chr 14, ERA I O Doi 42b, expressed, E3 I s, I iighily similar construction in the time I'm saciens]. Mus
				plastin [H.sapiens], ES1s, Highly S	plastin [H.sapiens], ES1s, Highly similar to Apoppo plastin, integrind the programmy and C:6362
				IIIOSCUIUS, CICIE IIII COMPLETE III	Indections, closed minimages of the contraction of
4055	16300	X70706	000	plastin 1 (I isoform), plastin 2, L, plastin 3 (T isoform)	astin 3 (T isoform)
4533	20001	\neg		DNA segment, Chr 15, Wayne Sta	DNA segment, Chr 15, Wayne State University //, expressed, E.S.I., Moderatery Smillion
				to K2C8_RAT Keratin, type II cytos	to K2C8_RAT Keratin, type II cytoskeletal 8 (Cytokeratin 5) (Cytokeratin endo A)
				[R.norvegicus], ES1s, Moderately	[R.norvegicus], ES18, Moderately Sittilia to 157,502 (2017). The part of the p
			, н, W,	mKNA; CDNA DKTZP454C101 (11)	mKNA; cDNA DKFZp-3+C-101 (non-gone 2).
		10000	General	basic, gene 8	
4076	1460	876034	Allelliale	DNA segment, Chr 17, ERATO Do	DNA segment, Chr 17, ERATO Doi 479, expressed, EGF-like module containing, inuciii-
				like, hormone receptor-like sequer	like, hormone receptor-like sequence 1, EST, Highly similar to 1,00003 hypotherical like, hormone receptor-like sequence 1, EST, Weakly similar to EMR1 MOUSE CELL
-				protein DRFZp3d401923.1 [113d4]	protein UKFZp3040192311 (1.53pp.15), ECT, SON (M.musculus), ESTs, Weakly similar SI IRFACE GLYCOPROTEIN EMR1 PRECURSOR [M.musculus], ESTs, Weakly similar
				to EMR1 MOUSE CELL SURFAC	to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR
				[M.musculus], KIAA0758 protein,	[M.musculus], KIAA0758 protein, cadherin EGF LAG seven-pas G-type receptor 2,
7007	14463	NM 139110 Z. AA	Z. AA	hypothetical protein FLJ22684, latrophilin	rophilin
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	-682-					T/U	JS03/031		7
DNA segment, Chr 17, ERATO Doi 479, expressed, EGF-like module containing, mucinlike, hormone receptor-like sequence 1, EST, Weakly similar to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR [M.musculus], ESTs, Highly similar to lectomedin-2; KIAA0821 protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to EMR1 MOUSE CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR [M.musculus]	DNA segment, Chr 18, ERATO Dol 240, expressed, mas massed. hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit, clone MGC:7126 IMAGE:3158015, mRNA, complete cds, RIKEN cDNA 0610011L04 gene, acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase), t-	complex protein 1, related sequelice 1	dehydrogenase 7 family, member A1, aldehyde dehydrogenase family 1, subfamily A2	DNA segment, Cnr 2, Erval O Dol 403, CAP C33258 IMAGE:5324816, mRNA, complete gene amplified in osteosarcoma, clone MGC:38258 IMAGE:5324816, mRNA, complete cds, RIKEN cDNA 2610507E10 gene, RIKEN cDNA 2810418J22 gene, conserved gene amplified in osteosarcoma	DNA segment, Chr 3, ERATO Doi 555, expressed, ESTs, Weakly similar to A35210 ferroxidase (EC 1.16.3.1) precursor - rat [R.norvegicus], ESTs, Weakly similar to MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to	KUHU ferroxidase [H.sapiens], cerulopiasmin, celulopiasmin (terroxidase), inchesion of cerulopiasmin, celulopiasmin (terroxidase), inchesion of celifornia at Los Angeles 1, ESTs, Moderately	Similar to stress-associated endoplasmic reticulum protein 1; ribosome asso; ribosome associated membrane protein 4 [Homo sapiens] [H.sapiens]	DNA segment, Chr 3, University of California at Los Angeles 1, E313, Moderatory similar to stress-associated endoplasmic reticulum protein 1; ribosome asso; ribosome similar to stress-associated endoplasmic reticulum protein 1; ribosome asso; ribosome	associated membrane protein 4 [Homo sapiens] [n.sapiens]
ш		K, U, FF, LL	W	MM, PPP,		> . 2	SB. CC		п
NM 022962	1	NM 130433 K, U, FF, LL	875019	v		NM_012532	NIM 030835 BB CC		NM_030835

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<u> </u>		ESTs, Mo	۵ 06 1001	10 0449	ar 10 2 13 toin 647	MOTERN 2014	R.norvegic	ıs] [M.mut		similar to	orvegicus]	ENT PRO	ulin-deper	ed non-	VOCA -4-10	lar to Aso.	SIS, MODE	ALASE 24	YEN CON	npanut B (I	rotein MD		or.otto	בי מוקים י		
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		s 0593 e)	gicus], RI	1	ESI, We	milar to ri	AL PROT	2A09 [Mu	. S10	, ESTs, M	7.1.123)1	ODULIN-	ıs], calciuı	regnancy	ine kinase	, ESIS, H	hain [H.St	ROTEIN	RM [H.sa	ly 2A), re	n/progeni	I, Mus mu Sideriio II)	Clouria III)			
		's Genetic	t [R.norve	line rich 2	xpressed	Weakly Si	IROSOM	A 221040	nal protei	xpressed	se (EC 2.	UM/CALN	A.muscult	505105, p	ine/threor	expressed	gulatory c	CONINE	A ISOFO	2 (forme	oietic ster	expressed	(glutaric a	electrori-		
		& Womer	rotein - ra	0312, pro	Joi 429, e	ns], EST,	ar to 2113 AT 40S F	KEN CDN	e, ribosor	Doi 263. 6	otein kina	SE CALCI	CHAIN [quence Al	nase, ser	Doi 753, (2-alpha re	INE/THRE	T B, ALP	osphatase	1 hemator	Doi 394,	lypeptide	piete cds,		
		Brigham	line rich p	otein FLJ2	ERATO ((H.sapie	gniy simiii	ilar to RI	2A09 ger	FRATO	endent pr	C4 MOUS	TALYTIC	essed sec	ed CaM ki	, ERATO	phatase 2	NAN SER	SUBUNI	rotein pho	racterized	, ERATO	alpha po	RNA, com		
		nt. Chr 4,	4899 prol	hetical pro	int, Chr 4,	rotein S10	ESIS, H	ıy sırımarı erately sin	A 221040	Chr	dep-ulin-deb	ilar to KC	PE IV CA	ise I, expr	expresse	ent, Chr 7	otein phos	ABA_HUN	JLATORY	9 gene, p	rm, uncha	ent, Chr 9	voprotein,	16522, mF	iduria II)	
		Known Genelname, Indinam nome 1993 Services Communication of the Indiana Representation of the I	similar to JC4899 proline rich protein - rat [R.norvegicus], RIKEN cDNA 0610011E17	gene, hypothetical protein FLJ20312, proline rich 2	DNA segment, Chr 4, ERATO Doi 429, expressed, EST, Weakly similar to 21132000	ribosomal protein S10 [H.sapiens], EST, Weakiy similar to ribosomal protein S10	[H.sapiens], ESTS, Highly Similar to ZTT3200G Tibosoffial process 210 to the captures.	ESTs, mighty similar to RIKEN cDNA 2210402A09 [Mus musculus] [M.musculus],	RIKEN cDNA 2210402A09 gene, ribosomal protein S10	DNA segment Chr 6 ERATO Doi 263, expressed, ESTs, Moderately similar to S50193	Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat [R.norvegicus], ESTs,	Weakly similar to KCC4 MOUSE CALCIUM/CALMODULIN-DEPENDENT PROTEIN	KINASE TYPE IV CATALYTIC CHAIN [M.musculus], calcium/calmodulin-dependent	protein kinase I, expressed sequence AI505105, pregnancy upregulated non-	ubiquitously expressed CaM kinase, serine/threonine kinase PSKHZ	DNA segment, Chr 7, ERATO Doi 753, expressed, ES1s, Hignly similar to Asason	phosphoprotein phosphatase 2-alpha regulatory chain [H.sapiens], ESTS, Moderatery	similar to 2ABA_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE ZA, 33	KDA REGULATORY SUBUNIT B, ALPHA ISOFORM [H.sapiens], KIKEN CUNA	1300017E19 gene, protein phosphatase 2 (formerly 2A), regulatory subunit B (PK 3Z),	alpha isoform, uncharacterized hematopoietic stem/progenitor cells protein MDSVZo	DNA segment, Chr 9, ERATO Doi 394, expressed, Mus musculus, Sillilla to electron-	transfer-flavoprotein, alpha polypeptide (glutaric aciduria II), cione ivioc. 0-10 i	IMAGE:2646522, mRNA, complete cds, electron-transier-navoprotein, alpina por prepriod	(glutaric aciduria II)	
	Snobo		<u></u>	Ö		Έ_	<u>ٿ ي</u>	<u>u w</u>	8		<u> </u>	<u> </u>	<u> </u>	<u>α</u>	<u> </u>		<u> </u>	_ <u> </u>	<u> </u>		10		<u>+-</u>		Ť	
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TABLE 8) (9)		4151					3607		· ·		· <u>-</u>		2966	3					4019				299	

TABL	TABUE S :				The control of the co
	ਜ਼ ਂ ਜ਼	Centenika Var or		Human Homologous	
; ; ; e		<u>,</u>	Model Gode	Known Genei Name	own Genei Namer Human Homologous Sequence Guster Title
			9 Section 10 Section 1		DNA segment, Chr 9, ERATO Doi 394, expressed, Mus musculus, Similar to electron-
					transfer-flavoprotein, alpha polypeptide (glutaric aciduria II), clone MGC:6481
					IMAGE:2646522, mRNA, complete cds, electron-transfer-flavoprotein, alpha polypeptide
299	16435	AA894174	J, M, U		(glutaric aciduria II)
					DNA segment, Chr X, Celltech Chiroscience 3, Mus musculus, serine threonine Kinase
					pim3, clone MGC:27707 IMAGE:4924687, mRNA, complete cds, pim-1 oncogene, pim-
3499	21115	NM 022602 JJ. KK	XX XX		2 oncogene, proviral integration site 1
3					DNA segment, EST 1068184, ESTs, Highly similar to S68418 protein phosphatase 1M
					chain M110 isoform - rat [R.norvegicus], ESTs, Weakly similar to S68418 protein
					phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus], ESTs, Weakly
					similar to T42713 ankyrin 3, splice form 1 - mouse [M.musculus], RIKEN cDNA
			General Core		1810037O03 gene, leukocyte receptor cluster (LRC) member 3, protein phosphatase 1,
2216	2532	A1176590	Tox Markers		regulatory (inhibitor) subunit 12A
277	3	222			DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily A,
					member 4, DnaJ (Hsp40) homolog, subfamily B, member 1, DnaJ (Hsp40) homolog,
					subfamily B, member 12, ESTs, Weakly similar to DJA1_MOUSE DnaJ homolog
		<u>.</u>			subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2)
			_		[R.norvegicus], ESTs, Weakly similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2
					[H.sapiens], Homo sapiens cDNA FLJ13992 fis, clone Y79AA1002139, weakly similar to
					DNAJ PROTEIN HOMOLOG 1, RIKEN CDNA 1700014P03 gene, RIKEN CDNA
_					2010306G19 gene, RIKEN cDNA 5730551F12 gene, similar to MRJ gene for a member
390	16318	AA859648	0		of the DNAJ protein family (H. sapiens)
3	2		3		

	IBS.	Centent Accor Resor	Modeli Godo	Human Homologous Known Gene Neme Human II	The Attorney Docket (4/92)-5033-0/1W0 The Document No. 1935328.1 The Manager of the Comment of
					DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily A, member 4, ESTs, Highly similar to HS44 MOUSE HEAT SHOCK 40 KDA PROTEIN 4
				[M.muscr	[M.musculus], ESTs, Moderately similar to DJA1_MOUSE DnaJ homolog subfamily A
				member	member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2)
				[R.norveç	[R.norvegicus], ESTs, Weakly similar to DnaJ-like protein [Rattus norvegicus]
				PROTEIN	PROTEIN 4 [M.musculus], Homo sapiens mRNA full length insert cDNA clone
				EUROIM	EUROIMAGE 730912, Mus musculus SEC63 (Sec63) mRNA, complete cds, similar to
100	6892	AA800551	ø	DNAJ	
				Hs) (Hs)	DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily A,
				member	member 4, ESTs, Highly similar to HS44 MOUSE HEAT SHOCK 40 KDA PROTEIN 4
				[M.muscr	[M.musculus], ESTs, Moderately similar to DJA1_MOUSE DnaJ homolog subfamily A
				memper	member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2)
				[R.norvec	[R.norvegicus], ESTs, Weakly similar to DnaJ-like protein [Rattus norvegicus]
				R.norvec	[R.norvegicus], ESTs, Weakly similar to HS44 MOUSE HEAT SHOCK 40 KDA
				PROTEIN	PROTEIN 4 [M.musculus], Homo sapiens mRNA full length insert cDNA clone
				EUROIM,	EUROIMAGE 730912, Mus musculus SEC63 (Sec63) mRNA, complete cds, similar to
3520	6891	NM_022934	EE	DNAJ	
				DnaJ (Hs	DnaJ (Hsp40) homolog, subfamily A, member 1, DnaJ (Hsp40) homolog, subfamily B,
				member	member 6, DnaJ (Hsp40) homolog, subfamily C, member 7, DnaJ-like protein, ESTs,
				Highly sir	Highly similar to HS44 MOUSE HEAT SHOCK 40 KDA PROTEIN 4 [M.musculus],
				Homo sa	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 730912, RIKEN cDNA
753	5003	AA924691	n n	49304831	4930483N21 gene
				DnaJ (Hs	DnaJ (Hsp40) homolog, subfamily A, member 2, DnaJ (Hsp40) homolog, subfamily B,
				member	member 2, DnaJ (Hsp40) homolog, subfamily B, member 6, RIKEN cDNA 2810451A06
	_			gene, RIF	gene, RIKEN cDNA 4930483N21 gene, RIKEN cDNA 5730496F10 gene, expressed
1727	5021	AI072308	RR	sedneuce	sequence Al506245

DnaJ (Hsp40) homolog, subfamily B, member 3, DnaJ (Hsp40) homolog, subfamily B,
DnaJ (HSp4U) nomolog, subfamily B, member 3, DnaJ (HSp4U) nomolog, subfamily B, member 6, RIKEN cDNA 2810451A06 gene, expressed sequence Al506245, expressed
ene, expressed sequer
-
sequence AU020082 DnaJ (Hsp40) homolog, subfamily C, member 8, Homo sapiens cDNA FLJ13613 fis,
molog, subfamily
sequence AU020082 DnaJ (Hsp40) homolog, subfamily C, member 8, Homo sapiens cDNA FLJ13613 fit clone PLACE1010856, Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone
sequence AU020082 DnaJ (Hsp40) homolog, subfamily C, member 8, Homo s clone PLACE1010856, Homo sapiens mRNA; cDNA DK
Seque clone
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TABLE 3	ତ୍ର ୍ବ				And the second of the second o
	eres. Idins.	Geneenak : Aee or ' Rafseq (D)	Model Code	Rumen Romologous Knovareene Nemer	nen Romologous warGene Namo - Humanikiomologous Sequence Cluster Titlo
4013	19150	NM_139324	V, UU, General Alternate	1. P	EH-domain containing 4, ESTs, Highly similar to intersectin 2 [Homo sapiens] [H.sapiens], SH3 domain protein 1B, expressed sequence Al197390, intersectin (SH3 domain protein 1A), intersectin 1 (SH3 domain protein)
561	19226	AA892394	ZZ, AAA	ш = = ш п = =	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B), ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C), ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), ESTs, Highly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus], ESTs, Moderately similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
				ш .	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B), ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C), ELAV (embryonic
561	19227	AA892394	Ξ	<u>я</u> ш а г	lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), ESTS, Highly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus], ESTs, Moderately similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
				ш э б	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B), ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), ESTs, Highly similar to ELV4 RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen
				<u> </u>	HuD) (Hu-antigen D) [R.norvegicus], ESTs, Moderately similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D)
	·			<u> </u>	IR.norvegicusj, ESTS, Moderately Similar to PABT MOUSE POLTADEN TLATE- BINDING PROTEIN 1 [M.musculus], ESTS, Weakly similar to PAB1 MOUSE POLYADENYLATE-BINDING PROTEIN 1 [M.musculus], RIKEN cDNA 4932702K14
775	10666	AA925212	SS, ZZ, AAA	<u> </u>	gene, poly A binding protein, cytoplasmic 1, poly(A) binding protein, cytoplasmic 4 (inducible form)
2331	17358	A1179147	PP, QQ	a	electron-transfer-flavoprotein, beta polypeptide
2205	17920	AI176422		9	electron-transferring-flavoprotein dehydrogenase

Attorney Docket (49271-5058-011WO	nani Homologous Humani Homologous Sequence Gluster Tittle En	ELL-related RNA polymerase II, elongation factor, ESTs, Weakly similar to ELL MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL [M.musculus], Mus musculus, clone IMAGE:3583970, mRNA, partial cds, RIKEN cDNA 9430098E02 gene, elevennineteen lysine-rich leukemia gene, hypothetical protein FLJ22637	embryonic ectoderm development embryonic ectoderm development crk-associated substrate related),	enhancer of filialite flatter (cas like cooking) of expressed, developmentally down-expressed sequence Al385681, neural precursor cell expressed, developmentally down-regulated gene 9, signal transduction protein (SH3 containing), v-crk-associated tyrosine kinase substrate	enhancer of rudimentary homolog (Drosophila)	carcinoma-associated antigen 64 (HCA64) mRNA, complete cds, RIKEN cDNA carcinoma-associated antigen 64 (HCA64) mRNA, complete cds, RIKEN cDNA 1300014E15 gene, RIKEN cDNA 1300017C12 gene, RIKEN cDNA 1810022C23 gene, RIKEN cDNA 2010015A21 gene, RIKEN cDNA 4930453I21 gene, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hypothetical protein FLJ10948, peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	ephrin A1, ephrin-A1 lepithelial membrane protein 3	EPS8 related protein 2, epidermal growth factor receptor pathway substrate 8 related protein 3 protein 1, epidermal growth factor receptor pathway substrate 8 related protein 3	phosphatase 2a, phosphatidic acid phosphatase type 2A, phosphatidic acid phosphatase type 2C, phosphatidic acid phosphatase type 2C, phosphatase type 2C, phosphatase type 2C, phosphatase type 2C
	M egoe IN	DD. EE. WW	General Core Tox Markers	T, III, JJJ, KKK, General Alternate	999	11 88 88		SS.	BB, CC, NN, OO, QQ, ZZ, AAA
	General			T X M 012931 MN	1	NM 053061	 	AA875641 S	NM_022538 /
		7913		18695	14962	16100	23194	21509	8597
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No. 1986		atalytic, sitol 4-ki	sione kinase,		ytosolic	rotein p6	ride	lar chann	norvegic		s, Moder	K.norve(N CDNA		ne 2 [Rat	r, SP-40	מושמשווי
Mionney weeke kaka keese-ende Doeument No. 1995323.1	1000	kinase, c te cds, hatidyline gamma p	kınase, d sitide-3-l		in S16, c	S16	Jene, chlo	ntracellul	Rattus		insj, EST	vegicus]	ne, RIKE	/ A7.) Boson o	is inhibito	ge z, apr
100 DO		nositol 4- A, comple de, phosp catalytic,	inositol 3 iosphoint	G, 01833	nal prote	protein	531E12 g	chloride i	n p64H1	-01 -01	: [H.sapie	attus nor	1 L 1 L 1 t 3 48F20 qe	subfamily	tetagrap	ement lys	te messa
		sphatidyll 73, mRN/ oolypeptic	sphatidyl te cds, pt	G-2-NII 193	6 riboso	ribosoma	NA 5730	annel 3,	nel protei	TUMAN.	GENASE	enase [R	V-rORW IA 18100	family 1,		ecandar.	ed prosta
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	ance Clu	ns, Simili 20 IMAG , catalytic hosphoin	lus, Simil 4, mRNA	phospr	similar t	ence AA	similal (Capital) Regions]. R	ide intrac	chloride	rmyitetra similar tr	ATED	rofolate (FIUH F	e dehydr	drogenas	terin; 1 es clusterin	osterone
	ris Sequi	mo sapie AGC:3193 4-kinase eptide, pl	s muscu :366109	Sypeptide rotrophin	r, Weakly	sed sedu	, weakiy R norve	1, chlor	acellular	to 10-10 T Highly	rorofo 7	Itetrahyd	similar to	aldehvd	ate dehy	r to Clusi vegicus],	in 2, test
	mologo.	7822, Ho e, clone N lylinositol eta polyp	7822, Mu 7 IMAGE	lamma po	7031, ES), expres	52, ES18	ar channe	drial), intr	ily similar	icusi, es TETRAH	10-formy	derately		ahydrofol	ıly similai is] [R.nor	lycoprote
	nzn Homologous own Genei Name Human Homologous Sequence Cluster III (18	EST AA437822, Homo sapiens, Similar to phosphatidylinositol 4-kinase, catalytic, alpha polypeptide, clone MGC:31920 IMAGE:4565073, mRNA, complete cds, phosphatidylinositol 4-kinase, catalytic, alpha polypeptide, phosphatidylinositol 4-kinase, catalytic, beta polypeptide, phosphoinositide-3-kinase, catalytic, gamma polypeptide	EST AA437822, Mus musculus, Similar to phosphatidylinositol 3-kinase, clone MGC:30377 IMAGE:3661094, mRNA, complete cds, phosphoinositide-3-kinase,	catalytic, gamma polypeptide, phosphoinosiide-3-kiilase, class o	EST A1317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic	[H.sapiens], expressed sequence AA420385, ribosomal protein S16	EST X83352, ESTS, Weakly Similar to intraceitate cristics of control of the property of the control of the cont	Indiana indiversional promotering intracellular channel 3, chloride intracellular channel 4 intracellular channel 4	(mitochondrial), intracellular chloride ion channel protein p64H1	EST, Highly similar to 10-formylitetranydrologiae derrydrogenado (************************************	[K.novegicus], ESTS, Inglify Silling Street of Procedures [H.sapiens], ESTS, Moderately FORMYLTETRAHYDROFOLATE DEHYDROGENASE [H.sapiens], ESTS, Moderately	similar to 10-formyltetrahydrofolate dehydrogenase [Rattus norvegicus] [K.norvegicus],	ESTs, Moderately similar to F1DH_HUMAN_10-F0KN11E1E1155011E15001 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	DEHYDROGENAGE [11.3aprend], http://dem.ii/ 1. subfamily A7,	formyltetrahydrofolate dehydrogenase	EST, Highly similar to Clusterin; Testostrone-Tepressed prostate incorpgion; SP-40,40, norvegicus] [R.norvegicus], clusterin, clusterin (complement lysis inhibitor, SP-40,40,	sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein 3,
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	nemk sor : Sæ (D		COOL ON INO	NM_022958_HH	NM_031073	A1009810			Al012221						NM 022547		NM 012679 . TT
	66 Acc				$\overline{}$	· . · · ·	7			1			- ·		12606 N		
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	ian Homologous Human Homologous Sequence Cluster Title	[R.norvegicus], ESTs, Highly similar to LMIP MOUSE LENS FIBER MEMBRANE [R.norvegicus], ESTs, Highly similar to LMIP MOUSE LENS FIBER MEMBRANE [R.norvegicus], ESTs, Highly similar to LMIP MOUSE LENS FIBER MEMBRANE [N.norvegicus], lens intrinsic membrane protein 2 (19kD), natural killer cell group 7 sequence intrinsic membrane protein 2 (19kD), natural killer cell group 7	EST, Highly similar to 1903270A phenylethanolamine N-meuryluansic actions of the mosculus of the methyltransferase [Rattus norvegicus] [R.norvegicus], Phenylethanolamine N-methyltransferase [Rattus norvegicus] [R.norvegicus], Phenylethanolamine N-methyltransferase, micotinamide N-methyltransferase, thioether S-methyltransferase	ES1, Highly similar to A43 (20 centrate A40043 notch protein homolog TAN-1 precursor [R.norvegicus], EST, Weakly similar to A40043 notch3 protein [H.sapiens], Notch homolog [H.sapiens], EST, Weakly similar to S78549 notch3 protein [H.sapiens], Notch homolog (2.0 nosophila)	EST, Highly similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUN I [H.sapiens], actin related protein 2/3 complex, subunit 1B (41 kD), actin related protein	2/3 complex, subunit 1B (41 kDa) EST Highly similar to AR41 HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT	[H.sapiens], actin related protein 2/3 complex, subunit 1B (41 kD), actin related protein 2/3 complex, subunit 1B (41 kDa) 2/3 complex, subunit 1B (41 kDa) EST Highly similar to BETA-1,4 N-ACETYLGALACTOSAMINYLTRANSFERASE	[M.musculus], RIKEN cDNA 4933429D13 gene, UDP-N-acetyl-alpha-D-[M.musculus], RIKEN cDNA 4933429D13 gene, UDP-N-acetylglucosaminylpolypeptide-beta-1, galactosamine:(N-acetylgalactosaminyltransferase, UDP-N-acetyl-alpha-D-galactosamine:(N-acetylgalactosaminyl)-galactosylglucosylceramide N-acetylgalactosaminyll-acetyl-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-(GalNAc-T), UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-	galactosylglucosylceramide-beta-1, 4-N-acetylgalactosalliilystation
	Humen Homologe Known Gene Nem								
		il	MM, III, JJJ, KKK, TTT		GG B 1 1 0 P	NN, 00, VV	A, O, NN, OO, VV		GG, WW
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G			5339		3693	10015	10016		179
RETIEW!	Seq.	12	3945 2406	3	1375	3387	3387		2853

4. 4. Feet 1	Z 90 1	v Z	Ic	<u> </u>	
Hogenment to be seed to the first of the fir	EST, Highly similar to C Chain C, Macrophage Migration Inhibitory Factor [H.sapiens], EST, Moderately similar to C Chain C, Macrophage Migration Inhibitory Factor [H.sapiens], EST, Moderately similar to MIF_RAT Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (Glutathione-binding 13 kDa protein) [R.norvegicus], ESTs, Moderately similar to MIF_HUMAN MACROPHAGE MIGRATION INHIBITORY FACTOR [H.sapiens], macrophage migration inhibitory factor, macrophage migration inhibitory factor (glycosylation-inhibiting factor)	EST, Highly similar to CA1B_HUMAN COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA1B MOUSE COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA1B_HUMAN COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [H.sapiens], ESTs, Highly similar to CA1B_HUMAN COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to CA1B MOUSE COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [M.musculus], RIKEN CA1B MOUSE COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [M.musculus], RIKEN CANA 223,000,7122, 2000.	1 1 The Calculation of the Company of the Calculation Channel alpha-1	EST, Highly similar to CCAC_RAT Voltage-uependent L-type cardian channel apprayed subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (RAT subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (RAT brain class C) (RBC) [R.norvegicus], ESTs, Highly similar to CCAC_HUMAN VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1C SUBUNIT [H.sapiens], ESTs, Highly similar to CCAD_HUMAN VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1D SUBUNIT [H.sapiens], Mus musculus putative ion channel protein CATSPER2 mRNA, complete cds, calcium channel, voltage-dependent, L type, alpha 1C subunit	EST, Highly similar to CYG2_HUMAN GUANYLATE CYCLASE SOLUBLE, BETA-2 CHAIN [H.sapiens], guanylate cyclase 1, soluble, beta 3
Human Homologous Known Gene Name					
Mecel Godo	>- H: 'U'		ш	>	A, B, M, FFF, HHH, KKK, NNN, OOO, General Core Tox Markers
ভেন্সোঃহুমার্য গুডুরু তুপ যুক্তিত্ব (টি	NM 031051		AI103332	302038	M57507
elec BNs.			13305	000	
\$ 000 mg	3590		1833		3024

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4630	010	4 P.OG. P.O.	A, B, EEE,	EST, Highly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus], Homo sapiens clone HQ0582, angiopoietin 2, angiopoietin-like 3, expressed sequence Al303526, fibrinogen, A alpha polypeptide, fibrinogen, alpha
1020	9304	Alcocola		polypeptide, florinogen, gamma polypeptide EST, Highly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus], Homo sapiens clone HQ0582, Mus musculus, Similar to angiopoietin-
1536	7891	AI043759	z	like factor, clone MGC:32448 IMAGE:5043159, mRNA, complete cds, angiopoietin, expressed sequence Al303526, fibrinogen, A alpha polypeptide, fibrinogen, gamma polypeptide
				EST, Highly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus], Homo sapiens clone HQ0582, Mus musculus, Similar to angiopoietin-like factor, clone MGC:32448 IMAGE:5043159, mRNA, complete cds, angiopoietin, expressed sequence Al303506, fibrinogen, Alpha polynomiale fibrinogen, alpha
2449	7892	AI229172	z	polypeptide, fibrinogen, gamma polypeptide
3224	22582	NM_013120	A, B, G, S, GGG, OOO, General Core Tox Markers	EST, Highly similar to GCKR RAT GLUCOKINASE REGULATORY PROTEIN [R.norvegicus], Mus musculus, Similar to Glucokinase regulatory protein, clone MGC:19300 IMAGE:4159892, mRNA, complete cds, glucokinase (hexokinase 4) regulatory protein
				EST, Highly similar to HEMO_RAT 5-AMINOLEVULINIC ACID SYNTHASE, ERYTHROID-SPECIFIC, MITOCHONDRIAL PRECURSOR (DELTA-AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-E) [R.norvegicus], ESTs, Highly similar to SYHUAE 5-aminolevulinate synthase
3232	16448	NM_013197_M, T	, т	[H.sapiens], aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia), aminolevulinic acid synthase 1, aminolevulinic acid synthase 2, erythroid, glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase), glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)

Known Gene Name Kuman Homologovs Sequence Gluster (116)		EST, Highly similar to HS9B MOUSE HEAT SHOCK PROTEIN HSP 90-BETA [M.musculus], ESTs, Highly similar to HS9A HUMAN HEAT SHOCK PROTEIN HSP 90-BETA [M.musculus], ESTs, Highly similar to T46243 hypothetical protein	DKFZp/61K0511.1 [H.sapiens], expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, heat shock protein, 86 kDa 1	EST, Highly similar to HS9B MOUSE HEAT SHOCK PROTEIN HSP 90-BETA [M.musculus], EST, Weakly similar to HHMS84 heat shock protein 84 - mouse [M.musculus], ESTs, Highly similar to HS9A_HUMAN HEAT SHOCK PROTEIN HSP 90-ALPHA [H.sapiens], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1 [H.sapiens], expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, heat shock protein, 86 kDa 1	EST, Highly similar to I53960 PRR2 alpha [H.sapiens]	EST, Highly similar to IM10_RAT MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10 [R.norvegicus], translocase of inner mitochondrial membrane 10 homolog (yeast), translocase of inner mitochondrial membrane 13 homolog a (yeast)
Model Gede	<u>.</u>		XX, YY	F, J, S, RR	General Core Tox Markers, General Alternate	MM, TTT
Reference	0.007820		A1008074	A1236795	AA900198	A1180367
77.03/12.3 Seq. (eugg Seq. (eugg	45 848		15849	15850	10555	22835
7ABL 3eq.	1.05.F.		1267	2753	705	2386

	EST, Highly similar to JT0752 lymphocyte activation-induced receptor ILA precursor [H.sapiens], tumor necrosis factor receptor superfamily, member 9	ĹĹ	A1236084	11465	2716
	(formerly 2A), regulatory subunit B (PR 52), alpha isoform	F, SS, NNN	NM_147214	16963	4036
	4833423D12 gene, caldesmon 1, major urinary protein 4, protein phosphatase 2			•	
	IMAGE:5148205, mRNA, complete cds, RIKEN cDNA 2410004D02 gene, RIKEN cDNA				
	[H.sapiens], Mus musculus, Similar to Caldesmon 1, clone MGC:30319			•	•
	similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin				•
	phosphoprotéin phosphatase 2-alpha regulatory chain [H.sapiens], ESTs, Weakly				_
	EST, Highly similar to JH0628 caldesmon [H.sapiens], ESTs, Highly similar to A38351				
	expressed gene 261	R	AA892260	24295	548
	[R.norvegicus], Homo sapiens, clone IMAGE:3855224, mRNA, partial cds, testis	•		•	
	EST, Highly similar to JC5386 steroidogenic acute regulatory protein - rat			· -	
	S15A [H.sapiens], ribosomal protein S15a	L .	NM_053982	15468	3862
	[R.norvegicus], ESTs, Highly similar to RS1A_HUMAN 40S RIBOSOMAL PROTEIN				
	EST, Highly similar to JC2234 ribosomal protein S15a, cytosolic [validated] - rat				L_
	moderately similar to 40S RIBOSOMAL PROTEIN S15A	X	NM_053982	19544	3862
	S15A [H.sapiens], Homo sapiens cDNA FLJ13026 fis, clone NT2RP3000968,				
	[R.norvegicus], ESTs, Highly similar to RS1A_HUMAN 40S RIBOSOMAL PROTEIN				
	EST, Highly similar to JC2234 ribosomal protein S15a, cytosolic [validated] - rat				·
	membrane 8 homolog b (yeast)	רור	NM_022541	9536	3485
•	inner mitochondrial membrane 8 homolog B (yeast), translocase of inner mitochondrial				
	subunit TIM8 B (Deafness dystonia protein 2 homolog) [R.norvegicus], translocase of				
	EST, Highly similar to IM8B_MOUSE Mitochondrial import inner membrane translocase				
	Kinowin Gene Name Humani Homologous Sequence Guster Mile	Model ලැලෙ		(D)	(ID)
	Human Homologous 1900 1900 1900 1900 1900 1900 1900 1900 1900 1900 1900 1900 1900		Ace or	<u>@</u>	Sed
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Part British	ogous ame	EST, Highly similar to KF1D_RAT Kinesin-like protein KIF1D [R.norvegicus], ESTs, Lizely, cimilar to KF1D_RAT KINESIN-I IKE PROTEIN KIF1C [H.sapiens], ESTs,	Weakly similar to KF1C_HUMAN KINESIN-LIKE PROTEIN KIF1C [H.sapiens], ESTs, woodly, similar to KF1C_HUMAN KINESIN-LIKE PROTEIN KIF1A [M.musculus], ESTs, Weakly similar	to RB6K MOUSE RABKINESIN-6 [M.musculus], KIAA1448 protein, Mus musculus kif1C	mRNA for kinesin superfamily protein 1C, complete cds, RIKEN cDNA 3000004C01 gene, Rab6, kinesin-like, kinesin 13B, kinesin family	member 1C	EST, Highly similar to M2GD_HUMAN DIME I HYLGLYCINE DENTUNCOLINGE.	MILOCHONDRIAL PRECONSON (1.134pts), CO. S. MONTOS (R.norvegicus), RIKEN CDNA DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR [R.norvegicus], RIKEN CDNA	1200014D15 gene, dimethylglycine dehydrogenase precursor, expressed sequence	AW495222, hypothetical protein FLJ100/9	EST, Highly similar to MZGD_HOMAN DIME ITTICAL CINE DELITION OF A MAINTOCHON DEFO. IRSOR IT saniens]. ESTS. Weakly similar to	MILLOCHONDRING INCOME INTEREST INTEREST (R. norvegicus), RIKEN CDNA	1200014D15 gene, dimethylglycine dehydrogenase precursor, expressed sequence	AW495222, hypothetical protein FLJ10079, sarcosine dehydrogenase	EST, Highly similar to MYHA_RAT Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) [R.norvegicus], ESTs, Highly similar to MYHA_MOUSE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) [M.musculus], Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA, Myosin heavy chain 11, RIKEN cDNA 5730504C04 gene, laminin, gamma 1
										RR			r, G, MN, CC,	Alternate	C, General Alternate
	<u>एकताइकात्र</u> शिख वर्गः सन्दर्भन्तः शि	5				A1136892				AA891589				NM_139102	Al009131
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					EST, Highly similar to MYHA_RAT Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B)
		_			type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) [M.musculus], Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly
4278	18031	X94551	RR.		similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mKNA, Myosin heavy chain 11, RIKEN cDNA 5730504C04 gene, laminin, gamma 1
			III, JJJ, 000,		EST, Highly similar to OM25_RAT MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25 (NPW16) [R.norvegicus], EST, Weakly similar to OM25_RAT Mitochondrial outer
370	21025	AA859241	General Core Tox Markers		membrane protein 25 (NPW16) [R.norvegicus], hypothetical protein FLJ11271, synaptojanin 2 binding protein
					EST, Highly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7 (PROTEASOME SUBUNIT XAPC7) [H.sapiens], EST_Highly similar to Se0038 multipatalytic and promitidate sounds (EC 3.4 99.48)
	<u> </u>				alpha chain RC6-1 - rat [R.norvegicus], Homo sapiens, similar to Proteasome subunit
2368	9032	A1179950	K, TT, LLL,		complete cds, RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, albha tvoe 7, proteasome (prosome, zubunit, albha tvoe 7, proteasome (prosome, macropain) subunit, albha tvoe 7, proteasome (prosome, macropain) subunit, albha tvoe 7
					EST, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus], EST, Weakly similar to E54024 protein kinase [H.sapiens], ESTs, Highly similar to ROTEIN L23A [R.norvegicus] ESTs, Highly similar to
					RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], Mus musculus, ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds, ribosomal protein
220	20845	2520 20845 AI231140	X, Y, AA, TT		L23a

	expressed sequence AL024098, ribosomal protein L8	F, G, H	15876 AA892582	15876	280
	Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus],				
	Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], ESTs,				_
	similar to R5RTL8 ribosomal protein L8, cytosolic [validated] - rat [R.norvegicus], ESTs,				
	Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly				
	EST, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus], EST,				
	L23a	Alternate	X65228	20844	4248
	ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds, ribosomal protein	General			
	RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], Mus musculus,				·
	similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus], ESTs, Highly similar to				
	[R.norvegicus], EST, Weakly similar to E54024 protein kinase [H.sapiens], ESTs, Highly				<u>.</u>
	EST, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat				
	L23a	N, XX, YY	2520 20846 AI231140	20846	2520
	ribosomal protein L23a, clone IMAGE:4988735, mRNA, partial cds, ribosomal protein				
	RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], Mus musculus,				
Ž	similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus], ESTs, Highly similar to				
	R.norvegicus], EST, Weakly similar to E54024 protein kinase [H.sapiens], ESTs, Highly				
	EST, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat				
	Known Genenkine / Human Homologous Sequence Quister, titue	Model Gode	RefSej [D	 ID (No.)	0
	HumaniHomologous Commenter		læer.	<u>@</u>	Seg
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e	16000		A Section of the sect	<u></u>	TABLE 3

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man Homelegous Homelegous Homelegous Seavence (cluster mile)	IRUS-R IRUS-R probable o S213 cDNA:	DKFZp547C014), Human kpni repeat mrna (cdna clone pcd-kpin-o), 3 cm, mas musculus, Similar to hypothetical protein FLJ10134, clone MGC:25912 IMAGE:4221959, mRNA, complete cds, RIKEN cDNA 4933411E06 gene, RIKEN cDNA 6820402119 gene, colon and small intestine-specific cysteine-rich protein precursor, smooth muscle cell-expressed and macrophage conditioned medium-induced protein smag-64	EST, Highly similar to S21348 probable pol polyprotein-related protein 4-1 at [R.norvegicus], ESTs, Highly similar to POL2 MOUSE RETROVIRUS-RELATED POL [R.norvegicus], ESTs, Highly similar to S21348 probable pol polyprotein-related protein 4 - rat [R.norvegicus], ESTs, Moderately similar to S21348 probable pol polyprotein-related protein 4 - rat [R.norvegicus], Homo sapiens cDNA: FLJ22714 fis, polyprotein-related protein 6 - rat [R.norvegicus], Homo sapiens cDNA: FLJ22714 fis, clone HSI13646, Homo sapiens mRNA; cDNA DKFZp547C014 (from clone pcd-kpni-8), 3' end, Mus	musculus, Similar to hypothetical protein FLJ10134, clone MGC::25912 IMAGE:4221959, mRNA, complete cds, RIKEN cDNA 4933411E06 gene, RIKEN cDNA 6820402119 gene, colon and small intestine-specific cysteine-rich protein precursor, smooth muscle cell-expressed and macrophage conditioned medium-induced protein smag-64
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	Attorney Booket (4492/1-5933-61/W) Document No. 1935/23.1	n Komologous A Gene Name Furnan Homologous Sequence Guster Wilde	EST, Highly similar to S611_HUMAN Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1) [R.norvegicus], ESTs, Highly similar to S611_HUMAN Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1) [R.norvegicus], SEC61, alpha subunit (S. cerevisiae), SEC61, alpha subunit 2 (S. cerevisiae), Sec61 alpha form	EST, Highly similar to STA3_RAT Signal transducer and activator of transcription 3 IR norvegicus], signal transducer and activator of transcription 3, signal transducer and	activator of transcription 3 (acute-phase response factor)	[R.norvegicus], stathmin-like 4	EST, Highly similar to 100333 hypothetical protein Not 300 (1.134) protein prote	EST, Highly similar to 114795 hypothetical protein DNI ZPASALLI (1.10272017)	PEX1, Highly similar to TEXA TOWAY [1.35p.c.iz], TOT I [H.sapiens], EST, Weakly PEX1_HUMAN PEROXISOME BIOGENESIS FACTOR 1 [H.sapiens], ESTs, Weakly similar to T46437 hypothetical protein DKFZp434K0126.1 [H.sapiens], ESTs, Weakly similar to T46437 hypothetical protein DKFZp434K0126.1 [H.sapiens],	similar to TERA MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE similar to TERA MOUSE TRANSITIONAL ENDOPLASMIC [M.musculus], ESTS, Weakly similar to TERA_RAT TRANSITIONAL ENDOPLASMIC DETICALL IN ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT)	(VALOSIN CONTAINING PROTEIN) (VCP) [CONTAINS: VALOSIN] [R.norvegicus]	EST, Moderately similar to acidic ribosonial protein For National Control of Section 19 (Rattus norvegicus) [R. norvegicus], EST, Weakly similar to acidic ribosomal protein P0 [Rattus norvegicus] [R. norvegicus], EST, Weakly similar to RLA0 MOUSE 60S ACIDIC PROTEIN P0 [M.musculus], ESTs, Highly similar to RLA0 MOUSE 60S ACIDIC processing PROTEIN P0 [M.musculus], ESTs, Highly similar to RLA0_HUMAN 60S	ACIDIC RIBOSOMAL PROTEIN P0 [H.sapiens], RIKEN cDNA 2610025P08 gene, acidic ribosomal phosphoprotein PO, ribosomal protein, large, P0
		Hrman Komologous Known Gene Name											
		Andreas Code			טט, ווו, אא	<u></u>	N. U. BBB				BB, CC		v, cc, ll, DDD
		Senistini Secor Refeq D		AI231217	A1008865			Т			AA956437		NM_022402
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				E6	EST, Moderately similar to HLA-B-associated transcript 1A; DNA segment, Chr 17, human DSS1F 1: nuclear RNA helicase Bat1 [Mus musculus] [M.musculus], EST,
				- N	Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47
				R	[R.norvegicus], ESTs, Moderately similar to IF41_HUMAN EUKARYOTIC INITIATION
				FA	FACTOR 4A-I [M.musculus], ESTs, Weakly similar to HE47 RAT PROBABLE ATP-
			0		DEPENDENT KINA HELICASE F47 [R. ildivegicus], Tilca-B-associated danisaript 17.; Biken cona 2410004K13 dene. RIKEN cona 2600001H07 dene, RIKEN cona
			Core Tox	26	2610307C23 gene, eukaryotic translation initiation factor 4A, isoform 1, eukaryotic
716	3822	AA900863	Markers	tra	translation initiation factor 4A1
<u>.</u>				3	EST, Moderately similar to HLA-B-associated transcript 1A; DNA segment, Chr 17,
				<u></u>	human D6S81E 1; nuclear RNA helicase Bat1 [Mus musculus] [M.musculus], EST,
· 				×	Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47
				<u>R</u>	[R.norvegicus], ESTs, Moderately similar to IF41_HUMAN EUKARYOTIC INITIATION
				74	FACTOR 4A-I [M.musculus], ESTs, Weakly similar to HE47 RAT PROBABLE ATP-
			FFF, GGG.	<u></u>	DEPENDENT RNA HELICASE P47 [R.norvegicus], HLA-B-associated transcript 1A,
<u>. </u>			HHH, General	<u>~</u>	RIKEN cDNA 2410004K13 gene, RIKEN cDNA 2600001H07 gene, RIKEN cDNA
•			Core Tox	26	2610307C23 gene, eukaryotic translation initiation factor 4A, isoform 1, eukaryotic
2609	3823	AI233147	Markers	tre	translation initiation factor 4A1
				Ü	EST, Moderately similar to mitochondrial intermediate peptidase [Rattus norvegicus]
				또.	[R.norvegicus], RIKEN cDNA 5730405E07 gene, mitochondrial intermediate peptidase,
3591	11899	NM 031052	000	\$	thimet oligopeptidase 1
					EST, Moderately similar to RIKEN cDNA 1700113017 [Mus musculus] [M.musculus],
	:			Ï	H2A histone family, member L, Homo sapiens, clone MGC:21597 IMAGE:4511035,
					mRNA, complete cds, Mus musculus, similar to H2A histone family, member O, clone
124	23115	AA801165	=	2	MGC:36202 IMAGE:5055276, mRNA, complete cds, expressed sequence R75370
				ú	EST, Moderately similar to tripeptidy/peptidase II [Rattus norvegicus] [R.norvegicus],
			Q, R, PPP,	<u>ú</u>	ESTs, Highly similar to TRIPEPTIDYL-PEPTIDASE II [M.musculus], tripeptidyl
3616	15487	NM 031137		ă	peptidase II

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erately	to 08061 OI [H.sapie	to 0806 30i [H.sapie	Jerately to 0806 SOI	[H.sapie derately	r to 0806 COI I [H.sapi	rotein U Moderal r to 8100	
HumaniHomologousiSequencei@luster/IIIIIle	similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], [M.musculus] ESTs, Weakly similar to 0806162C protein COI [M.musculus]	EST, Moderately similar to udoo lock protein Co. (with the same of	EST, Woderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 0806162C similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C similar to 0806162C protein COI	protein COI [M.musculus], LOIS, moderate [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI [M.musculus], EST, Moderately FET Moderately	similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C similar to 810024C cytochrome oxidase I [H.sapiens], EST, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI [M.musculus]	EST, Moderately similar to usua local protein on a final constant of the similar to 806162J protein URF4 similar to 810024J URF 4 [H.sapiens], EST, Weakly similar to 806162J protein URF4 [M.musculus], EST, Weakly similar to 810024J URF 4 [H.sapiens], ESTs, Moderately similar to 810024J similar to 0806162J protein URF4 [M.musculus] URF 4 [H.sapiens], ESTs, Weakly similar to 0806162J protein URF4 [M.musculus]	
.musculus], ES	, Weakly 06162C p onrome or us]	, Weakly 50162C (hrome of	culus], E r, Weakl 06162C	throme clus]	T, Weak 06162C chrome c chrome c	ar to 080 sapiens toderate otein UR	
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an Homologous HumaniHomologousiSequence Cluster (Title Win Gene Name)	similar to 810024C cytochrome oxidase I [H.sapiens], EST, W similar to 810024C cytochrome oxidase I [H.sapiens], EST, W protein COI [M.musculus], ESTs, Moderately similar to 800616 [M.musculus], ESTs, Weakly similar to 0806162C protein COI [M.musculus]	EST, Moderately similar to usua to brotein Cor (winnesconsimilar to 810024C cytochrome oxidase I [H.sapiens], EST, W protein COI [M.musculus], ESTs, Moderately similar to 08061 [M.musculus], ESTs, Moderately similar to 810024C cytochro [M.musculus], ESTs, Moderately similar to 810024C cytochro	tein CÖI [H.sapie telv simi	protein COI [M.Inusculus], LOIS, Moderately similar to 810024C cytochrol [M.musculus], ESTs, Moderately similar to 0806162C protein COI [M.musculus] ESTs, Weakly similar to 0806162C protein COI [M.muscult	similar to 810024C cytochrome oxidase I [H.sapiens], EST, W protein COI [M.musculus], ESTs, Moderately similar to 080610 [M.musculus], ESTs, Moderately similar to 810024C cytochroi [ESTs, Weakly similar to 0806162C protein COI [M.musculus]	ST, Wea 0024J U sculus],	
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jousise	cytoch sculus] Ts, Mod	similar u C cytoch usculus) Ts, Mod	similar I C cytoc	STS, Momilar to (similar control)	STS, Mo	/ similar 4.J URF ST, We& 62.J prot ns], EST	
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e <u>entenk</u> Aee or RefSeg ID			NM_053516 , JJJ	L, S NM_053516_HH	304		AA859612
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N.GI	0000	0767	3779	3779	000	P	386

differentially expressed nucleolar 1GT-beta1 target protein (DCLNT) EST, Moderately similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ES Moderately similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Moderately similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET translocation, SET translocation (myeloid [Rattus norvegicus]] [R.norvegicus], SET translocation, SET translocation (myeloid inferentially expressed nucleolar TGF-beta1 target protein (DENIT) GIFFERNIA (DESTS) (DESTS) (DESTS) (DESTA)			cus], EST, similar to 39A set et gene et gene sloid	YPE=1	in PHAS-I - liation otein 2,	YPE=1	in PHAS-I - tiation rotein 2,	
	EST, Moderately similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], EST, Moderately similar to 2008109A set gene [Rattus norvegicus], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Moderately similar to 2008109A set gene gene [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET translocation, SET translocation (myeloid leukemia-associated), cutaneous T-cell lymphoma-associated tumor antigen se20-4; leukemia-associated), cutaneous T-cell lymphoma-associated tumor antigen se20-4;	ally expressed nucleolar Or-Detail target protein (Corner)	EST, Moderately similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], EST, Moderately similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], ESTs, Moderately similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], SET translocation, SET translocation (myeloid [Rattus norvegicus], CET translocation, SET translocation antigen se20-4; leukemia-associated), cutaneous T-cell lymphoma-associated tumor antigen se20-4;	ally expressed nucleolar TGF-beta1 target protein (DENTT)	EST, Moderately similar to 20214134 initiation factor 45-300m; grocommodely by Nobel BHAS-1 [H.sapiens], ESTs, Weakly similar to A55258 insulin-stimulated phosphoprotein PHAS-1 at [R.norvegicus], RIKEN cDNA 1110004012 gene, eukaryotic translation initiation factor 4E binding protein 2,	eukaryotic translation initiation factor 4E binding protein 3	EST, Moderately similar to 202 14 134 initiation record 12 circuity properties of the Sapiens], ESTs, Weakly similar to A55258 insulin-stimulated phosphoprotein PHAS-I [H.sapiens], RIKEN cDNA 1110004O12 gene, eukaryotic translation initiation factor 4E binding protein 1, eukaryotic translation initiation factor 4E binding protein 2,	tic translation initiation factor 4E binding protein 5
	Known Gene Namo							
The management of the manageme		MM, TTT		D	D, V, NN, OO,	PP, EEE, JJJ, MMM		0, P
NN, OO,	Aes or Refect ID	AA858528 1		AI172405				NM_053857
D D, V, NN, OO, PP, EEE, JJJ, MMM 57 O, P	90.00 00.00 00.00	17461		23325		1572		1570
1572 NM_053857 O.P		334		2145		2320		3842

CAMOMEN CANALISES ON OF THE CANALISES OF	Humain Homologous		W eukaryotic translation initiation factor 4E binding protein 3	N, General EST, Moderately similar to 2113200F ribosomal protein S9 [H.sapiens] Alternate	Moderately similar to 40S RIBOSOMAL PROTEIN S23 [N. 10 vegicus], LOT, Moderately similar to R3RT25 ribosomal protein S25, cytosolic [validated] - rat	[R.norvegicus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S25 [R.norvegicus], EST, Mostly, similar to 101347 rihosomal protein S25, cytosolic [H.sapiens], ESTs,	Highly similar to JQ1347 ribosomal protein S25, cytosolic [H.sapiens], ribosomal protein			PP, QQ, YY 810024H URF 3 [H.sapiens] FST Weakly similar to A25074			NN, OO, VV,		Ent. Middelately silling to Account to the silling	Moderately similar to TCPA HUMAN T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	Moderately similar to TCPA_HUMAN T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA	Moderately similar to TCPA_HUMAN T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) [R.norvegicus], Homo sapiens, clone SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus], Homo sapiens, clone	Moderately similar to TCPA_HUMAN T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA [H.sapiens], ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus], Homo sapiens, clone IMAGE:4400828, mRNA, chaperonin containing TCP1, subunit 5 (epsilon), potassium large conductance calcium-activated channel, subfamily M, beta member 3-like, t-	Moderately similar to TCPA_HUMAN T-COMPLEX PROTEIN 1, ALPHA SUBUNIT Moderately similar to TCPA_HUMAN T-COMPLEX PROTEIN 1, ALPHA [H.sapiens], ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus], Homo sapiens, clone IMAGE:4400828, mRNA, chaperonin containing TCP1, subunit 5 (epsilon), potassium large conductance calcium-activated channel, subfamily M, beta member 3-like, t-
	HOUSE A COMMEN	***************************************	M	N, General Alternate			Z AA. 00.	UNN TOT		PP, QQ, YY		0, P, Z, AA,	NN, CO, VV,	וווווווו						
	CENSENI Recor		NM 053857	AA799369	T			X62482		84 AI170501			NIN 031140	OF LCO MINI						
TABLE 3	997 BES		3842 1571	14 18299				4241 15387	Т	2053 19884	I		46406	3010					·	

Altomey Docket 4492/1-5038-0/1W0	Human Homologous Sequence Cluster little		EST, Moderately similar to A55146 guanine nucleotide exchange factor elr-25 detact chain, long form - mouse [M.musculus], ESTs, Moderately similar to E2BA_HUMAN TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to 2112359A initiation factor elF-2B [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD), clone MGC:6458 IMAGE:2615801, mRNA, complete cds, Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD), clone MGC:7057 IMAGE:3156632, mRNA, complete cds, RIKEN cDNA 2410018C20 gene, eukaryotic translation factor 2B, subunit 1 (alpha, 26kD)	EST, Moderately similar to A55146 guanine nucleotide exchange factor elF-2B delta chain, long form - mouse [M.musculus], ESTs, Moderately similar to E2BA_HUMAN TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT [H.sapiens], ESTs, Weakly similar to 2112359A initiation factor elF-2B [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD), clone MGC:6458 IMAGE:2615801, mRNA, complete cds, Mus musculus, Similar to eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD), clone MGC:7057 IMAGE:3156632, mRNA, complete cds, RIKEN cDNA 2410018C20 gene, eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD)
	Human Homologous Known Gene Name			
	Model Gode	A, I, W, PP, QQ, VV, FFF, GGG, General Core Tox Markers	ш . С	.i
	ල බෙනෙ නියි ැ Aලේ ගේ RafSලේ ID	A1072634	24 010 010	AI031019
	elee Bro	1501	20040	23950
TABLE	Sed D	1737		1525

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See	<u>න</u> ම් ම	(Sewerns)		Humen Homologous	
((a)	[10] [No.]] යණුලේ (D	Model Code	Known Gene Name	wn Gene Name Human Homologous Sequence Guister unte
					EST, Moderately similar to A55146 guanine nucleotide exchange factor eIF-2B delta
					chain, long form - mouse [M.musculus], Mus musculus, Similar to eukaryotic translation
					initiation factor 2B, subunit 1 (alpha, 26kD), clone MGC:6458 IMAGE:2615801, mRNA,
			-		complete cds, Mus musculus, Similar to eukaryotic translation initiation factor 2B,
•					subunit 2 (beta, 39kD), clone MGC:7057 IMAGE:3156632, mRNA, complete cds,
					eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD), expressed sequence
3724	20793	NM_032058	ດດ		AA409345, expressed sequence C85417
			JJ, KK, NN,		EST, Moderately similar to APT_RAT ADENINE PHOSPHORIBOSYLTRANSFERASE
			00, EEE,		(APRT) [R.norvegicus], adenine phosphoribosyl transferase, adenine
2251	14384	AI177096	HHH, MMM		phosphoribosyltransferase, expressed sequence C85684
					EST, Moderately similar to COXI_MOUSE Cytochrome c oxidase polypeptide VIC-2
· 					[R.norvegicus], ESTs, Moderately similar to COXH_HUMAN CYTOCHROME C
	• •				OXIDASE POLYPEPTIDE VIC PRECURSOR [H.sapiens], cytochrome c oxidase
3402	23226	NM_019360	PP, 00		subunit VIc, cytochrome c oxidase, subunit VIc
<u>.</u>					CT Moderator cimilar to CVDM DAT Bootista International content of the property of the propert
_					121, Modelately annual to CITM I of the photographic contents isomerate.
٠.			-		milochondrial precursor (**Prase*) (Rolamase*) (Cyclobrillin **) [K.1101 vegicus], E.3.13,
	•				Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-1 RANS ISOMERASE A
					[M.musculus], ESTs, Weakly similar to CYPM_RAT Peptidyl-prolyl cis-trans isomerase,
					mitochondrial precursor (PPlase) (Rotamase) (Cyclophilin F) [R.norvegicus], KIKEN
					cDNA 2510026K04 gene, RIKEN cDNA 4930520F12 gene, expressed sequence
					AI256741, expressed sequence AW457192, peptidylprolyl isomerase A, peptidylprolyl
4159	15516	U68544	N		somerase E (cyclophilin E), peptidylprolyl isomerase F (cyclophilin F)
					EST, Moderately similar to DDH2_HUMAN NG,NG-DIMETHYLARGININE
!					UliMETHYLAMINOHYDKOLASE Z [H.sapiens], dimetnylarginine
2750	16978	AI236777	¥		dimethylaminohydrolase 1, dimethylarginine dimethylaminohydrolase 2



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TERRITOR (INC. 1) TERRITOR OF THE PROPERTY OF		EST, Moderately similar to DHBK MOUSE PUTATIVE STEROID DEHYDROGENASE KIK-I [M.musculus], ESTs, Weakly similar to DHBK MOUSE PUTATIVE STEROID DEHYDROGENASE KIK-I [M.musculus], RIKEN cDNA 6330410P18 gene, follicular	lymphoma variant translocation 1, hydroxysteroid (17-beta) dehydrogenase 12, retinal short-chain dehydrogenase/reductase 1, short-chain dehydrogenase/reductase 1	EST, Moderately similar to EF1D_HUMAN ELONGATION FACTOR 1-DELTA [H.sapiens], ESTs, Moderately similar to EF1D_HUMAN ELONGATION FACTOR 1-DELTA [H.sapiens], hypothetical protein FLJ20897	EST, Moderately similar to FGHUGB fibrinogen gamma-B chain precursor [H.sapiens], ESTs, Moderately similar to ANL2_MOUSE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2) [M.musculus], Mus musculus, Similar to angiopoietin-related protein 5, clone MGC:32467 IMAGE:5049765, mRNA, complete cds, Mus musculus, Similar to	fibrinogen-like 1, clone MGC:37822 IMAGE:5098805, mRNA, complete cds, angiopoietin-like 2, expressed sequence AI593246, fibrinogen, gamma polypeptide, fibrinogen-like 1	EST, Moderately similar to FIG1 MOUSE FIG-1 PROTEIN PRECURSOR [M.musculus], RIKEN cDNA 1110061B18 gene, RIKEN cDNA 4930438A08 gene, expressed sequence AW990848, interleukin-four induced gene 1,	monoamine oxidase B EST, Moderately similar to G02666 cysteine-rich protein 1 [H.sapiens], cysteine rich intestinal protein, cysteine-rich protein 1 (intestinal), expressed sequence AW743261	EST, Moderately similar to I48346 ribosomal protein fau - mouse [M.musculus], EST, Weakly similar to UBIM_HUMAN UBIQUITIN-LIKE PROTEIN FUBI (SUB 1-74 [H.sapiens], EST, Weakly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI R.norvegicus], Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously	expressed (fox derived)	EST, Moderately similar to ISI1_RAT Insulin-induced protein 1 (Insulin-induced growth response protein CL-6) (Immediate-early protein CL-6) [R.norvegicus], RIKEN cDNA 2900053111 gene, insulin induced gene 1, insulin induced protein 2
	Yuman Komologous Known Gene Namer Hu		lyn sh	<u> </u>	EE FE	fib an fib	<u> </u>	ES ES	以 多 王 区	ex	氏
	Model Code		BBB, CCC	General Alternate		·	00, 000, General Core	Tox Markers O, W		XX, YY	Ą B
	ලොඩොැ 		NM_032066	AI232006		Al059063 [NM_013198 AA925057		AI176302	NM_022392 A, B
	elege Id No.		9106	24501		5573		21396		20823	22413
			3725	2553		1628		3233 768		2197	3467



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Altienney Docket (4492/1-5038-911W)		precursor (ITI heavy chain H3) [R.norvegicus], inter-alpha (globulin) inhibitor, H1	polypeptide, inter-alpha (globulin) inhibitor, H2 polypeptide, inter-alpha trypsin inhibitor,	heavy chain 1, inter-alpha trypsin inhibitor, heavy chain 3, pre-alpha (globulin) inhibitor,	H3 polypeptide	EST, Moderately similar to JN0786 integrin beta-4 chain precursor - mouse	[M.musculus], ESTs, Moderately similar to JN0786 integrin beta-4 chain precursor -	mouse [M.musculus], expressed sequence AA407042, integrin beta 4, integrin, beta 4	EST, Moderately similar to KAPO_RAT CAMP-DEPENDENT PROTEIN KINASE TYPE I-	ALPHA REGULATORY CHAIN [R.norvegicus], EST, Weakly similar to KAP1 MOUSE	CAMP-DEPENDENT PROTEIN KINASE TYPE I-BETA REGULATORY CHAIN	[M.musculus], protein kinase, cAMP dependent regulatory, type I beta, protein kinase,	cAMP dependent regulatory, type I, alpha, protein kinase, cAMP-dependent, regulatory,	type I, alpha (tissue specific extinguisher 1)	EST, Moderately similar to LY6H_HUMAN LYMPHOCYTE ANTIGEN LY-6H	PRECURSOR [H.sapiens], ESTs, Moderately similar to D45835 Ly6 homolog RK3	precursor - rat [R.norvegicus], ESTs, Weakly similar to LY6F MOUSE LYMPHOCYTE	ANTIGEN LY-6F.1 PRECURSOR [M.musculus], expressed sequence AI789751,	lymphocyte antigen 6 complex, locus C, lymphocyte antigen 6 complex, locus E,	ymphocyte antigen 6 complex, locus H	EST, Moderately similar to MAS2_HUMAN MANNAN-BINDING LECTIN SERINE	PROTEASE 2 PRECURSOR [H.sapiens], ESTs, Moderately similar to CRAR_HUMAN	COMPLEMENT-ACTIVATING COMPONENT OF RA-REACTIVE FACTOR	PRECURSOR [H.sapiens], Mus musculus, Similar to complement component 1, s	subcomponent, clone MGC:19094 IMAGE:4196654, mRNA, complete cds, Mus	musculus, Similar to complement component 1, s subcomponent, clone MGC:28492	IMAGE:4166254, mRNA, complete cds, complement component 1, r subcomponent,	complement component 1, s subcomponent, mannan-binding lectin serine protease 2
Human Homologous	Known Gene Name L																											
	Wedal ලබෙ				D			RR				l, J, 000,	General	Alternate						D				I, J, U, X, Y, Z,	AA, GG, HH,	LL, FFF, GGG	LLL, RRR,	SSS, UUU
CONTENT	ිල් මිනිවේ				X83231			U60096						U75932						NM 020103								NM_138900
3 3 @L@G	No.				537			066						1314						18705								18867
MANBILE SI FER GOL	 @				4270		-	4150					_	4169						3418				-				3993

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Attomey Docket 4492/1-503-04000 Commant No. 1935828.1 Commant No.	EST, Moderately similar to MDHM_RAT MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to DEMSMM malate dehydrogenase [M.musculus], malate dehydrogenase 2, NAD (mitochondrial), malate dehydrogenase, mitochondrial	EST, Moderately similar to MDHM_RAT MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to DEMSMM malate dehydrogenase [M.musculus], malate dehydrogenase 2, NAD (mitochondrial), malate dehydrogenase, mitochondrial	EST, Moderately similar to MDHM_RAT MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to DEMSMM malate dehydrogenase [M.musculus], malate dehydrogenase 2, NAD (mitochondrial), malate dehydrogenase, mitochondrial	EST, Moderately similar to NDK3_MOUSE NUCLEOSIDE DIPHOSPHATE KINASE 3 (NDK 3) (NDP KINASE 3) (NM23-M3) (DR-NM23) [M.musculus], expressed in non-metastatic cells 4, protein (NM23-M4)(nucleoside diphosphate kinase), expressed sequence Al413736, non-metastatic cells 3, protein expressed in, non-metastatic cells 4, protein expressed in	EST, Moderately similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus], EST, Weakly similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus], Homo sapiens cDNA FLJ30126 fis, clone BRACE1000114, paraoxonase 1, paraoxonase 2	EST, Moderately similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus], EST, Weakly similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus], Homo sapiens cDNA FLJ30126 fis, clone BRACE1000114, paraoxonase 1, paraoxonase 2
Model Godo	, γ , γ	_	Λ	OO, III, JJJ, KKK, General Core Tox Markers	0, P, GG, PP, QQ, XX, YY	A, B, BB, CC, GG, HH, NN, OO, PP, QQ, BBB, CCC, HHH, PPP, QQQ
	AI010480	AI010480	NM_022516	NM_053507	U94856	U94856
39 GLGG ID No.	163	164	162	23558	9841	9842
TABLESS Seg @@ 100	1360	1360	3476	3776	4179	4179

	clone MGC:19156 IMAGE:4220620, mRNA, complete cds, mitochondrial acyl-CoA thioesterase thioesterase thioesterase	BBB, RRR, SSS	NM_138907	18083	3994
	peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene, Mus musculus, Similar to bile acid Coenzyme A: amino acid N-acyltransferase (alvcine N-cholovltransferase).				
	LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus				
	PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL				
	coenzyme A thioester hydrolase, mitochondrial precursor (Very-long-chain acyl-CoA thioesterase) (MTE-I) [R.norvegicus]. ESTs. Weakly similar to PTE2 HUMAN				
	THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to MTE1_RAT Acyl			_	
	THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA				
	EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A				
	5, proteasome (prosome, macropain) subunit, beta type, 5	GGG, LLL	AA891226	9136	472
	RIKEN cDNA 5830406J20 gene, proteasome (prosome, macropain) subunit, beta type	G, H, X, Y,			
	complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R.norvegicus],				
	(Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase				
	EST. Moderately similar to PSB5 RAT Proteasome subunit beta type 5 precursor				
_	AI786302, paraoxonase 1, paraoxonase 3	Tox Markers	AA818163	6016	160
	Homo sapiens cDNA FLJ30126 fis, clone BRACE1000114, expressed sequence	General Core			
	(Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus],	HHH, PPP,			
	EST, Moderately similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1)	B, H, GG,			
	IMAGE:3154583, mRNA, complete cds, paraoxonase 1, paraoxonase 2	РРР, ааа	AI169105	1335	1998
	clone BRACE1000114, Mus musculus, Similar to paraoxonase 2, clone MGC:11614				
_	PARAOXONASE/ARYLESTERASE 2 [H.sapiens], Homo sapiens cDNA FLJ30126 fis,				
	ESTs, Moderately similar to PON2_HUMAN SERUM				
	(Serum aryldiakylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus],				
	EST, Moderately similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1)				
	Known Genei Name = Hitimani Homologous Sequence Cluster IIIIe:	Model Gode	Raksag (D)	[ID No.*	@
	Human Homologous		Accor		S O
	The second secon				
	Attorney Docket 4/921-5038-01W0			RABLE 3	
	STATE OF THE PARTY				



EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COE THIOESTER HYDROLASE 2 (PEROXISOMAL CONG-CHAIN ACYL-COE THIOESTER HYDROLASE 2 (PEROXISOMAL CONG-CHAIN ACYL-COE THIOESTERASE 2) (ZAP128) [H.sapiens], PEROXISOMAL CONG-CHAIN ACYL-COENZYME 4 THIOESTER HYDROLASE 2 (PEROXISOMAL CONG-CHAIN ACYL-COENZYME 4 THIOESTERASE 2) (ZAP128) [H.sapiens], PONG-CHAIN ACYL-COENZYME 4 THIOESTERASE 2) (ZAP128) [H.sapiens], TONG-CHAIN ACYL-COENZY	Series	M M M M M M M M M M	/∕/લલ ભિ∵		Human Homologous	
5602 AI232611 RRR K, U, FF, BBB, GGG, LLL, UUU, General Core Tox M, X, W, DDD, GGG, LLL, UUU, General General Core 1479 U32314 Tox Markers 11321 AI137752 S			Refer ID		n Gene Name	
K, U, FF, BBB, 5602 Al232611 RRR M, W, DDD, GGG, LLL, UUU, General Core Tox 1478 U32314 Markers M, X, W, DDD, GGG, LLL, UUU, General Core 11321 Al137752 S						Moderately similar to PTE2 HUMAN PEROXISOMAL ACYL-COENZYME A
602 Al232611 RRR 5602 Al232611 RRR M, VV, DDD, GGG, LLL, UUU, General Core Tox 1478 U32314 Markers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					OHT	ESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA
K, U, FF, BBB, 5602 Al232611 RRR M, W, DDD, GGG, LLL, UUU, General Core Tox 1478 U32314 Markers M, X, W, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					OHT	ESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to PTE2_HUMAN
K, U, FF, BBB, 5602 Al232611 RRR M, W, DDD, GGG, LLL, UUU, General Core Tox M, X, W, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					PERC	DXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL
K, U, FF, BBB, 5602 Al232611 RRR M, WV, DDD, GGG, LLL, UUU, General Core Tox Anrkers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					FONC	3-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens
6602 AI232611 RRR M, W, DDD, GGG, LLL, UUU, General Core Tox AM, X, W, DDD, GGG, LLL, UUU, General Core LLL, UUU, General Core 1479 U32314 Tox Markers					PNG2	V FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus
K, U, FF, BBB, K, U, FF, BBB, RRR M, VV, DDD, GGG, LLL, UUU, General Core Tox M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers 11321 Al137752 S					perox	isomal long chain acyl-CoA thioesterase Ib (Pte1b) gene, Mus musculus, Similar
K, U, FF, BBB, S602 Al232611 RRR M, WV, DDD, GGG, LLL, UUU, General Core Tox MARKers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					to cyt	osolic acyl-CoA thioesterase 1, clone MGC:27572 IMAGE:4485973, mRNA,
5602 Al232611 RRR M, W, DDD, GGG, LLL, UUU, General Core Tox AM, X, W, DDD, GGG, LLL, UUU, General Core Tox AM, X, W, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers					dwoo	lete cds, RIKEN cDNA 4632408A20 gene, expressed sequence AW108394,
5602 AI232611 RRR M, VV, DDD, GGG, LLL, UUU, General Core Tox Anxers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers				K, U, FF, BBB,	mitoc	hondrial acyl-CoA thioesterase 1, peroxisomal acyl-CoA thioesterase 2A,
M, VV, DDD, GGG, LLL, UUU, General Core Tox Amarkers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers	2589	5602	AI232611	RRR	perox	isomal acyl-CoA thioesterase 2B, peroxisomal long-chain acyl-coA thioesterase
GGG, LLL, UUU, General Core Tox 1478 U32314 Markers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers				M, VV, DDD,		
1478 U32314 Markers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers	_			GGG, LLL,	EST,	Moderately similar to PYC_RAT Pyruvate carboxylase, mitochondrial precursor
Core Tox 1478 U32314 Markers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers 11321 Al137752 S				UUU, General	(Pyru	vic carboxylase) (PCB) [R.norvegicus], Mus musculus, Similar to Propionyl
1478 U32314 Markers M, X, VV, DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers 11321 Al137752 S				Core Tox	Coen	zyme A carboxylase, alpha polypeptide, clone MGC:11973 IMAGE:3601148,
M, X, VV, DDD, GGG, LLL, UUU, General Core Tox Markers 1479 U32314 Tox Markers	4118	1478	U32314	Markers	mRN	 A, complete cds, pyruvate carboxylase, pyruvate decarboxylase
DDD, GGG, LLL, UUU, General Core 1479 U32314 Tox Markers 11321 Al137752 S				M, X, VV,		
1479 U32314 Tox Markers 11321 Al137752 S				DDD, GGG,	EST,	Moderately similar to PYC_RAT Pyruvate carboxylase, mitochondrial precursor
General Core 1479 U32314 Tox Markers 11321 Al137752 S				LLL, UUU,	(Pyru	vic carboxylase) (PCB) [R.norvegicus], Mus musculus, Similar to Propionyl
1479 U32314 Tox Markers 11321 Al137752 S				General Core	Coen	zyme A carboxylase, alpha polypeptide, clone MGC:11973 IMAGE:3601148,
A1137752 S	4118	1479	U32314	Tox Markers	mRN	A, complete cds, pyruvate carboxylase, pyruvate decarboxylase
A1137752 S					EST,	Moderately similar to R5HU7 ribosomal protein L7, cytosolic [H.sapiens], EST,
Al137752 S					Weak	th similar to RL7 MOUSE 60S RIBOSOMAL PROTEIN L7 [M.musculus], ESTs,
AI137752 S					High	y similar to R5HU7 ribosomal protein L7, cytosolic [H.sapiens], ribosomal protein
	1960	11321		S	[F	



library, clone:1600029O15:hexokinase 1, full insert sequence, ribosomal protein L17	JJ, KK, HHH	17174 NM_013030 JJ, KK, HHH	17174	3200
[R.norvegicus], ESTs, Weakly similar to R5HU22 ribosomal protein L17, cytosolic				
[H.sapiens], ESTs, Highly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17				
[H.sapiens], ESTs, Highly similar to R5HU22 ribosomal protein L17, cytosolic				
[R.norvegicus], EST, Weakly similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17				
[H.sapiens], EST, Weakly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17				٠.
EST, Moderately similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17		,		
L11 [H.sapiens], RIKEN cDNA 2010203319 gene, ribosomal protein L11	Alternate	X62146	4441	4238
[M.musculus], ESTs, Moderately similar to RL11_HUMAN 60S RIBOSOMAL PROTEIN	GGG, General		•	
[H.sapiens], ESTs, Highly similar to RIKEN cDNA 2010203J19 [Mus musculus]	DDD, FFF,			
[R.norvegicus], EST, Weakly similar to RL11_HUMAN 60S RIBOSOMAL PROTEIN L11	II, JJ, KK,			
[H.sapiens], EST, Moderately similar to RL11_HUMAN 60S ribosomal protein L11		,		
EST, Moderately similar to RL11_HUMAN 60S RIBOSOMAL PROTEIN L11				
initiation factor 3, subunit 4 (delta, 44 kDa), nucleolin, pigpen	EE, NNN	AI044836	18205	1563
II, TATA box binding protein (TBP)-associated factor, 68 kDa, eukaryotic translation				
mRNA, complete cds, Nucleolin, RNA binding motif protein 8A, TAF15 RNA polymerase				
derived from t(12;16) malignant liposarcoma, clone MGC:18917 IMAGE:3153860,				
MGC:22221 IMAGE:4687764, mRNA, complete cds, Mus musculus, Similar to fusion,				
Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens], Homo sapiens, clone				
similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8 [H.sapiens], ESTs,				
[H.sapiens], ESTs, Moderately similar to NUCLEOLIN [M.musculus], ESTs, Moderately				
EST, Moderately similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8				
Known Genename Human Homologous Sequence Guster Mile	Model Code	RefSeq [D	(10 km)	
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7007	17175	08583X	II, JJ, KK, FFF,		[H.sapiens], ESTS, riighly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTS, Highly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTS, Weakly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600029O15:hexokinase 1, full insert sequence, ribosomal protein L17
1774					EST, Moderately similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], EST, Weakly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 In proposition 1 EST, Weakly similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17
					[K.notvegicus], L.S., Weary Similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], ESTs, Highly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTs, Highly similar to RL17 RAT 60S RIBOSOMAL PROTEIN L17
					[R.norvegicus], ESTs, Weakly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens], Mus musculus adult female placenta cDNA, RIKEN full-length enriched [H.sapiens], Mus musculus adult female placenta sequence, ribosomal protein L17
4233	17176	X60212	LL, SS		EST, Moderately similar to RL35_HUMAN 60S RIBOSOMAL PROTEIN L3 [H.sapiens].
1788	18642	AI102023	S		EST, Moderately similar to RL35_RAT 60S RIBOSOMAL PROTEIN L35 [R.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds, ribosomal protein L35
3017	17211	M34331	aga		EST, Moderately similar to RL35_RAT 60S RIBOSOMAL PROTEIN L35 [R.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds, ribosomal protein L35
3017	26030	M34331	F, DDD		EST, Moderately similar to RL35_RUMAN 605 RIBOSOMAL FNO LIN L3 [R.norvegicus], EST, Moderately similar to RL35_RAT 60S RIBOSOMAL PROTEIN L35 [R.norvegicus], Homo sapiens, clone IMAGE:4183312, mRNA, partial cds, ribosomal protein L35
					EST, Moderately similar to RS12_HUMAN 403 RIBOSOMAL PROTEIN 31 (1.32pp. 23). ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic [H.sapiens], ESTs, Moderately similar to RS12 MOUSE 40S RIBOSOMAL PROTEIN S12
3674	16918	NM_031709	9 F		[M.musculus], ribosomal protein S12

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Document No. 199522.1	TEIN SO IN	EST, Moderately similar to RS2 MOUSE 40S RIBOSOWAL PROTEIN 32 [w.m.bascaras]. EST, Weakly similar to ribosomal protein S2; 40S ribosomal protein S2 [Homo sapiens]	[H.sapiens], EST, Weakly similar to RS2_HUMAN 40S RIBOSOMAL PROTEIN 32 IH.sapiens], EST, Weakly similar to RS2_RAT 40S RIBOSOMAL PROTEIN S2	R.norvegicus], ESTs, Highly similar to ribosomal protein S2; 40S ribosomal protein S2 [R.norvegicus], ESTs, Highly similar to ribosomal protein S2; repeat family	[Homo sapiens] [H.sapiens], ESTS, rightly string to historial process 25, 55 per 3 gene [Mus musculus] [M.musculus], Homo sapiens, clone IMAGE:4816496, mRNA,	TEIN CO II	EST, Moderately similar to RS2 MOUSE 405 RIBOSOWAL PROTEIN 32 [willingsdates]	EST, Weakly similar to Tibosoffial protein 22, 400 figosoffial protein S2 III seriens FST Weakly similar to RS2 HUMAN 40S RIBOSOMAL PROTEIN S2	Hampiers EST, Weakly similar to RS2 RAT 40S RIBOSOMAL PROTEIN S2	R.norvegicus], ESTs, Highly similar to ribosomal protein S2; 40S ribosomal protein S2	[Homo sapiens] [H.sapiens], ESTs, Highly similar to ribosomal protein S2; repeat family	3 gene [Mus musculus] [M.musculus], Homo sapiens, clone IMAGE:4816496, mKNA,	CINI CO I	EST, Moderately similar to RS21_RA1 40S RIBOSOMAL FRO LEIN SZ 1 [13:110] v Sanday.	ribosomal protein Sz I		EST Moderately similar to S25111 alpha-2-macroglobulin receptor precursor - mouse	M.musculus], ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor	- mouse [M.musculus], ESTs, Weakly similar to S25111 alpha-2-macroglobulin receptor	ptor)	
		omal prot	RIBOSON OSOMAL	in S2; 405 ocomal pr	lone IMAC	000	WAL FRO	RIBOSON	OSOMAL	in S2; 40	posomal p	clone IMA	TOGG	-	AI PROT		ulin recep	-macroglo	1 alpha-2· in recepto	density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	
	man Homologous own, Gene Name Human Homologous Sequence Gluster IIIIIe	40S ribos	MAN 40S F 40S RIB	omal prote	sapiens, c		Alboard Alboard	MAN 40S	T 40S RIE	omal prote	nilar to ril	sapiens, (10000		MOSOBIC		nacroglob	1 alpha-2	to S2511 lipoprote	-macroglo	
	Duster Tilt	USE 40S rotein S2;	RS2_HUIRS2_RA	r to riboso	rligiliy sii s], Homo	101	JUSE 403	RS2 HU	RS2_RA	r to ribos	Highly sin	omoH ,[sr	2007	(A) 403 P	SOT ANS		alpha-2-r	to S2511	ıkty similar ow density	1 (alpha-2	
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	as snob	/ similar to nilar to rit	r, Weakly r, Weakly	ESTs, Hig	[H.saple⊓ sculus] [N	somal pro	y similar t	milar to rii T Weakly	T. Weakly	ESTS, Hig	[H.sapier)] [snInosr	somal pro	ly similar t ∵ coa	III 32 I	iy Siiriilai in S21	lv similar	STS, Hig	sculus], E	ein-relate	
	n Homolo	//oderatel //eakly sir	iens], ES	vegicus],	sapiensj • [Mus mu	partial cds, ribosomal protein S2	Moderate	Weakly SII	piens] ES	vegicus].	sapiens]	e [Mus m	partial cds, ribosomal protein SZ	Moderate	ribosomai protein 52 i	ES 1, Moderately silrill ribosomal protein S21	Moderate	usculus], [ise [M.mu	ty lipoprof	
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						3705							3705		3608	8086	3			2687	7007

	est, ghly v similar y similar	EST, ghly / similar y similar y similar 3 [Mus 3,	STS., STS., OTEIN d 4,
	EST, Moderately similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], EST, Weakly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Highly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus], ESTs, Weakly similar to RL3 MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like	EST, Moderately similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], EST, Weakly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Highly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus], ESTs, Weakly similar to RL3 MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like EST, Moderately similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], ESTs, Weakly similar to proteasome (prosome, macropain) subunit, beta type, 3 [Mus musculus] [M.musculus], proteasome (prosome, macropain) subunit, beta type 3,	proteasome (prosome, macropain) subunit, beta type, 3 EST, Moderately similar to S65792 ribosomal protein L9, cytosolic [H.sapiens], EST, Weakly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L9 [M.musculus], RIKEN cDNA 4930401B11 gene, ribosomal protein L9 EST, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Highly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Weakly similar to NED4 MOUSE NEDD-4 PROTEIN (fragment) [R.norvegicus], est expressed, developmentally down-regulated 4, neural precursor cell expressed, developmentally down-regulated gene 4a
THE PERSON NAMED IN COLUMN TWO IS NOT THE OWNER.	EST, Mode Weakly sim similar to Si to RL3_RA to RL3 MOI	EST, Mode Weakly sim similar to S. to RL3_RA to RL3 MOI 1110057H1 EST, Mode ESTs, Wearnsculus] [proteasome EST, Mode Weakly sim Weakly sim 4930401B1 EST, Mode [R.norvegic [R.norvegic (fragment) [M.musculu neural prec
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CONTRACTOR OF THE CONTRACTOR O	B, XX, YY, HHH	G, H, JJ, KK, UU, GGG, HHH, General Alternate	J, Z, AA
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	13647	13646	18252
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Altorney Decket (1921-5038-01000) The Booument No. 1935223.1 Tomologous France Clusterinis	EST, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Highly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Weakly similar to NED4 MOUSE NEDD-4 PROTEIN [M.musculus], neural precursor cell expressed, developmentally down-regulated 4, neural precursor cell expressed, developmentally down-regulated 4.	EST, Moderately similar to SCO2_HUMAN SCO2 PROTEIN HOMOLOG PRECURSOR [H.sapiens], EST, Weakly similar to SCO2_HUMAN SCO2 PROTEIN HOMOLOG PRECURSOR [H.sapiens] PRECURSOR [H.sapiens] EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Highly similar to SMHU1B metallothionein 1B [H.sapiens], H.sapiens mRNA for metallothionein isoform 1R, Homo sapiens metallothionein 1H-like protein mRNA, complete cds, Homo sapiens unknown mRNA, Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds, Mus musculus, metallothionein 2A, clone MGC:30400 IMAGE:4501155, mRNA, complete cds, metallothionein 1H, metallothionein 1X, metallothionein 2	EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Highly similar to SMHU1B metallothionein 1B [H.sapiens], H.sapiens mRNA for metallothionein isoform 1R, Homo sapiens metallothionein 1H-like protein mRNA, complete cds, Homo sapiens unknown mRNA, Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds, Mus musculus, metallothionein 2A, clone MGC:30400 IMAGE:4501155, mRNA, complete cds, metallothionein 1H, metallothionein 1X, metallothionein 2 EST, Moderately similar to T08727 probable H+-transporting ATP synthase [H.sapiens]
Artineni Rumeni Known			
Model Gode	Σ	A, Y, GGG, QQQ, General Core Tox Markers	C, E, L, T, W, DD, SS, WW, III, JJJ, KKK, NNN
	AI101003	Al176247	
B & S	10573	19363	
TABLES Sed @ D	1766	2195	2206 270



Attorney Docket (4924-5038-611W)	HumaniHomologous Known Gene Namer HumaniHomologous/Séguence/Gluster/Ilitle	EST, Moderately similar to 131432 K-Cl cotransport protein 2, turoserning 351, 311, 121, 121, 121, 121, 121, 121, 12	EST, Moderately similar to TCPA_HUMAN I-COMPLEX PROTEIN 1, ALT IN SOCIATION IS IN SOCIATION IN THE SOCIATION IN THE SOCIATION IS IN SECUENTIAL SOCIATION IN THE SOCIATION IN SECRETARY SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)	[R.norvegicus], chaperonin containing TCP1, subunit 5 (epsilon), potassium large conductance calcium-activated channel, subfamily M, beta member 3-like, t-complex 1	EST, Moderately similar to TVRITE OFF Directing Processing Section 1. RAB-1A [M.musculus], RAB1B, member RAS oncogene family, RAB33B, member RAS oncogene family and the processing section RAB oncogene family.	EST, Moderately similar to IVKLITP GIF-billuling protein hard and protein RAB-1A [M.musculus], RAB1B, member RAS oncogene family, RAB33B, member RAS oncogene family
	તેલી હેલ્લ	DD, EE, KKK,		A, B, H, S, GGG, HHH	11	aa, RR, UU
	eemeenii Vee ortii Refeeg ID	AA799691		AI233731	A1178239	X13905
	alee Dine	21679		13294	19586	19584
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Hiomologous HumanilHomologous Sequence Queter IIII le	[M.musculus], ESTs, Moderately similar to 199303 updation 301/28/2019 001/28/2019 001/28/2019 001/2019	insert, Homo sapiens cDNA FLJ13857 fis, clone THYRO1001003, weakly similar to UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19), Homo sapiens cDNA	FLJ25157 fis, clone CBR08008, highly similar to UBIQUI IN-CONJUGATING ENZ INC. INC. INC. ENZ. INC. E2-23 KDA (EC 6.3.2.19), Mus musculus, ubiquitin-conjugating enzyme E2D 1 (UBC4/5)	homolog, yeast), clone MGC:28550 IMAGE:4205941, mRNA, complete cds, KINEN conclog, yeast), clone ubjunitin-conjugating enzyme E2D 1 (UBC4/5 homolog,	yeast), ubiquitin-conjugating enzyme E2D 2, ubiquitin-conjugating enzyme E2D 2	(UBC4/5 homolog, yeast), ubiquitin-conjugating elizying czc. 3 (CC) (CC	ES1, Moderately Similar to 1034-1046711.	protein, helicase with zinc finger domain	[H.sapiens], block of proliferation 1	EST, Weakly similar to aldo-keto reductase ramily 1, member of lancing of concessions of lancing of the land of	reductase family 1, member A1 (aldehyde reductase), aldo-keto reductase family 1,	member A4 (aldehyde reductase)
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Human Homologous Comment No. 1935233.1 Human Homologous Comment Homologous Sequence Gluster Mile	EST, Weakly similar to carnitine/acylcarnitine translocase; mitochondrial carnitine-acylcarnitine translocase gene [Mus musculus] [M.musculus], ESTs, Weakly similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens], Homo sapiens, similar	to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20, clone MGC:35539 IMAGE:5200129, mRNA, complete cds, Mus musculus, Similar to CG4995 gene product, clone MGC:7958 IMAGE:3584570, mRNA, complete cds, expressed sequence AW491445, expressed sequence W51672, ornithine transporter 2, solute	carrier family 25 (carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carritine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 3, solute carrier	family 25 (mitochondrial carrier; ornithine transporter) member 15	EST, Weakly similar to carnitine/acylcarnitine translocase; mitochondrial carnitine-acylcarnitine translocase gene [Mus musculus] [M.musculus], ESTs, Weakly similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus	norvegicus] [R.norvegicus], ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens], Homo sapiens, similar	to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20, clone MGC:35539 IMAGE:5200129, mRNA, complete cds, Mus musculus, Similar to CG4995	gene product, clone MicC.7 936 IMAGE.3364370, mKNA, complete cds, expressed sequence W51672, ornithine transporter 2, solute carrier family 25 (carnitine/acylcarnitine translocase) member 20 solute carrier family	25 (mitochondrial carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3, solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
Model Godo			U, FF, LL, BBB, CCC,	RRR, SSS			····		RRR. SSS
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					EST, Weakly similar to cyclin-dependent kinase 4 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to cyclin-dependent kinase 4 [Rattus norvegicus] IR norvegicus]	
3799 2	20802	NM_053593	С, G, Н		[Nation vegicus], Lot is, industriated with a CONA industrial CELL Division FRO Lain KINASE 4 [M.musculus], cyclin-dependent kinase 6	
			LLL. SSS.		EST, Weakly similar to ectonucleotide pyrophosphatase/phosphodiesterase 1 [Rattus norveoicus] [Rattus Weakly similar to A39216 plasma cell membrane	Г
			UUU, General		glycoprotein PC-1 [H.sapiens], ectonucleotide pyrophosphatase/phosphodiesterase 1,	
143	2544	AA817968	Alternate		ectonucleotide pyrophosphatase/phosphodiesterase 5	
3887	15838	NM 057143 KK	XX		EST, Weakly similar to fertility protein SP22 [Rattus norvegicus] [R.norvegicus], RNA binding protein regulatory subunit RNA-binding protein regulatory subunit	
\top	1		Q, R, JJ, KK,		EST, Weakly similar to fertility protein SP22 [Rattus norvegicus] [R.norvegicus], RNA	T
3887	15839	NM_057143 NNN	NNN		binding protein regulatory subunit, RNA-binding protein regulatory subunit	
					EST, Weakly similar to histone H2A.F/Z variant [Homo sapiens] [H.sapiens], ESTs,	
_					Weakly similar to H2AZ_HUMAN HISTONE H2A [H.sapiens], H2A histone family,	
22	0254	0.00000	0		member Z, Homo sapiens cDNA FLJ32241 fis, clone PLACE6005231, RIKEN cDNA	
T	1	-1	C, n, 9, 000		COSUUVZEL I I gene, nistone mza. 772 variant	Т
			T, MM, PPP,		EST, Weakly similar to integral membrane protein 2B [Homo sapiens] [H.sapiens],	
22	16942	AA799520	GQQ,		ıntegral membrane protein 28	П
					EST, Weakly similar to integral membrane protein 2B [Homo sapiens] [H.sapiens],	
2717	16943	AI236097	PPP, aga		integral membrane protein 2B	
					EST, Weakly similar to Kruppel associated box (KRAB) zinc finger 1 [Rattus	
	-				norvegicus] [R.norvegicus], EST, Weakly similar to ZINC FINGER PROTEIN 91	
	-				[H.sapiens], ESTs, Moderately similar to DNA-binding protein; zinc finger protein 253	
					[Homo sapiens] [H.sapiens], ESTs, Moderately similar to ZINC FINGER PROTEIN 91	
	_				[H.sapiens], Mus musculus, Similar to RIKEN cDNA 2610036F08 gene, clone	
					MGC:28645 IMAGE:4224834, mRNA, complete cds, expressed sequence AI790734,	
	Š	1167000	2		expressed sequence AU021768, zinc finger protein 386 (Kruppel-like), zinc finger	
4130	\$	790/00	חחח		protein 91 (HPF7, HTF10)	٦



TABLES	(M)				Attorn
		Consent			
<u> </u>	S CONTRACTOR OF THE CONTRACTOR		Model Gode		
				EST, Weakly similar to pro	EST, Weakly similar to proline rich protein 2 [Mus musculus] [M.musculus], EST,
				Weakly similar to ZAP3_Mt	Weakly similar to ZAP3_MOUSE Nuclear protein ZAP3 [M.musculus], ESTs, Weakly
				similar to proline rich prote	similar to proline rich protein 2 [Mus musculus] [M.musculus], expressed sequence
				AA408880, pantothenate k	AA408880, pantothenate kinase, proline rich protein 2, protein phosphatase 1,
3525	21491	NM_022951	ZZ, AAA	regulatory subunit 10	
				EST, Weakly similar to ribo	EST, Weakly similar to ribosomal protein L18a; 60S ribosomal protein L18a [Homo
				sapiens] [H.sapiens], ESTs	sapiens] [H.sapiens], ESTs, Highly similar to ribosomal protein L18a; 60S ribosomal
75	20811	AA799899	RR	protein L18a [Homo sapiens] [H.sapiens]	ns] [H.sapiens]
				EST, Weakly similar to ribo	EST, Weakly similar to ribosomal protein L18a; 60S ribosomal protein L18a [Homo
				sapiens] [H.sapiens], ESTs	sapiens] [H.sapiens], ESTs, Highly similar to ribosomal protein L18a; 60S ribosomal
4197	20810	X14181	EEE, MMM	protein L18a [Homo sapiens] [H.sapiens]	ns] [H.sapiens]
				EST, Weakly similar to ribo	EST, Weakly similar to ribosomal protein, mitochondrial, S22 [Mus musculus]
1133	3496	AA997304	F	[M.musculus], mitochondrial ribosomal protein S22	al ribosomal protein S22
				EST, Weakly similar to SC	EST, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus]
				[R.norvegicus], ESTs, Wea	[R.norvegicus], ESTs, Weakly similar to SC65 synaptonemal complex protein [Rattus
				norvegicus] [R.norvegicus],	norvegicus] [R.norvegicus], SC65 synaptonemal complex protein, cartilage associated
"				protein, growth suppressor	protein, growth suppressor 1, nucleolar autoantigen (55kD) similar to rat synaptonemal
497	18269	AA891769	D, N	complex protein	
				EST, Weakly similar to trop	EST, Weakly similar to tropomyosin 3, gamma [Rattus norvegicus] [R.norvegicus],
				ESTs, Highly similar to TPN	ESTs, Highly similar to TPMN_HUMAN TROPOMYOSIN, CYTOSKELETAL TYPE
				[H.sapiens], ESTs, Modera	[H.sapiens], ESTs, Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE
3893	14126	NM_057208	W	[M.musculus]	
			- C	C	
177	21010	21010 AA925306	D, U, FF, BBB, RRR, SSS	EST, Weakly similar to 1701410A cnoline a [R.norvegicus], carnitine acetyltransferase	ES Ι, Weakly similar to 1701410A choline acetylitransferase [καπυs norvegicus] [R.norvegicus], carnitine acetyltransferase



TABLE 3	83 8			第二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十	
- S (2) (3)	GLGG DNG	<u> Consenk </u>	Model Gode	HumantHomologous htt Known GanoNeme	antitioniologous mentential to the second of
					EST, Weakly similar to 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus], EST, Weakly similar to R6HUP2 acidic ribosomal protein P2, cytosolic [H.sapiens], ESTs, Highly similar to MT 11 MOI ISE DNA I PROTEIN HOMOI OG MT 11 IM musculus
					ESTS, Weakly similar to RLA1 MOUSE 60S ACIDIC RIBOSOMAL PROTEIN P1
					[M.musculus], Homo sapiens cDNA FLJ31504 fits, clone N1ZNEZ005604, Weakly similar to 60S ACIDIC RIBOSOMAL PROTEIN P2, expressed sequence Al255964, ribosomal
4220	24577	X55153	C, F, K, DDD		protein, large, P1
3859	15135	NM 053971	G. H. FFF		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L6 IM.musculus]. ribosomal protein L6
			M, X, Y, KK,		
			HHH, General		
			Core Tox		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ESTs, Weakly
3859	15136	NM_053971	Markers		similar to 60S RIBOSOMAL PROTEIN L6 [M.musculus], ribosomal protein L6
					EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis,
					clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746,
118	22025	AA800849	8, π	_	RIKEN cDNA 3830414F09 gene
					EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis,
					clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746,
279	22027	AA850060	۷, 000		RIKEN cDNA 3830414F09 gene
					EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis,
					clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746,
279	22028	AA850060	ccc		RIKEN cDNA 3830414F09 gene
					EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis,
					clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746,
806	22029	AA945284	Z,	_	RIKEN cDNA 3830414F09 gene
					EST, Weakly similar to 810024L URF 5 [H.sapiens], Homo sapiens cDNA FLJ10784 fis,
		 	0		cione NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746,
13/1	22030	AIU11//	IN, BB, CC		KIKEN CUNA 36304 14F09 gene

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	- George - George - Telesco	Centena Récor Récej (D	Model Gode	Human Homologous Known Genei Namen Human Homologous Sequence Cluster III 1	mologous Sequence Gluster Mile
3755	11319	NM_053357	HH	EST, Weakly similar Armadillo Repeat Co (88kD), catenin beta	Of The Xtcf3-Cbd nerin-associated
				EST, Weakly simi similar to UDB5 N	EST, Weakly similar to A27878 glucuronosyltransferase [H.sapiens], ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE 2B5 PRECURSOR, MICROSOMAL [M.musculus]. Mus musculus. Similar to UDP alvoosyltransferase 2
2989	24860	M13506	E, K, M, X, TT, BBB, DDD, EEE, MMM		family, polypeptide B4, clone MGC:37823 IMAGE:5098890, mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2 family, polypeptide B15, UDP-glucuronosyltransferase 2 family, member 5, expressed sequence AA986709
			BB, CC, II,	EST, Weakly simi [R.norvegicus], Et [M.musculus], RIK	EST, Weakly similar to A32852 membrane alanyl aminopeptidase (EC 3.4.11.2) - rat [R.norvegicus], ESTs, Weakly similar to AMPN MOUSE AMINOPEPTIDASE N [M.musculus], RIKEN cDNA 2010111101 gene, RIKEN cDNA 4833403115 gene, alanyl
3005	1540	M25073	NNN, General Alternate		(membrane) aminopeptidase, alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)
1381	3995	AI011678	GGG, General Core Tox Markers		EST, Weakly similar to A33880 syndecan 2 [H.sapiens], Mus musculus, clone IMAGE:4983756, mRNA, partial cds, syndecan 2, syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
			S, FFF, GGG, OOO, UUU, General Core	EST, Weakly simi IMAGE:4983756,	EST, Weakly similar to A33880 syndecan 2 [H.sapiens], Mus musculus, clone IMAGE:4983756, mRNA, partial cds, syndecan 2, syndecan 2 (heparan sulfate
3042	1529	M81687	Tox Markers	proteoglycan 1, co	proteoglycan 1, cell surface-associated, fibroglycan)
800	17540	17540 00055014	a a	EST, Weakly simi MOUSE FIBRILL/ M.m.isculus] avg	EST, Weakly similar to A38712 fibrillarin [H.sapiens], EST, Weakly similar to FBRL MOUSE FIBRILLARIN [M.musculus], ESTs, Moderately similar to FIBRILLARIN [M.musculus], ESTs, Moderately similar to FIBRILLARIN
330	2	1160060	۵ ' ز	וויויווחפרווייוול ליבי ליבי ליבי ליבי ליבי ליבי לי	הפספת ספקתפונים ארת לכססט, וומווומווו



EST, Weakly similar to A3B1_MOUSE Adapter-related protein complex 3 beta 1 subunit (Beta-adaptin 3A) (AP-3 complex beta-3A subunit) (Beta-3A-adaptin) [M.musculus], Mus

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musculus, clone MGC:36656 IMAGE:5364848, mRNA, complete cds, adaptor-related protein complex 3, beta 1 subunit, adaptor-related protein complex AP-3, beta 1 subunit, adaptor-related protein complex AP-3, beta 2 subunit	EST, Weakly similar to A41120 prostaglandin transporter - rat [R.norvegicus], ESTs, Weakly similar to JC7286 liver-specific organic anion transporter-1 - mouse [M.musculus], ESTs, Weakly similar to PGT_HUMAN PROSTAGLANDIN TRANSPORTER [H.sapiens], expressed sequence Al060904, solute carrier family 21 (organic anion transporter), member 11, solute carrier family 21 (organic anion transporter), member 12, solute carrier family 21 (orostaglandin transporter), member 2	EST, Weakly similar to A42148 GTP-binding protein rab8 - rat (fragment) [R.norvegicus], ESTs, Weakly similar to cell line NK14 derived transforming oncogene [Mus musculus] [M.musculus], ESTs, Weakly similar to RAB8_HUMAN RAS-RELATED PROTEIN RAB-8 [H.sapiens], RIKEN cDNA 0610007N03 gene, RIKEN cDNA 2310012G06 gene, SOCS box containing protein RAR3, cell line NK14 derived transforming oncogene, mel transforming oncogene (derived from cell line NK14)- RAB8 homolog EST, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens], ESTs, Weakly	similar to A43932 mucin 2 precursor, intestinal [H.sapiens], Homo sapiens mRNA for FLJ00219 protein, hepatitis A virus cellular receptor 1	EST, Weakly similar to A44437 regenerating liver inhibitory factor RL/IF-1 - rat [R.norvegicus], Homo sapiens, Similar to GA binding protein transcription factor, beta subunit 1 (53kD), clone MGC:29891 IMAGE:5139830, mRNA, complete cds, ankyrin repeat domain 2 (stretch responsive muscle), molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha, testis-specific ankyrin motif containing protein
BB, CC	3	RR	Σ	EE, PP, QQ, III, JJJ, NNN
AI170332	NM 022667	NM 053998	NM_133308	AA944727

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Attorney Docket 4/1921-5033-0100 Document No. 1935328.1	Homologous Homologous Genernemen Homologous Sequence Guster Mis	EST, Weakly similar to A45377 transcription factor ATF4 [H.sapiens], ESTs, Highly similar to A45377 transcription factor ATF4 [H.sapiens], activating transcription factor 4, 100 topological property (100 topological property (transcription factor 5	EST, Weakly similar to A45377 transcription factor ATF4 [H.sapiens], ESTs, Highly similar to A45377 transcription factor ATF4 [H.sapiens] activating transcription factor A	activating transcription factor 4 (tax-responsive enhancer element B67), activating	transcription factor 5	EST, Weakly similar to A48045 ribosomal protein S27, cytosolic [H.sapiens], ESTs,	S27 (metallopanstimulin 1), ribosomal protein S27-like	EST, Weakly similar to A48045 ribosomal protein S27, cytosolic [H.sapiens], ESTs,	Highly similar to A48045 ribosomal protein S27, cytosolic [H.sapiens], ribosomal protein	S27 (metallopanstimulin 1), ribosomal protein S27-like	EST, Weakly similar to A55749 spliceosome-associated protein SAP 61 [H.sapiens],	splicing factor 3a, subunit 3, 60kD	EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR	[H.sapiens], Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched	library, clone:5330437D01:serine protease inhibitor 2-1, full insert sequence, kallikrein	binding protein	EST, Weakly similar to AACT HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR	[H.sapiens], RIKEN cDNA 4833409F13 gene, serine protease inhibitor 2-2	EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR	[H.sapiens], serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,	pigment epithelium derived factor), member 2, serine protease inhibitor 2-2	EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR	[H.sapiens], serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,	pigment epithelium derived factor), member 2, serine protease inhibitor 2-2
	Humani Kaowi																								
	Kadel Gode Kaowa		W			Σ		*			RR		L			H, O, P, GG,	PPP, QQQ	E, 88, III, JJJ,	KKK, NNN			W			L, TT
	Keinsenik Glec Accor D'No. Refseq D		NM_024403			NM_024403		AA851135			A1008511		AA818612				X69834		D00753			M38566			17147 NM_012657 L, TT
ଡ ^{non}	ම <u>ු ලේ</u> ම No.		13633			13634		2103			22126		6234				588		3292			17145			17147
TABLES	Sed (10)		3558			3558		302			1277		176				4252		2841			3023			3106

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Seq.	elec Base	Constant Accor Rakig (D	The coll code	Human Homologous Known Gene Name	nan Homologous Nan Gene Nemo Human Homologous Sequence @uster Mile
					EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR If saniens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin
3106	17148	NM_012657	нн, тт		pigment epithelium derived factor), member 2, serine protease inhibitor 2-2
					EST, Weakly similar to AACT_HUMAN ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR
					[H.sapiens], serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,
4282	17146	Y07534	J		pigment epithelium derived factor), member 2, serine protease inhibitor 2-2
					EST, Weakly similar to B41222 ubiquitin-protein ligase [H.sapiens], ESTs, Highly
					similar to ubiquitin conjugating enzyme [Rattus norvegicus] [R.norvegicus], ESTs,
					Highly similar to A41222 ubiquitin-protein ligase [H.sapiens], ESTs, Moderately similar
					to B41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN
					UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA
					2610301N02 gene, expressed sequence Al327276, ubiquitin-conjugating enzyme E2A
					(RAD6 homolog), ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae),
					ubiquitin-conjugating enzyme E2B (RAD6 homolog), ubiquitin-conjugating enzyme E2B,
42	17380	AA799612	MM, TTT		RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C
					EST, Weakly similar to B41222 ubiquitinprotein ligase [H.sapiens], ESTs, Highly
					similar to ubiquitin conjugating enzyme [Rattus norvegicus] [R.norvegicus], ESTs,
					Highly similar to A41222 ubiquitinprotein ligase [H.sapiens], ESTs, Moderately similar
					to B41222 ubiquitinprotein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN
					UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA
			R, DD, EE,		2610301N02 gene, expressed sequence Al327276, ubiquitin-conjugating enzyme E2A
			MM, ww,		(RAD6 homolog), ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae),
			TTT, General		ubiquitin-conjugating enzyme E2B (RAD6 homolog), ubiquitin-conjugating enzyme E2B,
3617	17379	NM_031138 Alternate	Alternate		RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C



TABLE	3.9 8.5	ಗುಟ್ಟು ನಿ			Alionney Doekel 44.821-5086-01/We
Sed (D	GLGG BND	Consent Accor Roksq (D	epos (epow	Human Hemologous Krovn Gene Name	en Homologous vnj Gene Keme Hvman Homologous Sequence Gluster III lê
					EST, Weakly similar to beta-fibrinogen precursor [H.sapiens], ESTs, Moderately similar to ANL2_MOUSE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2)
					[M.musculus], E.S.I.S, Weany Silling to Fibb_NST Fibrilloger beta chair precusor. [Contains: Fibrinopeptide B] [R.norvegicus], Mus musculus, Similar to angiopoietin-
			E, S, MM,		musculus, Similar to fibrinogen-like 1, clone MGC:37822 IMAGE:5098805, mRNA,
4091	2010	U05675	KKK, TTT		complete cds, angiopoietin-like 2, expressed sequence Al593246
			General Core		EST, Weakly similar to C10 MOUSE PUTATIVE C10 PROTEIN [M.musculus],
865	2762	AA944165	Tox Markers		hypothetical protein BC009925
					EST, Weakly similar to CAHB_HUMAN CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECLIRSOR (CARP 2) (CA-R) (CA-R) (CARBONIC ANHYDRASE-RELATED
					PROTEIN 11) (CARP XI) [H.sapiens], ESTs, Weakly similar to A Chain A, Crystal
					Structure Of S-Glutathiolated Carbonic Anhydrase lii [R.norvegicus], Mus musculus,
					Carbonic anhydrase-related protein 10, clone MGC:27641 IMAGE:4507552, mRNA,
					complete cds, RIKEN cDNA 2700029L05 gene, carbonic anhydrase 11, carbonic
					anhydrase 13, carbonic anhydrase 14, carbonic anhydrase VI, carbonic anhydrase VII,
2423	9038	AI228419	<u>}-</u>		carbonic anhydrase XI
					EST, Weakly similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus], ESTs,
·- <u>-</u>	·				Highly similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus], ESTs,
					Moderately similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus], ESTs,
					Weakly similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus], bromodomain
321	14292	AA851791	<u>د</u>		containing 2
					EST, Weakly similar to CBX3_HUMAN CHROMOBOX PROTEIN HOMOLOG 3
31	19211	AA851329	XX HH HH		[H.sapiens], ESTS, Moderately similar to CBA3_HUMAN CHROMOBOA FROTEIN [HOMOLOG 3 IH.sapiens], Homo sapiens, clone IMAGE:4798132, mRNA, partial cds
					EST, Weakly similar to CLN3 HUMAN CLN3 PROTEIN [H.sapiens], Homo sapiens
2313	2825	A1178752	WW		clone 319 CLN3 protein (CLN3) mRNA, complete cds, expressed sequence Al323623



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					EST, Weakly similar to COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR [M.musculus],
					Mus musculus, Similar to splicing factor, arginine/serine-rich 8 (suppressor-of-white-
					apricot homolog, Drosophila), clone MGC:31019 IMAGE:5006904, mRNA, complete
					cds, RIKEN cDNA 3010033P07 gene, expressed sequence AL022771, expressed
3606	16929	NM 031108	I		sequence AL022885, ribosomal protein S9
					EST, Weakly similar to DYJ2_HUMAN DYNEIN LIGHT INTERMEDIATE CHAIN 2,
					CYTOSOLIC [H.sapiens], LIC-2 dynein light intermediate chain 53/55, RIKEN cDNA
					1110053F02 gene, dynein light chain-A, dynein, cytoplasmic, light intermediate
2900	9745	H31847	g R		polypeptide 2, expressed sequence AA409702
			KK, GGG,		EST, Weakly similar to G02526 NADH dehydrogenase [H.sapiens], NADH
			HHH, General		dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13), RIKEN cDNA
22	15654	AA799501	Alternate		2900002J19 gene
					EST, Weakly similar to G02526 NADH dehydrogenase [H.sapiens], NADH
					dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13), RIKEN cDNA
3187	20943	NM_012985 MM, TTI	MM, TTT		2900002J19 gene
L_					EST, Weakly similar to G02526 NADH dehydrogenase [H.sapiens], NADH
					dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13), RIKEN cDNA
4198	15653	X14210	= '55		2900002J19 gene
					EST, Weakly similar to GBG9 RAT GUANINE NUCLEOTIDE-BINDING PROTEIN
					G(I)/G(S)/G(O) GAMMA-9 SUBUNIT [M.musculus], ESTs, Highly similar to AF188180 1
					G-protein gamma 8 subunit [M.musculus], ESTs, Weakly similar to GBG8_MOUSE
					Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-8 subunit (Gamma-9)
					[R.norvegicus], G-protein gamma 8 subunit, guanine nucleotide binding protein (G
			XX, YY, PPP,		protein), gamma 2 subunit, guanine nucleotide binding protein (G protein), gamma 4
2972	1695	L35921	000		subunit, guanine nucleotide binding protein 4



France Figure F		Tables				
D, EE D, EE, GG, OO , R		elec [.] One	consenz Les or Rese (D		Here Kino	ous Sequence, cluster utitie
15186 NM_030861 DD, EE 15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					EST, Weakly simi	lar to GNT1_RAT Alpha-1,3-mannosyl-glycoprotein beta-1,2-N-
15186 NM_030861 DD, EE 15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					acetyiglucosariiii)	/itransferase (iv-glycosyl-oligosaccinalide-glycophotein iv- /itransferase I) (GNT-I) (GlcNAc-T I) [R.norvegicus], RIKEN cDNA
15186 NM_030861 DD, EE 15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					4930467B06 gene	e, mannoside acetylglucosaminyltransferase 1, mannosyl (alpha-1,3-)-
15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R		15186	NM_030861	DD, EE	glycoprotein beta-	1,2-N-acetylglucosaminyltransferase
15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R	ı				EST, Weakly simi	lar to GNT1_RAT Alpha-1,3-mannosyl-glycoprotein beta-1,2-N-
15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AAB92297 D 17734 NM_031970 Q, R					acetylglucosaminy	/Itransferase (N-glycosyl-oligosaccharide-glycoprotein N-
15187 NIM_030861 FF, TT, NNN 15188 NIM_030861 OOO 17734 NIM_031970 Q, R 17735 NIM_031970 Q					acetylglucosaminy	/Itransferase I) (GNT-I) (GICNAc-T I) [R.norvegicus], RIKEN cDNA
15187 NM_030861 FF, TT, NNN 15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					4930467B06 gene	e, mannoside acetylglucosaminyltransferase 1, mannosyl (alpha-1,3-)-
15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R	٠.	15187	NM_030861	FF, 17	glycoprotein beta-	1,2-N-acetylglucosaminyltransferase
15188 NM_030861 OOO 7226 AAB92297 D 17734 NM_031970 Q, R	ı				EST, Weakly simi	lar to GNT1_RAT Alpha-1,3-mannosyl-glycoprotein beta-1,2-N-
15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					acetylglucosaminy	/Itransferase (N-glycosyl-oligosaccharide-glycoprotein N-
15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R					acetylglucosaminy	/Itransferase I) (GNT-I) (GICNAc-T I) [R.norvegicus], RIKEN cDNA
15188 NM_030861 OOO 7226 AA892297 D 17734 NM_031970 Q, R 17735 NM_031970 Q				DD, EE, GG,	4930467B06 gene	e, mannoside acetylglucosaminyltransferase 1, mannosyl (alpha-1,3-)-
7226 AAB92297 D 17734 NM_031970 Q, R 17735 NM_031970 Q		15188	NM_030861		glycoprotein beta-	.1,2-N-acetylglucosaminyltransferase
7226 AA892297 D 17734 NM_031970 Q, R 17735 NM_031970 Q	l				EST, Weakly simi	lar to HDA2_HUMAN HISTONE DEACETYLASE 2 [H.sapiens], Mus
7226 AA892297 D 17734 NM_031970 Q, R 17735 NM_031970 Q					musculus, Similar	to hypothetical protein FLJ22237, clone MGC:27683
17734 NM_031970 Q, R 17735 NM_031970 Q		7226	AA892297	٥	IMAGE:4913322,	mRNA, complete cds, histone deacetylase 2
17734 NM_031970 Q, R 17735 NM_031970 Q	l				EST, Weakly simi	lar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly similar
17734 NM_031970 Q, R 17735 NM_031970 Q					to HHHU27 heat	shock protein 27 [H.sapiens], ESTs, Moderately similar to HHHU27
17734 NM_031970 Q, R 17735 NM_031970 Q					heat shock proteir	127 [H.sapiens], heat shock 27kD protein 1, hypothetical protein
17735 NM_031970 Q	٠.	17734	NM_031970	Q	MGC10974	
17735 NM_031970 Q	l				EST, Weakly simi	lar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly similar
17735 NM_031970 Q					to HHHUZ/ neat	snock protein z7 [H.sapiens], ESTS, Wioderately Similar to HHHUZ/
1//35 INIM_UST8/U IQ	_		A184 004070		MOCAOCA PIOCE	127 [m.sapielis], ileat silven 27 nd ploteli 1, lighottietical plotelii
	- 1		NIVI OS ISTO	2	+1601 JON1	



1772 17736 MM 031970 CCC COCC COCC COCC COCC COCC CCC CC	TABLE 9	ଜ ଜ				THE TANK TO THE TANK THE
17736 NM_031970 CCC 15615 NM_053800 DDD 17100 NM_022179 F 17101 NM_022179 F 17101 NM_022179 HHH CGG, HHH OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T		GLGC BNG	ලේඛ:දිතැ? Ace or ි RefSeq (D	Model Gode	ran H. P. Ian Homologous wn Gene Name	
17736 NM_031970 CCC 15615 NM_053800 DDD 17100 NM_022179 F 17101 NM_022179 F 17101 NM_022179 HHH OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						EST, Weakly similar to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Highly similar
17736 NM_031970 CCC 15615 NM_053800 DDD 17100 NM_022179 F 17101 NM_022179 F A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						to HHHU27 heat shock protein 27 [H.sapiens], ESTs, Moderately similar to HHHU27
15615 NM 053800 DDD 17100 NM 022179 F 17101 NM 022179 F 17101 NM 022179 HHH GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers Z0827 AA963185 T	,	000	20700			neat shock protein 27 [H.sapiens], heat shock 27kD protein 1, hypothetical protein
15615 NM_053800 DDD 17100 NM_022179 F 17101 NM_022179 HHH JJ, KK, FFF, HHH GGG, HHH, OOO, General Core Tox 9191 Al072107 Markers 20827 AA963185 T	3712	17/36	NM 0319/0			MGC10974
17100 NM_022179 F JJ, KK, FFF, JJ, KK, FFF, HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T	3829	15615	NM 053800			EST, Weakly similar to human Thioredoxin [n.sapiens], Kincin CDNA 4930429324 gene, thioredoxin, thioredoxin 1
17100 NM_022179 F 17101 NM_022179 HHH 17101 NM_022179 HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs,
17100 NM_022179 F JJ, KK, FFF, 17101 NM_022179 HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						Moderately similar to HXK3_HUMAN HEXOKINASE TYPE III [H.sapiens], ESTs,
17100 NM_022179 F JJ, KK, FFF, JJ, KK, FFF, A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T			· · ·			Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase 2,
JJ, KK, FFF, JJ, KK, FFF, HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T	3445	_	NM_022179	щ		hexokinase 3 (white cell)
JJ, KK, FFF, HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 A072107 Markers Z0827 A9963185 T						EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs,
JJ, KK, FFF, HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						Moderately similar to HXK3_HUMAN HEXOKINASE TYPE III [H.sapiens], ESTs,
17101 NM_022179 HHH A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 Al072107 Markers 20827 AA963185 T				JJ, KK, FFF,		Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase 2,
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers	3445	17101	NM_022179			hexokinase 3 (white cell)
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers						EST, Weakly similar to I73674 chlordecone reductase homolog [H.sapiens], ESTs,
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers						Highly similar to 2008147B protein RAKc [Rattus norvegicus] [R.norvegicus], ESTs,
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 Al072107 Markers 20827 AA963185 T						Highly similar to DBDD_HUMAN TRANS-1,2-DIHYDROBENZENE-1,2-DIOL
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 Al072107 Markers 20827 AA963185 T						DEHYDROGENASE [H.sapiens], ESTs, Moderately similar to DBDD_HUMAN TRANS-
A, B, OO, FFF, GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T						1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE [H.sapiens], ESTs, Weakly
GGG, HHH, OOO, General Core Tox 9191 AI072107 Markers 20827 AA963185 T				A, B, 00, FFF,		similar to DHBX MOUSE ESTRADIOL 17 BETA-DEHYDROGENASE, A-SPECIFIC
9191 Al072107 Markers 20827 AA963185 T				GGG, HHH,		[M.musculus], Homo sapiens truncated AKR mRNA for truncated aldo-keto reductase
9191 AI072107 Markers 20827 AA963185 T				000, General		type B, partial cds, aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-
9191 AI072107 Markers 20827 AA963185 T		:		Core Tox		alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4),
20827 AA963185 T	1723	9191	AI072107	Markers		hydroxysteroid (17-beta) dehydrogenase 5
20827 AA963185 T						EST, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens],
20827 AA963185 T						ESTs, Highly similar to RS28_HUMAN 40S RIBOSOMAL PROTEIN S28 [H.sapiens],
20827 AA963185 T						ESTs, Moderately similar to RS28_HUMAN 40S RIBOSOMAL PROTEIN S28
	1047			<u> </u>		[M.musculus], RNA polymerase 1-1 (40 kDa subunit), ribosomal protein S28



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(Asimional)	Human Homologous	EST, Weakly similar to IF37 MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 7 [M.musculus], eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67 kDa), eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	EST, Weakly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens], Homo sapiens cDNA FLJ12978 fis, clone NT2RP2006321, RAN binding protein 6, importin 4	EST, Weakly similar to JC1365 FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens], FK506 binding protein 7, FK506 binding protein precursor	EST, Weakly similar to JC1365 FK506/rapamycin-binding protein FKBP13 precursor [H.sapiens], FK506 binding protein 7, FK506 binding protein precursor	EST, Weakly similar to JC2324 LIM protein [H.sapiens], Homo sapiens cDNA FLJ13238 fis, clone OVARC1000440, RIKEN cDNA 2410002J21 gene, expressed sequence	AV278559, expressed sequence AW123232, hypothetical protein FLJ10044, paxillin, transforming growth factor beta 1 induced transcript 1	EST, Weakly similar to JC2369 ribosomal protein L15, cytosolic [validated] - rat	[H.sapiens], Homo sapiens, clone MGC:2392 IMAGE:2961444, mRNA, complete cds, RIKEN cDNA 2510008H07 gene, ribosomal protein L15	EST, Weakly similar to JC5111 cyclin-dependent kinase-related protein 1b - rat	[R.norvegicus], EST, Weakly Similar to ST0869 proine-rich protein [n.sapiens], ESTS, Highly similar to KPT1 MOUSE SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	[M.musculus], ESTs, Weakly similar to KPT1 MOUSE SERINE/THREONINE-PROTEIN	kinase 1	EST, Weakly similar to JC7286 liver-specific organic anion transporter-1 - mouse	mouse [M.musculus], RIKEN cDNA 1700022M03 gene, expressed sequence Al060904,	solute carrier family 21 (organic anion transporter), member 10, solute carrier family 21	(organic anion transporter), member 6
	Model Gode	General Core Tox Markers	R	a	F, HH		nnn	V EEF	General Core				PP, QQ		B, PPP,	General Core	Tox Markers
ICABELLE 30	%ee or : '` Re(Seq (D	AA891553	A1137586	AA998471			AA799637		NM 139114	l			NM 031077				AI169779
ନ ଜୁନ	(1900) (1900)	17225	7414	26116	26117		20093		15239				6348				20503
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	GLGG" ID No.	 Ace ගේ RatScq (D	Keit Este	Numan Homologows Known Gene Name Human Homologows Sequence Gluster IIIIle	Works and the second se
				[M.musculus], ESTs, Weakly similar to JC7286 liver-specific organic anion transporter-1 - mouse [M.musculus], ESTs, Weakly similar to JC7286 liver-specific organic anion transporter-1 mouse [M.musculus], RIKEN cDNA 1700022M03 gene, expressed sequence Al060904,	organic anion transporter-1 - mouse 86 liver-specific organic anion transporter-1 2M03 gene, expressed sequence Al060904,
3664	20502	NM_031650	z ď	solute carrier farmiy z i (organic anior transporter), member 10, solute carrier farmiy z i (organic anion transporter), member 6	odiel), membel 10, solute carrier larmiy 2.1
			DD, EE, JJ, OO, III, JJJ,		
			000, General	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE	INE/ETHANOLAMINE KINASE
434	16327	AA875050	Core Tox Markers	[M.musculus], RIKEN cDNA 4930555L11 gene, choline kinase-like, expressed sequence Al197444, hypothetical protein FLJ10761	ne, choline kinase-like, expressed J10761
				EST, Weakly similar to MAN2_HUMAN ALPHA-MANNOSIDASE II [H.sapiens], KIAA0935 protein. mannosidase 2. alpha B1. mannosidase 2.	HA-MANNOSIDASE II [H.sapiens], mannosidase 2. aloha B1. mannosidase 2.
			(alpha B2, mannosidase, alpha, class 2A, member 2, mannosidase, alpha, class 2B,	mber 2, mannosidase, alpha, class 2B,
2319	6628	AI178793	99	member 1	
				EST, Weakly similar to MLRV_RAT Myosin regulatory light chain 2, ventricular/cardiac muscle isoform (MLC-2) [R.norvegicus], ESTs, Weakly similar to MLRV_RAT Myosin	regulatory light chain 2, ventricular/cardiac
				regulatory light chain 2, ventricular/cardiac muscle isoform (MLC-2) [R.norvegicus], myosin light chain 2, precursor lymphocyte-specific, myosin light chain,	nuscle isoform (MLC-2) [R.norvegicus], specific, myosin light chain,
2082	17883	M11851	PP, QQ, Ⅲ,	phosphorylatable, cardiac ventricles, myosin, light polypeptide 2, regulatory, cardiac,	i, light polypeptide 2, regulatory, cardiac,
				EST, Weakly similar to MLRV_RAT Myosin regulatory light chain 2, ventricular/cardiac	regulatory light chain 2, ventricular/cardiac
		·		muscle isoform (MLC-2) [R.norvegicus], Rat heart myosin light chain 2 (MLC2) mRNA,	heart myosin light chain 2 (MLC2) mRNA,
				3' end, myosin light chain 2, precursor lymphocyte-specific, myosin light chain, phosphoniatable cardiac ventricles myosin light polynentide 2 regulatory cardiac	nocyte-specific, myosin light chain, light polypertide 2 regulatory cardiac
473	18397	AA891242	KK	slow	
i i				EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form [H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,	cali light chain 6, nonmuscle form uscle, myosin, light polypeptide 6, alkali,
400	24470	AA875523	55	Smooth muscle and non-muscle	

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See		जिन्ना हिन्ता हुन्। शब्द वर्ण		ເພັກຂາກ ເກີອ ຕົວໄວ ອີບອ	neni Komologous
	. (10) No.	 	शिन्त्री (दर्बर्व)	Known Gene Nameh	Human Homologous Sequence Guster mile
					EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form
					[H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,
699	24473	AA894200	Z, AA		smooth muscle and non-muscle
					EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form
					[H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,
699	24474	AA894200	99		smooth muscle and non-muscle
			J, Q, R, GG, II,		EST, Weakly similar to MOHU6N myosin alkali light chain 6, nonmuscle form
			EEE, FFF,		[H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali,
4077	24469	S77858	HHH, MMM		smooth muscle and non-muscle
					EST, Weakly similar to MOT2_RAT Monocarboxylate transporter 2 (MCT 2)
					[R.norvegicus], ESTs, Weakly similar to MOT2 MOUSE MONOCARBOXYLATE
					TRANSPORTER 2 [M.musculus], ESTs, Weakly similar to MOT2_RAT
					Monocarboxylate transporter 2 (MCT 2) [R.norvegicus], ESTs, Weakly similar to
			V, III, JJJ,		MOT3_HUMAN MONOCARBOXYLATE TRANSPORTER 3 [H.sapiens], solute carrier
			General Core		family 16 (monocarboxylic acid transporters), member 6, solute carrier family 16
2476	12587	AI229979	Tox Markers		(monocarboxylic acid transporters), member 7
					EST, Weakly similar to NPT1_RAT RENAL SODIUM-DEPENDENT PHOSPHATE
	_				TRANSPORT PROTEIN 1 (SODIUM/PHOSPHATE COTRANSPORTER 1) (NA(+)/PI
					COTRANSPORTER 1) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 1)
	_				(RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 1) [R.norvegicus],
		· ·			ESTs, Weakly similar to RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT
					PROTEIN 1 [M.musculus], Mus musculus, Similar to solute carrier family 17 (sodium
					phosphate), member 2, clone MGC:19073 IMAGE:4193755, mRNA, complete cds,
			-		expressed sequence AW261723, solute carrier family 17 (sodium phosphate), member
					1, solute carrier family 17 (sodium phosphate), member 2, solute carrier family 17
		_			(sodium phosphate), member 3, solute carrier family 17 (sodium phosphate), member 4,
4114	1558	U28504	GG, JJJ, NNN		solute carrier family 17 vesicular glutamate transporter), member 1



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		:			EST, Weakly similar to NPT1_RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 (SODIUM/PHOSPHATE COTRANSPORTER 1) (NA(+)/PICOTRANSPORTER 1) (NENAL SODILIM-PHOSPHATE TRANSPORT PROTEIN 1)
<u>,</u>	-				(RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 1) [R.norvegicus],
					ESTS, Weakiy similar to REIVAL SOUTOW-DEPENDENT PROSPINTE TRANSPORT PROTEIN 1 [M.musculus], Mus musculus, Similar to solute carrier family 17 (sodium
					phosphate), member 2, clone MGC:19073 IMAGE:4193755, mRNA, complete cds,
					expressed sequence Avvzo 1723, solute carrier family 17 (sodium phosphate), member 1, solute carrier family 17 (sodium phosphate), member 2, solute carrier family 17
					(sodium phosphate), member 3, solute carrier family 17 (sodium phosphate), member 4,
4114	1559	U28504	FF, GG, NNN		solute carrier family 17 vesicular glutamate transporter), member 1
			E, General		EST, Weakly similar to PPOX MOUSE PROTOPORPHYRINOGEN OXIDASE
393	14138	AA859700	Alternate		[M.musculus], protoporphyrinogen oxidase
			E, III, JJJ,		
			NNN, General		EST, Weakly similar to PPOX MOUSE PROTOPORPHYRINOGEN OXIDASE
393	14139	AA859700	Alternate		[M.musculus], protoporphyrinogen oxidase
					EST, Weakly similar to PRC5 MOUSE PROTEASOME COMPONENT C5 [M.musculus],
					ESTs, Weakly similar to PRC5 MOUSE PROTEASOME COMPONENT C5
	0,000				[M.musculus], proteasome (prosome, macropain) subunit, beta type 1, proteasome
3/8/	20842	053590 MN	X, Y, KK, UUU		(prosome, macropain) subunit, beta type, 1
					EST, Weakly similar to PRO1 MOUSE PROFILIN [M.musculus], EST, Weakly similar
130	2100	A A 8 1 7 8 8 7	}		10 FNOZ TOWNAN FNOT ILIN II (1.38pielis), ESTS, weakly similar (0 FNOZ TOWAN) PROFIL IN II (H sanians) Mk1 protein profilin 1
3					EST, Weakly similar to PRO1 MOUSE PROFILIN I [M.musculus], EST, Weakly similar
					to PRO2 HUMAN PROFILIN II [H.sapiens], ESTs, Weakly similar to PRO2 HUMAN
2626	3073	AI233494	JJ, KKK, NNN		PROFILIN II [H.sapiens], profilin, profilin 1
_					EST, Weakly similar to PRO1 MOUSE PROFILIN I [M.musculus], EST, Weakly similar
			-		to PRO2_HUMAN PROFILIN II [H.sapiens], ESTs, Weakly similar to PRO2_HUMAN
2626	3074	AI233494	JJ		PROFILIN II [H.sapiens], profilin, profilin 1

	TABLES	中国 中			. Attorney Docket (K. K. K.) - Attorney Docket (K. K. K.) - Attorney Document No. 1935328,1
	<u>erec</u>				man Homologious
, @	ID No.		Model Gode	Known Gene Name	own eene Name Human Homologove Sequence Cluster Mue
					EST, Weakly similar to PRO1 MOUSE PROFILIN I [M.musculus], EST, Weakly similar
	-				to PRO2_HUMAN PROFILIN II [H.sapiens], ESTs, Weakly similar to PRO2_HUMAN
2626	3 3075	AI233494	F, JJ		PROFILIN II [H.sapiens], profilin, profilin 1
					EST, Weakly similar to PRP2 MOUSE PROLINE-RICH PROTEIN MP-2 PRECURSOR
	<u></u>				[M.musculus], ESTs, Weakly similar to PRP2 MOUSE PROLINE-RICH PROTEIN MP-2
	-				PRECURSOR [M.musculus], ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION
					INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens], Mus musculus brain
					cDNA, clone MNCb-3966, RIKEN cDNA 1110020C13 gene, TAF4 RNA polymerase II,
					TATA box binding protein (TBP)-associated factor, 135 kD, hypothetical protein
3915	5 17413	08090NN	F		FLJ20152, proline rich protein, reticulon 3
					EST, Weakly similar to PRS7 MOUSE 26S PROTEASE REGULATORY SUBUNIT 7
			S, BBB, CCC,		[M.musculus], RIKEN cDNA 2300001E01 gene, proteasome (prosome, macropain) 26S
2868	3 2578	D50694	999		subunit, ATPase 2, syntaxin 8
					EST, Weakly similar to PRS7 MOUSE 26S PROTEASE REGULATORY SUBUNIT 7
					[M.musculus], RIKEN cDNA 2300001E01 gene, proteasome (prosome, macropain) 26S
3735	5 2577	NM_033236	Α, Υ		subunit, ATPase 2, syntaxin 8
					EST, Weakly similar to PRS8 MOUSE 26S PROTEASE REGULATORY SUBUNIT 8
					[M.musculus], Homo sapiens mRNA; cDNA DKFZp586i1420 (from clone
					DKFZp586I1420); partial cds, YME1-like 1 (S. cerevisiae), hypothetical protein
					DKFZp667C165, protease (prosome, macropain) 26S subunit, ATPase 5, proteasome
					(prosome, macropain) 26S subunit, ATPase, 5, proteasome (prosome, macropain) 26S
1199	9 1291	AB000491	SΉ		subunit, ATPase, 6
					EST, Weakly similar to PSD4_HUMAN 26S PROTEASOME REGULATORY SUBUNIT
3627	7 18375	NM_031331	G, H, S		S5A [H.sapiens], proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
					EST, Weakly similar to PSD4_HUMAN 26S PROTEASOME REGULATORY SUBUNIT
3627	7 18376	NM_031331	SS		S5A [H.sapiens], proteasome (prosome, macropain) 26S subunit, non-ATPase, 4



TABLE 3	ශ ස				Attorney Doctot 44921-5039-01000 Document No. 1985328.1
88 (<u>a</u>	elec D No.	<u>କ୍ରେଲ୍ଲେମ୍ଲ୍ୟ</u> Ace ତିନ୍	Model Gode	Himen Homologous Kinown Gene Neme	Hameral Homologous Sequence Guster We
					EST, Weakly similar to R6HUP1 acidic ribosomal protein P1, cytosolic [H.sapiens],
					ESTs, Highly similar to R6HUP1 acidic ribosomal protein P1, cytosolic [H.sapiens],
					ESTs, Weakly similar to RLA1 MOUSE 60S ACIDIC RIBOSOMAL PROTEIN P1
921	24521	AA945636	aaa		[M.musculus], expressed sequence Al255964, ribosomal protein, large, P1
					EST, Weakly similar to R6RT30 ribosomal protein L30, cytosolic [validated] - rat
					[R.norvegicus], EST, Weakly similar to S45004 ribosomal protein L30, cytosolic
					[H.sapiens], ESTs, Highly similar to S45004 ribosomal protein L30, cytosolic
					[H.sapiens], ESTs, Moderately similar to S45004 ribosomal protein L30, cytosolic
3511	19375	NM_022699	₩		[H.sapiens]
					EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus],
					ESTs, Weakly similar to Crystal Structure Of The Small G Protein Rap2a With Gdp
	÷				{SUB 1-167 [H.sapiens], ESTs, Weakly similar to RALA MOUSE RAS-RELATED
					PROTEIN RAL-A [M.musculus], v-ral simian leukemia viral oncogene homolog A (ras
3299	15201	NM_031093	F		related)
					EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus],
					ESTs, Weakly similar to Crystal Structure Of The Small G Protein Rap2a With Gdp
					{SUB 1-167 [H.sapiens], ESTs, Weakly similar to RALA MOUSE RAS-RELATED
					PROTEIN RAL-A [M.musculus], v-ral simian leukemia viral oncogene homolog A (ras
3299	15202	NM_031093	V, LL, WW		related)
			G, H, CC,		
			ppp, ggg,		
			HHH, General		EST, Weakly similar to RL12_HUMAN 60S RIBOSOMAL PROTEIN L12 [H.sapiens],
	:		Core Tox		ESTs, Weakly similar to RL12_HUMAN 60S RIBOSOMAL PROTEIN L12 [H.sapiens],
4216	18606	X53504	Markers		ribosomal protein L12
4202	19244	X15013	G, H, JJJ		EST, Weakly similar to RL7A MOUSE 60S RIBOSOMAL PROTEIN L7A [M.musculus], RIKEN cDNA 4632404N19 gene, ribosomal protein L7a



TABL	TABLE 3				Attorney Docket 44,924-5038-641W0 Document No. 1995228.1
Sed	GLGG (ID No.	ල්කාදේකායි /2ලේ ගේ යිරෙදීලේ 10	Medi Gede	Humen Homologous Known Gene Neme	an Homologous The factor of
					EST, Weakly similar to RS27_HUMAN 40S RIBOSOMAL PROTEIN S27 [H.sapiens],
					ESTs, Highly similar to RS27_HUMAN 40S RIBOSOMAL PROTEIN S27 [H.sapiens],
218	17097	AA819501	=,		ESTS, Moderately similar to RSZ/HOWAN 40S RIBOSOWAL PROTEIN SZ/ [H.sapiens], RIKEN cDNA 3200001M24 gene, ribosomal protein S27-like
					EST, Weakly similar to S13101 cytochrome P450 c117 - rat [R.norvegicus], Mus
	-				musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA
					2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29,
	_				cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19,
3706	10947	NM_031839	PP, QQ		expressed sequence Al159681, expressed sequence AW107714
					EST, Weakly similar to S13101 cytochrome P450 c117 - rat [R.norvegicus], Mus
					musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA
					2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29,
			FF, EEE,		cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19,
3706	10949	NM_031839	MMM		expressed sequence A1159681, expressed sequence AW107714
					EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat
					[R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1 alpha-
_					1 chain [H.sapiens], ESTs, Weakly similar to S21055 translation elongation factor eEF-1
					alpha chain - rat [R.norvegicus], G1 to S phase transition 1, G1 to phase transition 1, G1
3738	24419	NM_033539	Y		to phase transition 2, eukaryotic translation elongation factor 1 alpha 1
					EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat
					[R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1 alpha-
					1 chain [H.sapiens], G1 to phase transition 1, eukaryotic translation elongation factor 1
2467	23573	AI229595	D		alpha 1
					EST, Weakly similar to S21977 Pm5 protein [H.sapiens], Homo sapiens cDNA:
					FLJ23491 fis, clone LNG00825, highly similar to HSPM5 Human mRNA for pM5 protein,
1383	23768	AI011709	 <u>≻</u>		pM5 protein



Centerny Ace or Refseq (D) Model Godlo,	ر مول	Kumen Homologovs Known Genettemer Humen Homologous Sequence Gluster Mile.
		EST, Weakly similar to S37583 RING finger protein rfp - mouse [M.musculus], ESTs, Moderately similar to JE0343 terf protein - rat [R.norvegicus], ESTs, Weakly similar to
		JE0343 terf protein - rat [R.norvegicus], Homo sapiens, clone IMAGE:3678120, mRNA, partial cds, RIKEN cDNA 1810012B10 gene, expressed sequence AW538890, gene
Z, AA		overexpressed in astrocytoma, hypothetical protein FLJ22612, hypothetical protein MGC13061, ring finger protein 27, tripartite motif-containing 17
		EST, Weakly similar to S44204 procollagen-proline dioxygenase (EC 1.14.11.2) alpha
		chain - rat [R.norvegicus], ESTs, Weakly similar to DAHUA2 procollagen-proline
Q R		idoxygeriase [n.sapieris], norito sapieris, dorie images rozz ro, nikiva, partiai cus, hypothetical protein FLJ20262
		EST, Weakly similar to S49326 nascent polypeptide-associated complex alpha chain
		[H.sapiens], EST, Weakly similar to T30827 nascent polypeptide-associated complex
		alpha chain, non-muscle splice form - mouse [M.musculus], FKSG17, KIAA0363 protein,
		expressed sequence AL022831, nascent-polypeptide-associated complex alpha
N, <		polypeptide
		EST, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII precursor,
	2	hepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa, heme-regulated
		initiation factor 2-alpha kinase
		EST, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII precursor,
F, LL, RRR	RRR,	hepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa, heme-regulated
nnn		initiation factor 2-alpha kinase
		EST, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII precursor,
		hepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa, heme-regulated
F		initiation factor 2-alpha kinase
		EST, Weakly similar to S71929 cytochrome-c oxidase (EC 1.9.3.1) chain VIII precursor,
		hepatic - mouse [M.musculus], cytochrome c oxidase, subunit VIIIa, heme-regulated
<u> </u>		initiation factor 2-alpha kinase

TABU	ଡ	TABUES	9 m. 4 m. 1		Attorney Decket 4921-5038-01000
නිලේ [ලි	GLGC DNG	eensenk Aee or Reiseg (D	जिल्ला हिन्द्र हैं। अञ्चान हिन्द्र हैं।	Human Homologous Known Gene Name	Human Hömölögövis Sequence Cluster Mila
					EST, Weakly similar to secreted cyclophilin-like protein [H.sapiens], ESTs, Weakly
					similar to cyclophilin B [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 3732410E19
					gene, peptidylprolyl isomerase (cyclophilin)-like 1, peptidylprolyl isomerase B,
					peptidylprolyl isomerase B (cyclophilin B), peptidylprolyl isomerase C, peptidylprolyl
3481	8097	NM_022536	BB, CC		somerase C (cyclophilin C)
					EST, Weakly similar to SYFB_MOUSE PHENYLALANYL-TRNA SYNTHETASE BETA
					CHAIN (PHENYLALANINETRNA LIGASE BETA CHAIN) (PHERS) [M.musculus],
					Homo sapiens cDNA FLJ30727 fis, clone FEBRA2000007, highly similar to Homo
					sapiens putative phenylalanyl-tRNA synthetase beta-subunit mRNA, KIAA1185 protein,
					RIKEN cDNA 2900010D03 gene, expressed sequence C76708, phenylalanine-tRNA
2300	6502	AI178283	×		synthetase-like, phenylalanyl-tRNA synthetase beta-subunit
					EST, Weakly similar to T00637 hypothetical protein H_GS541B18.1 [H.sapiens], golgi
1376	24022	AI011474	000		phosphoprotein 2
					EST, Weakly similar to T02345 hypothetical protein KIAA0324 [H.sapiens], ESTs,
					Weakly similar to T02345 hypothetical protein KIAA0324 [H.sapiens], Homo sapiens
_					cDNA FLJ31094 fis, clone IMR321000165, polymerase I and transcript release factor,
1084	24166	AA964630	W		serine/arginine repetitive matrix 2
					EST, Weakly similar to T10086 alcohol sulfotransferase (EC 2.8.2.2) - mouse
					[M.musculus], ESTs, Weakly similar to SUH2_RAT Probable alcohol sulfotransferase
	_				(Hydroxysteroid sulfotransferase) (ST) (Senescence marker protein 2) (SMP-2)
					(Androgen-repressible liver protein) (Dehydroepiandrosterone sulfotransferase) (DST)
					[R.norvegicus], RIKEN cDNA 2810007J24 gene, sulfotransferase family, cytosolic, 2A,
					dehydroepiandrosterone (DHEA) -preferring, member 1, sulfotransferase family,
3119	18718	NM_012695	××		cytosolic, 2B, member 1, sulfotransferase, hydroxysteroid preferring 2
					EST, Weakly similar to T12456 hypothetical protein DKFZp564M2423.1 [H.sapiens],
					ESTs, Highly similar to T12456 hypothetical protein DKFZp564M2423.1 [H.sapiens], PAI
					1 mRNA-binding protein, RIKEN cDNA 1200009K13 gene, intracellular hyaluronan-
1036	22358	AA957624	٦, ٧		binding protein

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889 10	GLGC ID No.	ිල්බාවෙකි. Ace ගේ Ref පිලේ [D	्रहेळ्जू स्ट्रिक्स	Human Homologous KnowniGene Name Human Homologous Sequence Gluster Title	ter Title
743	4942	AA924396	Q, R	EST, Weakly similar to T43481 probable mucin DKFZp434C196.1 [H.sal Weakly similar to T43481 probable mucin DKFZp434C196.1 [H.sapiens]	EST, Weakly similar to T43481 probable mucin DKFZp434C196.1 [H.sapiens], ESTs, Weakly similar to T43481 probable mucin DKFZp434C196.1 [H.sapiens]
တ	21815	AA686423	RRR, UUU	EST, Weakly similar to T46390 hypothetical prot hepatocellular carcinoma-associated antigen 59	EST, Weakly similar to T46390 hypothetical protein DKFZp434C1920.1 [H.sapiens], hepatocellular carcinoma-associated antigen 59
1142	21812	AA997588	၁၁၁	EST, Weakly similar to T46390 hypothetical prothetical	EST, Weakly similar to T46390 hypothetical protein DKFZp434C1920.1 [H.sapiens], hepatocellular carcinoma-associated antigen 59
3461	17158	NM 022298	9,0	EST, Weakly similar to TBA1 MOUSE 1 alpha 1, tubulin, alpha 2, tubulin, alpha alpha, ubiquitous	EST, Weakly similar to TBA1 MOUSE TUBULIN ALPHA-1 CHAIN [M.musculus], tubulin, alpha 1, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha 6, tubulin, alpha 7, tubulin, alpha, ubiquitous
3461	17161	NM_022298 V, XX, YY	v, xx, v	EST, Weakly similar to TBA1 MOUSE 1 alpha 1, tubulin, alpha 2, tubulin, alpha alpha, ubiquitous	EST, Weakly similar to TBA1 MOUSE TUBULIN ALPHA-1 CHAIN [M.musculus], tubulin, alpha 1, tubulin, alpha 2, tubulin, alpha 6, tubulin, alpha 7, tubulin, alpha, ubiquitous
411	13974	AA860030	0, P, W	EST, Weakly similar to TBB5 MOUSE CONA 2310061K05 gene, RIKEN cDNA gene, tubulin, beta 5, tubulin, beta polyr	EST, Weakly similar to TBB5 MOUSE TUBULIN BETA-5 CHAIN [M.musculus], RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 5, tubulin, beta, 5
1208	13973	AB011679	O, P	EST, Weakly similar to TBB5 MOUSE CDNA 2310061K05 gene, RIKEN cDNA gene, tubulin, beta 5, tubulin, beta poly	EST, Weakly similar to TBB5 MOUSE TUBULIN BETA-5 CHAIN [M.musculus], RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 5, tubulin, beta 6, tubuli
1005	11050	AA956164	HHH, General Alternate	EST, Weakly similar to TCPE MOUSE [M.musculus], ESTs, Weakly similar to T-complex 1, chaperonin containing TC TCP1, subunit 7 (eta), chaperonin subucomplex protein 1	EST, Weakly similar to TCPE MOUSE T-COMPLEX PROTEIN 1, EPSILON SUBUNIT [M.musculus], ESTs, Weakly similar to JQ0866 T-complex protein 1 - rat [R.norvegicus], T-complex 1, chaperonin containing TCP1, subunit 5 (epsilon), chaperonin containing TCP1, subunit 7 (eta), chaperonin subunit 5 (epsilon), chaperonin subunit 7 (eta), t-complex protein 1
1700	-		JJ, KK	EST, Weakly similar to TESTIN 2 [M.m. clone NT2RI2003338, Homo sapiens cl	EST, Weakly similar to TESTIN 2 [M.musculus], Homo sapiens cDNA FLJ31627 fis, clone NT2RI2003338, Homo sapiens cDNA FLJ31929 fis, clone NT2RP7006160

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Attorney Docket 41921-5038-61WO	nani Homologous Human Homologous Sequence Guster Wite Municene Name Est, Weakly similar to TRI9 HUMAN THYROID RECEPTOR INTERACTING EST, Weakly similar to TRI9 HUMAN THYROID RECEPTOR INTERACTING	PROTEIN 9 [H.sapiens], nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells	mRNA; cDNA DKFZp586L1121 (from clone DKFZp586L1121), fer (ms/rps related) protein kinase, testis specific 2	ES1, Weakly Similar to CD20—1000. (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 3) [R.norvegicus], ES1s, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Homo sapiens EST from clone 37208, full insert, RIKEN cDNA 1100001F19 gene, RIKEN cDNA 1600028117 gene, prefoldin 5, ubiquitin-conjugating enzyme E2D 3	(UBC4/5 homolog, yeast) (UBC4/5 homolog, yeast) Capacitation Capacitation	(Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 3) [K.norvegicus], E3 13, (Ubiquitin-protein ligase) (Ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Weakly similar to S53358 ubiquitin-conjugating enzyme E2D 3	(UBC4/5 homolog, yeast) (UBC4/5 homolog, yeast) EST Weakly similar to UB5C HUMAN Ubiquitin-conjugating enzyme E2-17 kDa 3	(Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2(17)KB 3) [R.norvegicus], E313, (Ubiquitin-protein ligase) (Ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus], Weakly similar to S53358 ubiquitin-conjugating enzyme E2 gene, Homo sapiens EST from clone 37208, full insert, RIKEN cDNA 1100001F19 gene, RIKEN cDNA 1600028117 gene, prefoldin 5, ubiquitin-conjugating enzyme E2D 3	(UBC4/5 homolog, yeast) (UBC4/5 homolog, yeast) (ST-COA EST, Weakly similar to VLCS_HUMAN VERY-LONG-CHAIN ACYL-COA	SYNTHETASE [H.sapiens], Homo sapiens cDNA FLJ23764 IIS, GOIDE III, 2723, AND SAME SYNTHETASE [H.sapiens], Homo sapiens cDNA FLJ23764 IIS, GOIDE III, 27 (fatty-acid-Coenzyme A ligase, very long-chain 1, hypothetical protein family 27 (fatty acid transporter), member 2, solute carrier family 27 (fatty acid transporter), member 3	ומווון בי נימני כסים מסים הייין
		General Alternate	ססם, נונ		Ŧ.		Q		PPP, QQQ		E
	seniseuu Vee or Refisee ID	G AA925318 A	A1044892 D		AA894258 L		AA900187		NM 031237	·	AA850055
9	9 9 9 9 9 9 9 9 9	23159	6941		15274		15275		15273		21310
] Sed (D	778	1565	T	672		704		3621		278
	·										

TABLES					Aitemey Doeket 44524-5038-011W0
	GLGG DND	Genisemk Aee or RefSeq (D	Model Gode	Humen Homologous Known Gene Neme	Ruman Homologous Scalance Cluster IIIIe
					EST, Weakly similar to WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG
					[M.musculus], ESTs, Highly similar to WASL_RAT Neural Wiskott-Aldrich syndrome
				<u> </u>	protein (N-WASP) [R.norvegicus], ESTs, Weakly similar to WISKOTT-ALDRICH
					SYNDROME PROTEIN HOMOLOG [M.musculus], Homo sapiens, clone MGC:24665
					IMAGE:4252688, mRNA, complete cds, RIKEN cDNA 2600017H02 gene, RIKEN cDNA
				7	4930474A20 gene, RIKEN cDNA 4930487N19 gene, Wiskott-Aldrich syndrome
					homolog (human), Wiskott-Aldrich syndrome-like, Wiskott-Aldrich syndrome-like
					(human), expressed sequence AA960202, fragile X mental retardation 1, hypothetical
					protein FLJ10159, hypothetical protein MGC12679, leukocyte receptor cluster (LRC)
1280	949	A1008687	ww		member 3
					EST, Weakly similar to ZF37_RAT Zinc finger protein 37 (Zfp-37) [R.norvegicus], ESTs,
					Moderately similar to 137961 zinc finger protein kox21 [H.sapiens], ESTs, Moderately
				<u> </u>	similar to ZF93_MOUSE ZINC FINGER PROTEIN 93 (ZFP-93) [M.musculus], ESTs,
. — .					Weakly similar to Z232_HUMAN ZINC FINGER PROTEIN 232 [H.sapiens], ESTs,
					Weakly similar to ZF93_MOUSE ZINC FINGER PROTEIN 93 (ZFP-93) [M.musculus],
					Mus musculus, Similar to zinc finger protein 85 (HPF4, HTF1), clone MGC:28872
				_	IMAGE:4527362, mRNA, complete cds, hypothetical protein MGC13250, zinc finger
•					protein 232, zinc finger protein 37, zinc finger protein 37 homolog (mouse), zinc finger
2606	13377	AI233056	SS	1	protein 93
					EST, Weakly similar to ZF37_RAT Zinc finger protein 37 (Zfp-37) [R.norvegicus], ESTs,
					Weakly similar to ZF29 MOUSE ZINC FINGER PROTEIN 29 [M.musculus], ESTs,
					Weakly similar to ZF93_MOUSE ZINC FINGER PROTEIN 93 (ZFP-93) [M.musculus],
	·. :				expressed sequence AW557864, zinc finger protein 29, zinc finger protein 37, zinc
4129	1623	U41164	Z		finger protein 37 homolog (mouse)
					EST, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein
					Y1) (RLZF-Y) [R.norvegicus], ESTs, Moderately similar to 137956 zinc finger protein
					kox17 [H.sapiens], ESTs, Weakly similar to MLZ4 MOUSE ZINC FINGER PROTEIN
1830	2064	A140341E	DO, EE, PP,	<u> </u>	MLZ-4 [M.musculus], RIKEN cDNA 2500002G23 gene, Rattus norvegicus zinc finger protein V1 /DI ZE V) mDNA complete cds zinc finder protein 00
1028	7	AI 1034 13	2		Totali I I (NEZF-1) IIINIAA, COTIPIETE COS, ZITC III gel protein 39

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	-743-			PCT/US03	/03194
EST, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein Y1) (RLZF-Y) [R.norvegicus], ESTs, Moderately similar to 137956 zinc finger protein kox17 [H.sapiens], ESTs, Weakly similar to S47072 finger protein HZF10, Krueppelrelated [H.sapiens], ESTs, Weakly similar to TC17 MOUSE TRANSCRIPTION FACTOR 17 [M.musculus], Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds, hypermethylated in cancer 2, zinc finger protein 354A, zinc finger protein 99	EST, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein Y1) (RLZF-Y) [R.norvegicus], ESTs, Moderately similar to I37956 zinc finger protein kox17 [H.sapiens], ESTs, Weakly similar to ZF94_MOUSE ZINC FINGER PROTEIN 94 (ZFP-94) [M.musculus], ESTs, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein Y1) (RLZF-Y) [R.norvegicus], Homo sapiens cDNA FLJ30551 fis, clone BRAWH2001503, KIAA0426 gene product, hypothetical protein FLJ12298, zinc finger protein 99	ESTs, Highly similar to 130kDa-Ins(1,4,5)P3 binding protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to 130kDa-Ins(1,4,5)P3 binding protein [Rattus norvegicus] [R.norvegicus], phospholipase C, delta, phospholipase C-like 1, phospholipase C-like 2	ESTs, Highly similar to calcitonin gene-related peptide-receptor component protein [Homo sapiens] [H.sapiens], calcitonin gene-related peptide-receptor component protein	ESTs, Highly similar to eukaryotic translation elongation factor 1 beta 2; eukaryotic translation elongation elongation factor 1 beta 1 [Homo sapiens] [H.sapiens], eukaryotic translation elongation factor 1 beta 2	ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
Z, AA	RR .	RR), UU,	n, General Core Tox Markers, General Alternate	a, R
Al235511	16345 NM 145724	E12159	NM_053670 C, UU	A1175551	8
14740	16345	930	24204	18507	15303
	I	1			1 1

TABLE 3					Attomay Docket 4/1921-5033-01000 The Bocument Nov 1995228.
8ed (10	GLGC DNo.	Ceneral Ace or Research	Model Gode	Human Homologous Known Geno Neme	nen Homologous) van GenelNemen Human Homologous Sequence (divister tittle):
36	16576	AA799570	О, В		ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
1886	18742	AI105131	U, FF, LL, XX, BBB, RRR, SSS, UUU		ESTs, Highly similar to lung alpha/beta hydrolase 1; alpha/beta hydrolase-1 [Mus musculus] [M.musculus], lung alpha/beta hydrolase 1, lung alpha/beta hydrolase 3
					ESTs, Highly similar to lymphocyte activation-associated protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to KEAP_RAT Kelch-like ECH-associated protein 1
	-				(Cytosolic inhibitor of Nrt2) (INrt2) [K.norvegicus], Kelch-like ECH-associated protein 1, Mus musculus, Similar to KIAA0952 protein, clone MGC:25591 IMAGE:4011475, mRNA, complete cds, RIKEN cDNA 2700038B03 gene, kelch-like ECH-associated
30	17599	AA799539	Д, В		protein 1
	·				ESTs, Highly similar to lymphocyte activation-associated protein [Homo sapiens] H sepiens ESTs Weakly similar to KEAP RAT Kelch-like FCH-associated protein 1
					(Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus], Kelch-like ECH-associated protein 1,
		a			Mus musculus, Similar to KIAA0952 protein, clone MGC:25591 IMAGE:4011475, mRNA.complete.cds. RIKEN cDNA 2700038B03 gene, kelch-like ECH-associated
1145	13330	AA997716	≻,×		protein 1
					ESTs, Highly similar to MAP-kinase activating death domain; Rab3 GDP/GTP exchange protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to MAP-
					kinase activating death domain; Rab3 GDP/GTP exchange protein [Rattus norvegicus]
	_				[R.norvegicus], MAP-kinase activating death domain, Mus musculus, Similar to MAP-
258	21171	AA848979	۵		kinase activating death domain, clone MGC:7838 IMAGE:3500720, mRNA, complete cds, RIKEN cDNA 2010004M01 gene, suppression of tumorigenicity 5
					ESTs, Highly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], ESTs. Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus].
1818	4898	AI102879	Q, R		KIAA1266 protein, KIAA1610 protein, metastasis associated 1, metastasis associated 3



						-		_
Actionary Docket Levis - 1925-01000 Docket Levis - 1925-01000 Docket Levis - 1925-01000 Docket Levis - 1925-0100 Docket Levis - 1925-020 Actional Plants - 1	ESTs, Highly similar to microtubule-associated protein 1a [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to microtubule-associated protein 1a [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to microtubule-associated protein 1a [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to MAPA_MOUSE Microtubule-associated protein 1A (MAP 1A) [M.musculus], chromatin assembly factor 1, subunit A (p150), expressed sequence Al853608, microtubule-associated protein 1A	ESTs, Highly similar to neuronal protein 17.3; similar to mouse neuronal protein 15.6 [Homo sapiens] [H.sapiens], nuclear protein 15.6	ESTs, Highly similar to neuronal protein 17.3; similar to mouse neuronal protein 15.6 [Homo sapiens] [H.sapiens], nuclear protein 15.6	ESTs, Highly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], NF-E2-related factor 2, nuclear factor (erythroid-derived 2)-like 1, nuclear factor (erythroid-derived 2)-like 1, nuclear factor, erythroid derived 2,-like 1, nuclear, factor, erythroid derived 2,-like 1, nuclear, factor, erythroid	ESTs, Highly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], nuclear factor (erythroid-derived 2)-like 2, nuclear factor, erythroid derived 2, like 3, nuclear, factor, erythroid derived 2, like 3	ESTs, Highly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus], nuclear factor (erythroid-derived 2)-like 2, nuclear factor, erythroid derived 2, like 3, nuclear, factor, erythroid derived 2, like 2	ESTs, Highly similar to phosphoribosylpyrophosphate synthetase-associated protein (39 kDa) [Rattus norvegicus] [R.norvegicus], Mus musculus, phosphoribosyl pyrophosphate synthetase-associated protein 2, clone MGC:36957 IMAGE:4947226, mRNA, complete cds, RIKEN cDNA 2610101M19 gene, RIKEN cDNA 5730409F23	gene, phosphoribosyl pyrophosphate synthetase-associated protein 1
Avinen Homologovs Known Gene Neme								
odel Gode	n	I, J, Z, AA, LL	000	AA	GG, HH, II, FFF, KKK	J, GG, HH, KKK		M, HH
Content Cont	M83196	AA893690	AI228236	AI179123	A1177161	A1177161		NM_022545 M, HH
No.	1991	16912	16913	17890	1169	1170		12192
TABLE 3 Seq (0)	3045	650	2413	2328	2258	2258		3488



TABU	TABLE 8				Aliomay boakel 44921-5038-01Wo
, , , , , ,	GLGG TO No.	Content Ace or Resea ID	Model Gode	Human Homologous Known Gene Name	en Homologous Yn Gene Name Human Homologous Sequence Oluster Mile
					ESTs, Highly similar to phosphoribosylpyrophosphate synthetase-associated protein
					(39 kDa) [Rattus norvegicus] [R.norvegicus], Mus musculus, phosphoribosyl
					pyropnospnate syntretase-associated protein 2, clore inoc.3039.1 imAGE.4347.220, mRNA complete cds. RIKEN cDNA 2610101M19 gene. RIKEN cDNA 5730409F23
3488	12193	NM 022545	M, EE		gene, phosphoribosyl pyrophosphate synthetase-associated protein 1
					ESTs, Highly similar to protein translocation complex beta; protein transport protein
431	16215	AA874999	I, FF		SEC61 beta subunit [Homo sapiens] [H.sapiens], protein translocation complex beta
					ESTs, Highly similar to proteoglycan 3 (megakaryocyte stimulating factor, articular
					superficial zone protein) [Mus musculus] [M.musculus], proteoglycan 4 (megakaryocyte
					stimulating factor, articular superficial zone protein), proteoglycan 4, (megakaryocyte
			V, 8B, EEE,		stimulating factor, articular superficial zone protein, camptodactyly, arthropathy, coxa
1926	4969	AI113008	III, JJJ, MMM		vara, pericarditis syndrome), vitronectin
			000, General		
			Core Tox		
			Markers,		ESTs, Highly similar to RAN binding protein 16 [Mus musculus] [M.musculus], ESTs,
			General		Moderately similar to RAN binding protein 16 [Homo sapiens] [H.sapiens], RAN binding
720	16465	AA901042	Alternate		protein 16
					ESTs, Highly similar to ribosomal protein S27a [Mus musculus] [M.musculus], ESTs,
					Highly similar to ubiquitin / ribosomal protein S27a [H.sapiens], Mus musculus, Similar to
					ubiquitin-like 4, clone MGC:19132 IMAGE:4215699, mRNA, complete cds, ribosomal
2591	14070	AI232649	H.		protein S27a
				-	ESTs, Highly similar to TLS-associated serine-arginine protein 1, isoform 1; TLS-
-			•		associated serine-arginine protein 1; TLS-associated protein TASR [Homo sapiens]
					[H.sapiens], ESTs, Weakly similar to splicing factor, arginine/serine-rich (transformer 2
					Drosophila homolog) 10 [Rattus norvegicus] [R.norvegicus], Mus musculus
_					hexaribonucleotide binding protein 3 (Hrnbp3) mRNA, partial cds, RIKEN cDNA
					1500010G04 gene, neural-salient serine/arginine-rich, silica-induced gene 41, splicing
3881	23307	NM_057119	HHH		factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)

TABLE 3					Attorney Decket 44921-5033-01WG
8 9		eemsemk Aee or ReÆeq (b	Medel Godez	Human Homologous Known Genei Name	ren Homologotts van Gene Namen Homologous Sequence Gluster Mile
					ESTs, Highly similar to TLS-associated serine-arginine protein 1, isoform 1; TLS-associated serine-arginine protein 1; TLS-associated protein TASR IHomo sapiens]
_					[H.sapiens], ESTs, Weakly similar to splicing factor, arginine/serine-rich (transformer 2
					Drosophila homolog) 10 [Rattus norvegicus] [R.norvegicus], Mus musculus
					hexaribonucleotide binding protein 3 (Hrnbp3) mRNA, partial cds, KIKEN cDNA 4500040004 app. poural ealiont sorine/arcining-rich eilica-induced cene 41 enlicind
3881	23309	NM 057119	>		factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
					ESTs, Highly similar to 0506206A histone H2B [Rattus norvegicus] [R.norvegicus],
				-	ESTs, Weakly similar to 148401 histone H2b - mouse [M.musculus], H2B histone family,
			-		member A, H2B histone family, member D, H2B histone family, member G, H2B histone
				, -	family, member K, Mus musculus, Similar to H2B histone family, member J, clone
3501	12542	NM_022647	A, B	-	MGC:29103 IMAGE:5003093, mRNA, complete cds
					ESTs, Highly similar to 0506206A histone H2B [Rattus norvegicus] [R.norvegicus], H2B
					histone family, member A, H2B histone family, member B, H2B histone family, member
					D, H2B histone family, member G, H2B histone family, member H, H2B histone family,
1409	2250	AI012354	a, R	-	member K, histone family member
					ESTs, Highly similar to 1814460A p53-associated protein [H.sapiens], Mdm2,
					transformed 3T3 cell double minute 2, p53 binding protein (mouse), transformed mouse
2828	20082	AI639488	F, II, W		3T3 cell double minute 2
					ESTS, Highly similar to 2008147A protein RARD [Rattus norvegicus] [R.norvegicus],
					ESTS, Woderately Similar to 2006 147 brotein MAND [Nation fine vegicus]
			A, I, J, FFF,		ESTs, Weakly similar to DHBX MOUSE ESTRADIOL 17 BETA-DEHYDROGENASE, A-
			000, General		SPECIFIC [M.musculus], aldo-keto reductase family 1, member C1 (dihydrodiol
		-	Core Tox		dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase), aldo-keto
128	5934	AA817695	Markers		reductase family 1, member C12, aldo-keto reductase family 1, member C13
					ESTs, Highly similar to 40S RIBOSOMAL PROTEIN S23 [H.sapiens], Mus musculus,
			X, Y, LLL,		Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358,
2620	23296	AI233316	000		mKINA, complete cds, mitochondrial ribosomal protein 3 iz, ribosomal protein 323

Control Cont	TABLES	ଜ୍ଞ				Aniomsy Docket 4.9221-5058-01000
14124 AA859305 VV, HHH 14125 NM_057208 VV 4 8368 AI007808 DD, EE 6 20848 NM_017343 A, B, P 16 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R	Seq.	@ <u>r</u> @@	ලේඛනෙකුදු රුලේ මැ Raksaa 10			
14124 AA859305 VV, HHH 13 14125 NM 057208 VV 4 8368 AI007808 DD, EE 6 20849 NM_017343 A, B, P 16 20849 NM_053999 Q, R 70 16964 NM_053999 Q, R 71 16969 NM_147215 O, P						ESTs, Highly similar to A25530 tropomyosin, fibroblast [H.sapiens], ESTs, Highly similar
14124 AA859305 VV, HHH 14125 NM_057208 VV 4 8368 AI007808 DD, EE 5 20848 NM_017343 A, B, P 6 20849 NM_017343 A, TT 70 16964 NM_053999 Q, R 70 16965 NM_053999 Q, R 71 16969 NM_147215 O, P						to TPMN_HUMAN TROPOMYOSIN, CYTOSKELETAL TYPE [H.sapiens], ESTs,
14125 NM 057208 VV 8368 AI007808 DD, EE 20849 NM 017343 A, B, P 16964 NM 053999 Q, R 16965 NM 053999 Q, R 16965 NM 147215 O, P	371	14124	AA859305	W, HHH		Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE [M.musculus]
14125 NM_057208 VV 8368 Al007808 DD, EE 20848 NM_017343 A, B, P 16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P						ESTs, Highly similar to A25530 tropomyosin, fibroblast [H.sapiens], ESTs, Highly similar
14125 NM_057208 VV 8368 AI007808 DD, EE 20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R						to TPMN_HUMAN TROPOMYOSIN, CYTOSKELETAL TYPE [H.sapiens], ESTs,
8368 AI007808 DD, EE 20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R	3893	14125				Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE [M.musculus]
8368 A1007808 DD, EE 20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R						ESTs, Highly similar to A37056 AMP deaminase (EC 3.5.4.6), brain - rat (fragment)
8368 AI007808 DD, EE 20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P						[R.norvegicus], Homo sapiens cDNA: FLJ22545 fis, clone HS100239, RIKEN cDNA
8368 Al007808 DD, EE 20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P						1200014F01 gene, adenosine monophosphate deaminase 2 (isoform L), expressed
20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R	1254	8368	A1007808	DD, EE		sequence Al553520
20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R	L					ESTs, Highly similar to A37100 myosin regulatory light chain A, smooth muscle - rat
20848 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R		:				[R.norvegicus], RIKEN cDNA 2900073G15 gene, myosin light chain, phosphorylatable,
20849 NM_017343 A, B, P 20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R		· ·				cardiac ventricles, myosin regulatory light chain, myosin, light polypeptide, regulatory,
20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R	3346	20848	NM_017343	A B		non-sarcomeric (20kD)
20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R						ESTs, Highly similar to A37100 myosin regulatory light chain A, smooth muscle - rat
20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P	-	•				[R.norvegicus], RIKEN cDNA 2900073G15 gene, myosin light chain, phosphorylatable,
20849 NM_017343 A, TT 16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P		•				cardiac ventricles, myosin regulatory light chain, myosin, light polypeptide, regulatory,
16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P	3346			∢		non-sarcomeric (20kD)
16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P						ESTs, Highly similar to A38351 phosphoprotein phosphatase 2-alpha regulatory chain
16964 NM_053999 Q, R 16965 NM_053999 Q, R 16969 NM_147215 O, P						[H.sapiens], RIKEN cDNA 2410004D02 gene, protein phosphatase 2 (formerly 2A),
16965 NM_053999 Q, R 16969 NM_147215 O, P	3870	16964	NM_053999			regulatory subunit B (PR 52), alpha isoform
16965 NM_053999 Q, R 16969 NM_147215 O, P						ESTs, Highly similar to A38351 phosphoprotein phosphatase 2-alpha regulatory chain
16965 NM_053999 Q, R 16969 NM_147215 O, P		:	,			[H.sapiens], RIKEN cDNA 2410004D02 gene, protein phosphatase 2 (formerly 2A),
16969 NM_147215 O, P	3870				-	regulatory subunit B (PR 52), alpha isoform
16969 NM_147215 O, P	<u> </u>					ESTs, Highly similar to A38351 phosphoprotein phosphatase 2-alpha regulatory chain
16969 NM_147215 O, P		_				[H.sapiens], RIKEN cDNA 2410004D02 gene, protein phosphatase 2 (formerly 2A),
	4037	_		О, Р		regulatory subunit B (PR 52), alpha isoform

1.52
II.
F, S, U, BB, CC, TT, Ⅲ,
JJJ, LLL, 000, SSS,
UUU, General M83143 Alternate
E, F, G, U, LL,
CCC, LLL, RRR, SSS,
M83143 UUU
E, J, W, UU,
NM 057101 NNN
F, M, DDD,
LLL, RRR,
UUU, General NM 012645 Alternate
NM 021585 F
W 139096 W
2000 (2,1,5 00, 2,2



		-750- 			
Attorney Dockret 44221-5036-011Wo Locument No. 1995323,1 Think in Homologous Remain Homologous Sequence (Auster Mile)	ESTs, Highly similar to A54602 microtubule-associated serine/threonine protein kinase MAST205 - mouse [M.musculus], ESTs, Moderately similar to A54602 microtubule-associated serine/threonine protein kinase MAST205 - mouse [M.musculus], Homo sapiens cDNA: FLJ21699 fis, clone COL09829, KIAA0303 protein, KIAA0807 protein, Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130026D18:syntrophin associated serine/threonine kinase, full insert sequence, microtubule associated testis specific serine/threonine protein kinase,	Syntrophin associated serine/threonine kinase ESTs, Highly similar to A56011 transcription factor IIIC alpha chain - rat [R.norvegicus], ESTs, Moderately similar to A56011 transcription factor IIIC alpha chain - rat [R.norvegicus], ESTs, Weakly similar to A56011 transcription factor IIIC alpha chain - rat	polypeptide 1 (alpha subunit, 220kD) ESTs, Highly similar to ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR [M.musculus], acetyl-Coenzyme A dehydrogenase, medium chain, acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain, expressed sequence Al266902, expressed sequence D17825, glutaryl-Coenzyme A dehydrogenase, hypothetical protein FLJ12592	ESTs, Highly similar to AP19_HUMAN CLATHRIN COAT ASSEMBLY PROTEIN AP19_[H.sapiens], ESTs, Highly similar to clathrin-associated protein AP17 delta [H.sapiens], ESTs, Weakly similar to A2S1_MOUSE Clathrin coat assembly protein AP17 (Clathrin coat associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein) (HA2 17 kDa subunit) (Clathrin assembly protein 2 small chain) [R.norvegicus], Homo sapiens, clone MGC:17284 IMAGE:4340257, mRNA, complete cds, adaptor-related protein complex 2. sigma 1 subunit, expressed sequence Al043088	ESTs, Highly similar to ARG2_RAT Arginase II, mitochondrial precursor (Non-hepatic arginase) (Kidney-type arginase) [R.norvegicus], RIKEN cDNA 5033405N08 gene, agmatine ureohydrolase (agmatinase), arginase type II, arginase, type II
Model Gode		дд 'd 'О	RR, 000	i S	; 3
Establish Research Research III		AA866276	L28801 A169321	022952	AA945580
38 @1@@ @1.00 .00		15884	1791	20681	22606
TABLES Seq (S) (D)		415	2971	35.76	915



	TABLE 3				Attomey Decket 4/9221-5038-010VO
	etec Id No.	<u>ලේකවෙනැයි</u> Aලේ ගේ RefSeq (D	Medel Gode	Humen Homologous Hum Known Gene Nemc Hum	an Homologows ***********************************
					ESTs, Highly similar to ARG2_RAT Arginase II, mitochondrial precursor (Non-hepatic arginase) (Kidney-type arginase) [R.norvegicus], RIKEN cDNA 5033405N08 gene,
915	22607	AA945580	3	agm	agmatine ureohydrolase (agmatinase), arginase type II, arginase, type II
				EST	ESTs, Highly similar to B Chain B, Peptide-In-Groove Interactions Link Target Proteins
				ToT	To The B-Propeller Of Clathrin [R.norvegicus], RIKEN cDNA 1700034F02 gene,
				clath	clathrin, heavy polypeptide (Hc), clathrin, heavy polypeptide-like 1, expressed sequence
3391	17507	NM_019299	A, B, ∏	R74732	732
				EST	ESTs, Highly similar to BMHU6 bone morphogenetic protein 6 precursor [H.sapiens],
				EST	ESTs, Moderately similar to S37618 vgr protein - rat (fragment) [R.norvegicus], bone
				mont	morphogenetic protein 5, bone morphogenetic protein 6, bone morphogenetic protein 7,
_				pone	bone morphogenetic protein 7 (osteogenic protein 1), bone morphogenetic protein 8
3289	18925	NM_017147 Z, AA, HH	Z, AA, HH	(oste	(osteogenic protein 2)
				EST	ESTs, Highly similar to C Chain C, Structure Of A Cbl-Ubch7 Complex: Ring Domain
				Func	Function In Ubiquitin-Protein Ligases [H.sapiens], ESTs, Weakly similar to ubiquitin-
				conji	conjugating enzyme E2D 2 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA
				1700	1700013N18 gene, ubiquitin-conjugating enzyme 8, ubiquitin-conjugating enzyme E2D
2141	21564	AI172301	ш	2, ut	2, ubiquitin-conjugating enzyme E2L 3, ubiquitin-conjugating enzyme E2L 6
				EST	ESTs, Highly similar to C560_HUMAN SUCCINATE DEHYDROGENASE
2203	20001	AI176396	ᆲ	CYT	CYTOCHROME B560 SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens]
				EST	ESTs, Highly similar to Cdc42 From Human, Nmr, 20 Structures [H.sapiens], Mus
				snu	musculus mRNA for small GTPase Tc10, complete cds, cell division cycle 42 (GTP
				bind	binding protein, 25kD), cell division cycle 42 homolog (S. cerevisiae), ras homolog gene
				famil	family, member J, ras-related C3 botulinum toxin substrate 1 (rho family, small GTP
3780	19205	NM 053522	a a	bind	binding protein Rac1)



TABLE 3	1 <u>3</u> 3				Aironney Docket 44921-5038-01WO
	GLGG BNG	<u>ලංකෑනෙයි</u> ! ලංකුම් ලංකුම්	Medal Goda	Human Homologous R Known Gene Names Human Ho	Humanikomologous Sequence Quster iide
				ESTs, High MITOCHON MOUSE 60	ESTs, Highly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to CH60 MOUSE 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR
3451	20385	NM_022229	G, H, S, T, U	[M.musculu PROTEIN, I (chaperonin	[M.musculus], ESTs, Weakly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens], heat shock 60kD protein 1 (chaperonin), heat shock protein, 60 kDa
				ESTs, High MITOCHON MOUSE 60	ESTs, Highly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to CH60 MOUSE 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR
044	20286	03031	Q, R, S, T,	[M.musculu PROTEIN, I	[M.musculus], ESTs, Weakly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens], heat shock 60kD protein 1 (Abanaronin), heat shock protein, 60 kDa
100	00007	700000	200, 000	ESTS, High	ESTs, Highly similar to CIA1_HUMAN WD40-REPEAT CONTAINING PROTEIN CIAO 1
				[H.sapiens] acetylhydro	[H.sapiens], ESTs, Weakly similar to LIS1_MOUSE Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45
	_			kDa subuni [R.norvegic	kDa subunit) (PAF-AH alpha) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1) [R.norvegicus], F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila),
				Homo sapik	Homo sapiens cDNA FLJ31861 fis, clone NT2RP7001319, Homo sapiens, clone MGC:4710 IMAGE:3534806, mRNA, complete cds, Mus musculus F-box-WD40 repeat
	_			protein 6 (F 1500041N1	protein 6 (Fbxw6) mRNA, complete cds, Mus musculus, Similar to RIKEN cDNA 1500041N16 gene, clone MGC:12066 IMAGE:3708188, mRNA, complete cds, nuclear
·		.		receptor co acetvihydro	receptor co-repressor/HDAC3 complex subunit, platelet-activating factor acetylhydrolase, acetylhydrolase,
993	12426	AA955760	<u>}</u>	isoform 1b, subunit (45)	isoform 1b, beta1 subunit, platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD), transducin (beta)-like 1
3926	18846	NM_130755	L.	ESTs, Highly sir citrate synthase	ESTs, Highly similar to citrate synthase [H.sapiens], RIKEN cDNA 1700007H16 gene, citrate synthase

TABLE 3	ം അ ബ				Attorney Doetset 4492A-5033-011W0 Doeument No. 1985323.1
Stan	ला लेट जि.	Consent		Humen Homologous	
{ <u> </u>	98 98 9		() () () () () () () ()	Known Cene Neme	wan Ceae Nemeri Humen Hemologous Sequence Custer mile
					ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], ESTs,
					Highly similar to ROA3_HUMAN HETEROGENEOUS NUCLEAR
					RIBONUCLEOPROTEIN A3 [H.sapiens], ESTs, Highly similar to S12520 core protein
					A1 [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1
					[H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1
					[H.sapiens], ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR
					RIBONUCLEOPROTEINS A2/B1 [M.musculus], Mus musculus, similar to
					heterogeneous nuclear ribonucleoprotein A3 (H. sapiens), clone MGC:37309
		····			IMAGE:4975085, mRNA, complete cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA
					3010025E17 gene, heterogeneous nuclear ribonucleoprotein A1, heterogeneous
					nuclear ribonucleoprotein A2/B1, heterogeneous nuclear ribonucleoprotein A3,
2734	17571	AI236484	×, ×,		hypothetical protein 23851
					ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], ESTs,
					Highly similar to S12520 core protein A1 [H.sapiens], ESTs, Highly similar to
					heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to
					heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to
					ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1
			B, JJ, WW,		[M.musculus], Mus musculus, similar to heterogeneous nuclear ribonucleoprotein A3 (H.
			DDD, HHH,		sapiens), clone MGC:37309 IMAGE:4975085, mRNA, complete cds, RIKEN cDNA
			General		2610510D13 gene, RIKEN cDNA 3010025E17 gene, heterogeneous nuclear
23	17613	17613 AA799511	Alternate		ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A2/B1

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Document No. 1935323.1	S Human Homologous Sequence Gueter Mile	ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], ESTs, Highly similar to S12520 core protein A1 [H.sapiens], ESTs, Highly similar to	heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to	heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/81	[M.musculus], Mus musculus, similar to heterogeneous nuclear ribonucleoprotein A3 (H.	sapiens), clone MGC:37309 IMAGE:4975085, mRNA, complete cds, RIKEN cDNA	2610510D13 gene, RIKEN cDNA 3010025E17 gene, heterogeneous nuclear	ribonucleoprotein A1, neterogeneous nuclear ribonucleoprotein A2/B1	ESTS, DIGITIS SITTING TO DENGE TO DIVING TO MAN DECAT RIBONOCEEASE GRIVING TO DECATE TO DESCRIPTION OF THE STATE OF THE ST	Precondor [n.sapiers], rinein convision gene, deuxymonidiease i-line 3 deuxyribonidease Liike 1 deuxyribonidease Liike 3	ESTs, Highly similar to ERR3 HUMAN ESTROGEN-RELATED RECEPTOR GAMMA	[H.sapiens], estrogen related receptor, alpha, estrogen-related receptor alpha, estrogen-	related receptor gamma	ESTs, Highly similar to FMO3_HUMAN DIMETHYLANILINE MONOOXYGENASE	[H.sapiens], ESTs, Weakly similar to FMO3_HUMAN DIMETHYLANILINE	MONOOXYGENASE [H.sapiens], Mus musculus flavin-containing monooxygenase 4	mRNA, complete cds, flavin containing monooxygenase 2, flavin containing	monooxygenase 3, flavin containing monooxygenase 5	ESTs, Highly similar to GBG5_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN	G(I)/G(S)/G(O) GAMMA-5 SUBUNIT [H.sapiens], G protein gamma-5 subunit, Mus	musculus, guanine nucleotide binding protein (G protein), gamma 5, clone MGC:12061	IMAGE:3707994, mRNA, complete cds, Mus musculus, guanine nucleotide binding	protein (G protein), gamma 5, clone MGC:8292 IMAGE:3593324, mRNA, complete cds,	guanine nucleotide binding protein (G protein), gamma 5	ESTs, Highly similar to GFRP RAT GTP CYCLOHYDROLASE I FEEDBACK DECT II ATODY DEOTEIN IS propositive! GTB evolutivations I feedback requisitory	protein	
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				(A)	ESTs, Highly similar to GTO1_RAT Glutathione transferase omega 1 (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) [R.norvegicus], ESTs, Weakly similar to GTXH_HUMAN GLUTATHIONE-S-TRANSFERASE HOMOLO [H.sapiens], RIKEN cDNA 1700020F09 gene, glutathione S-transferase omega 1, glutathione transferase zeta 1 (maleylacetoacetate isomerase), glutathione-S-transferase zeta 1 (maleylacetoacetate isomerase), glutathione-S-transferase like;
1996	17812	AI169075	PPP, QQQ	JB	glutathione transferase omega
1344	15644	AI010256	C, L, W, WW	Ш X	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
1905	24211	Al111853	ш	<u> </u>	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
1936	24212	AI136747	PPP, QQQ	ű Ÿ	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
2009	24213	AI169289	ור	ü Ұ	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
3863	15642	NM_053985	C, I, J, N, W, II, MM, WW, 000, TTT	31 光	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
3863	15643	NM_053985	W	ШŸ	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene
3863	15645	W 053985 W	M	ŭŸ	ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B), RIKEN cDNA 1810027O10 gene



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3 19109 NM_012963 3 19110 NM_012963 19433 AA819776	ESTs, Highly similar to HMG1_HUMAN HIGH MOBILITY GROUP PROTEIN HMG1 [H.sapiens], ESTs, Moderately similar to HMG1 MOUSE HIGH MOBILITY GROUP
3 19109 NM_012963 19110 NM_012963 19433 AA819776	PROTEIN HMG1 [M.musculus], ESTs, Moderately similar to high mobility group protein homolog HMG4 IM misculus] ESTs Weakly similar to HMG1 HUMAN HIGH
3 19109 NM_012963 3 19110 NM_012963 19433 AA819776	MOBILITY GROUP PROTEIN HMG1 (H.sapiens), RIKEN cDNA 4932431P20 gene,
3 19109 NM_012963 3 19110 NM_012963 19433 AA819776	Rattus norvegicus epidermal Langerhans cell protein LCP1 mRNA, complete cds, high
3 19110 NM_012963 19433 AA819776	mobility group 20A, high mobility group box 1, high-mobility group (nonhistone
3 19110 NM_012963 19433 AA819776	ESTS, Highly similar to HMG1 HUMAN HIGH MOBILITY GROUP PROTEIN HMG1
3 19110 NM_012963 19433 AA819776	[H.sapiens], ESTs, Moderately similar to HMG1 MOUSE HIGH MOBILITY GROUP
3 19110 NM_012963 19433 AA819776	PROTEIN HMG1 [M.musculus], ESTs, Moderately similar to high mobility group protein
3 19110 NM_012963 19433 AA819776	homolog HMG4 [M.musculus], ESTs, Weakly similar to HMG1_HUMAN HIGH
3 19110 NM_012963 19433 AA819776	MOBILITY GROUP PROTEIN HMG1 [H.sapiens], RIKEN cDNA 4932431P20 gene,
3 19110 NM_012963 19433 AA819776	
3 19110 NM_012963 19433 AA819776	
19433 AA819776	chromosomal) protein 1, high-mobility group 20A
19433 AA819776	ESTs, Highly similar to HS9A_HUMAN HEAT SHOCK PROTEIN HSP 90-ALPHA
19433 AA819776	[H.sapiens], ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP
19433 AA819776	84) [R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein
19433 AA819776	DKFZp761K0511.1 [H.sapiens], Mus musculus, clone IMAGE:3584589, mRNA, partial
19433 AA819776	cds, expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein,
	84 kDa 1, heat shock protein, 86 kDa 1
	ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84)
	[R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1
	[H.sapiens], Mus musculus, clone IMAGE:3584589, mRNA, partial cds, expressed
	sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, heat
876 20795 AA944397 K	shock protein, 86 kDa 1



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Altomey Deckel 4,921-5038-01Wo	Komologous France Kuman Bonologous Seguence Guster Milo	ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84)	[H.sapiens], Mus musculus, clone IMAGE:3584589, mRNA, partial cds, expressed	sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, heat	shock protein, 86 kDa 1	ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84)	[R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1	[H.sapiens], RIKEN cDNA 1810014B01 gene, expressed sequence C81438, heat shock	90kD protein 1, beta, heat shock protein, 84 kDa 1, tumor rejection antigen (gp96) 1,	tumor rejection antigen gp96	ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84)	[R.norvegicus], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1	[[H.sapiens], RIKEN cDNA 1810014B01 gene, expressed sequence C81438, heat shock	90kD protein 1, beta, heat shock protein, 84 kDa 1, tumor rejection antigen (gp96) 1,	tumor rejection antigen gp96	ESTs, Highly similar to Human Translation Initiation Factor Eif1, Nmr, 29 Structures	[H.sapiens], putative translation initiation factor, suppressor of initiator codon mutations,	related sequence 1 (S. cerevisiae)	ESTs, Highly similar to Human Translation Initiation Factor Eif1, Nmr, 29 Structures	[[H.sapiens], putative translation initiation factor, suppressor of initiator codon mutations,	related sequence 1 (S. cerevisiae)	ESTs, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3'end -	mouse [M.musculus], RIKEN cDNA 1600013K19 gene, hypothetical protein MGC16332,	tumor necrosis factor, alpha-induced protein 2	ESTs, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3'end -	mouse [M.musculus], RIKEN cDNA 1600013K19 gene, similar to S. cerevisiae Sec6p	and R. norvegicus rsec6, tumor necrosis factor, alpha-induced protein 2
	Rumen Komologous Knovn Gene Nemo																										
	Model Gode				H, T, II					SS					רר			KKK			C			А			99
TABLES	Content Ace or Roßej (D				AI176546					AA963782					S69316			AI009501			AI232021			AI102578			AA851443
89 010	GLEC ONO.				16518					18648					18647			19092			19094			22487			21489
TABL					2214					1058					4071			1319			2554			1807			315



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Sed (D	GLGG (D No.)	Content Accordad Refector	Medal Gede	TIME STORES HOUSE STORES HAVE STORES HAVE STORES HAVE STORES TO STORES THE ST	En Homologous It The Third In the Comment of the
4119	21488	U32575	GG, PP, QQ	EST mou and	ESTs, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3'end - mouse [M.musculus], RIKEN cDNA 1600013K19 gene, similar to S. cerevisiae Sec6p and R. norvegicus rsec6, tumor necrosis factor, alpha-induced protein 2
				EST simi	ESTs, Highly similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs, Weakly similar to
				1386 NIZ 97. 9	138616 zinc finger protein ZNF139 [H.sapiens], ESTs, Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Mus musculus, Similar to zinc finger protein 97, clone MGC:6111 IMAGE:3494875, mRNA, complete cds. Pancreas zinc finger
2602	12873	AI232984		prot	protein, see also D1Bda10\2, zinc finger protein 260, zinc finger protein 63, zinc finger protein 97
				EST Simi	ESTs, Highly similar to I49636 DNA-binding protein - mouse [M.musculus], ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately similar to I40636 DNA-binding protein - mouse IM musculus] ESTs, Moakly similar to
				OZF_1 	OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Weakly similar to Z177_HUMAN ZINC FINGER PROTEIN 177 [H.sapiens], Homo sapiens mRNA; cDNA
				DKF	DKFZp547C146 (from clone DKFZp547C146), Mus musculus, Similar to zinc finger protein 97, clone MGC:6111 IMAGE:3494875, mRNA, complete cds, Pancreas zinc
2377	19828	AI180087	u.	finge	finger protein, see also D1Bda10\2, zinc finger protein 177, zinc finger protein 260, zinc finger protein 63, zinc finger protein 97
				EST	ESTs, Highly similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately
				SIMI OZF Z17	similar to 149636 UNA-binding protein - mouse [m.musculus], ESTs, Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Weakly similar to Z177 HUMAN ZINC FINGER PROTEIN 177 [H.sapiens], Homo sapiens mRNA; cDNA
	·			DKF	DKFZp547C146 (from clone DKFZp547C146), Mus musculus, Similar to zinc finger protein 97, clone MGC:6111 IMAGE:3494875, mRNA, complete cds, Pancreas zinc
3830	19827	NM_053806	PP, QQ, YY, PPP, QQQ	finge	finger protein, see also D1Bda10\(\mathbb{2}\), zinc finger protein 177, zinc finger protein 260, zinc finger protein 63, zinc finger protein 97

TABLE 9	ලි දූ				7) Aitomay Dodkat (49271-5059-611W6) (2) (2) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4
8ed (D	elec In No.	Cealseal. Lee or ReÆeq (D	Model Gode	Kumen Komologous Known Genei Neme	an Komologous
					ESTs, Highly similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately similar to 149636 DNA-binding protein - mouse [M.musculus], ESTs, Weakly similar to
1689	26184	A1070784	=		OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Mus musculus, Similar to zinc finger protein 97, clone MGC:6111 IMAGE:3494875, mRNA, complete cds, Pancreas zinc finger protein, see also D18da10\(\mathcal{Q}\), zinc finger protein 260, zinc finger protein 260, zinc finger protein 260, zinc finger protein 260, zinc finger protein 83, zinc finger protein 97
1125	8786	AA996993	ᅩ		ESTs, Highly similar to I58408 IK factor [H.sapiens], IK cytokine
996	23584	AA955071	J, GG, HH, General Core Tox Markers		ESTs, Highly similar to 167428 retinoic acid receptor homolog - rat (fragment) R norvectors retinoid X recentor gamma retinoid X recentor
1222	19649	AF016387	≿ X		ESTs, Highly similar to 167428 retinoic acid receptor homolog - rat (fragment) [R.norvegicus], retinoid X receptor gamma, retinoid X receptor.
					ESTs, Highly similar to IEFS_HUMAN TRANSFORMATION-SENSITIVE PROTEIN IEF
<u>. </u>					SSP 3521 [H.sapiens], ESTs, Weakly similar to small glutamine-rich tetratricopeptide repeat (TPR) containing protein (SGT) [Rattus norvegicus] [R.norvegicus], Mus
				-	musculus, clone MGC:27660 IMAGE:4527683, mRNA, complete cds, RIKEN cDNA
					5330427H01 gene, hypothetical protein FLJ12788, small glutamine-rich tetratricopeptide reoeat (TPR) containing protein (SGT), small glutamine-rich tetratricopeptide repeat
					(TPR)-containing, stress-induced phosphoprotein 1, stress-induced-phosphoprotein 1
96	11840	NM_138911	H, Z, AA, DD		(Hsp70/Hsp90-organizing protein)
	: :		FFF, General		ESTs, Highly similar to IF34 MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 4 [M.musculus], ESTs, Moderately similar to NUCLEOLIN
			Core Tox		[M.musculus], ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens],
			Markers,		Nucleolin, RIKEN cDNA 0610008K04 gene, eukaryotic translation initiation factor 3,
1667	2906	AI070087	General Alternate		subunit 4 (delta, 44 kDa), eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD), nucleolin, pigpen

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	ubiquitin B, ubiquitin C		EE	AA818069	
, 00	MGC:24263 IMAGE:3934516, mRNA, complete cds, expressed sequence AL033289,				
	UQHUC polyubiquitin 9 [H.sapiens], Homo sapiens, Similar to orosomucoid 1, clone				
-, -	transcription elongation factor A (SII), 3		Alternate	AI172272	- 1
	sapiens mRNA for transcription elongation factor TFIIS, PHD finger protein 3,		XX, General		
	Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo				
U	to JC5430 transcription elongation factor S-II-T1, testis-specific - mouse [M.musculus],				
	Highly similar to Transcriptional Elongation Factor Sii [H.sapiens], ESTs, Weakly similar				
	ESTs, Highly similar to JC4577 transcription elongation factor T1 [H.sapiens], ESTs,				1
	[H.sapiens], brain and reproductive organ-expressed (TNFRSF1A modulator)		99	AI171289	7
	ESTs, Highly similar to JC2472 brain and reproductive organ-expressed protein				ı
	protein 1 (9-27), interferon induced transmembrane protein 3 (1-8U)		PP, aa, LLL	X61381	
	[H.sapiens], RIKEN cDNA 1110004C05 gene, interferon induced transmembrane		HH, NN, 00,		
	PROTEIN 3 [H.sapiens], ESTs, Highly similar to S17182 interferon-induced protein 1-8U		BB, CC, GG,		
	ESTs, Highly similar to IFM3_HUMAN INTERFERON-INDUCED TRANSMEMBRANE				1
1-	protein 1 (9-27), interferon induced transmembrane protein 3 (1-8U)		MMM	AI169751	21660
76:	[H.sapiens], RIKEN cDNA 1110004C05 gene, interferon induced transmembrane		88, EEE,		_
-	PROTEIN 3 [H.sapiens], ESTs, Highly similar to S17182 interferon-induced protein 1-8U				
	ESTs, Highly similar to IFM3_HUMAN INTERFERON-INDUCED TRANSMEMBRANE				l
	protein 1 (9-27), interferon induced transmembrane protein 3 (1-8U)		1	AI010584	21659
	[H.sapiens], RIKEN cDNA 1110004C05 gene, interferon induced transmembrane				
	PROTEIN 3 [H.sapiens], ESTs, Highly similar to S17182 interferon-induced protein 1-8U				
	ESTs, Highly similar to IFM3_HUMAN INTERFERON-INDUCED TRANSMEMBRANE				1
	like 3		œ	X83399	
1	gene, eukaryotic translation initiation factor 4E, eukaryotic translation initiation factor 4E-				
	FACTOR 4E [H.sapiens], RIKEN cDNA 1300018P11 gene, RIKEN cDNA 2700069E09				
	ESTs, Highly similar to IF4E_HUMAN EUKARYOTIC TRANSLATION INITIATION				
	Sene Name Human Homologous Sequence Quister Mile """ "	Kinowii Gene Neme	(ගිම්මේ ලිමේම	RefSeq (D	(1) (1)
		Human Homologous			<u> </u>
					20 I I
	A VIVIONARY DOCKER (49271-6023-01VWO				
				The second secon	



			-762-			<u></u>	
Movin Gene Name: Highly similar to JE0190 polyubiquitin unit [H.sapiens], ESTs, Highly similar to	UQHUC polyubiquitin 9 [H.sapiens], Homo sapiens, Similar to orosomucoid 1, clone MGC:24263 IMAGE:3934516, mRNA, complete cds, expressed sequence AL033289, ubiquitin B, ubiquitin C	ESTs, Highly similar to K6A1_RAT Ribosomal protein S6 kinase alpha 1 (S6K-alpha 1) (90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1) (RSK-1) (pp90RSK1) [R.norvegicus], Mus musculus, clone IMAGE:3156601, mRNA, S6 protein kinase (Rsk-1), ribonuclease P1, ribosomal protein S6 kinase polypeptide 1, ribosomal protein S6 kinase polypeptide 1, ribosomal	ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE [H.sapiens], ESTs, Weakly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE [H.sapiens], Homo sapiens, clone IMAGE:4793702, mRNA, Mus musculus, clone MGC:32469 IMAGE:5050433, mRNA, complete cds, crystallin, zeta, fatty acid synthase,	ESTS, Highly similar to LCK MOUSE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK [M.musculus], RIKEN cDNA 8430404F20 gene, hemopoietic cell kinase, lymphocyte-specific protein tyrosine kinase, lymphocyte-specific protein tyrosine kinase, src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	ESTs, Highly similar to LCT2_HUMAN LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2 PRECURSOR [H.sapiens], leukocyte cell-derived chemotaxin 2	ESTs, Highly similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus], ESTs, Weakly similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus], MAX dimerization protein, MAX interacting protein 1, Max interacting protein 1	ESTs, Highly similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus], ESTs, Weakly similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus], MAX dimerization protein, MAX interacting protein 1, Max interacting protein 1
Model Code	⊢	۵	>		G, GG, НН, VV	ZZ, AAA	_ ш
Sent Sent Sent Sent Sent Sent Sent Sent	NM_138895	Al227953	0827630	NM 013185 VV	AA945596	AA893611	AI237835
33 33 (C)	3015	12413	2846	1258	12314	3465	3467
TABLE 3 899 (例 100 (D	3991	2407	461	3231	917	644	2788



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Canoly Emily (V.C.Z.) - Colors Sequence (U.C.) - Colors (U.C.)	ESTs, Highly similar to MYHA_MOUSE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) [M.musculus], ESTs, Weakly similar to JC5837 364K Golgi complex-associated protein rat [R.norvegicus], ESTs, Weakly similar to MYHA_MOUSE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain, type B) (Nonmuscle myosin heavy chain, type B) (Nonmuscle myosin heavy	antigen-2 - mouse [M.musculus], RB1-inducible coiled-coil 1, RIKEN cDNA 2400004E04 gene, RIKEN cDNA 4930428L02 gene, RIKEN cDNA 5730504C04 gene, coiled-coil protein BICD2, expressed sequence AL022610, expressed sequence AU042952, golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1, hypothetical protein FLJ13031, myosin heavy chain IX, similar to rat myomegalin	ESTs, Highly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus], NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae), RIKEN cDNA 2410130M07 gene, nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs), sperm specific antigen 1	ESTs, Highly similar to NPA1 MOUSE NEURONAL PAS DOMAIN PROTEIN 1 [M.musculus], ESTs, Moderately similar to NPA1_HUMAN NEURONAL PAS DOMAIN PROTEIN 1 [H.sapiens], ESTs, Weakly similar to NPA1_HUMAN NEURONAL PAS DOMAIN PROTEIN 1 [H.sapiens], basic-helix-loop-helix-PAS protein, neuronal PAS domain protein 1	ESTs, Highly similar to NPM_HUMAN NUCLEOPHOSMIN [H.sapiens], ESTs, Weakly similar to NPM_HUMAN NUCLEOPHOSMIN [H.sapiens], nucleoplasmin 3	ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately similar to 138937 DNA/RNA-binding protein [H.sapiens], ESTs, Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Pancreas zinc finger protein, see also D1Bda10 hypothetical protein, MGC:7160, zinc finger protein	260, zinc finger protein 63
Known Gene Name							
Model Gode		၁၁၁	nnn	D, E	А, В, ННН		FF
eenseni Aee or Refeeq (D		NM 138885	Al236338	AI071989	A1009376		AI170270
38 % % % % % % % % % % % % % % % % % % %		5656	19298	9795	3665		18671
TABLES See GI		3990	2730	1718	1313		2043

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		Mo <u>c</u> el Gode	Human Komologous Known Gene Name	rentificinologous
				ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs, Moderately similar to 138937 DNA/RNA-binding protein IH sapiens] FSTs_Weakly
	-			similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Pancreas zinc
		H, General		finger protein, see also D1Bda10\2, hypothetical protein, MGC:7160, zinc finger protein
2290 18672 AI178	AI178189	Alternate		260, zinc finger protein 63
				ESTs, Highly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], ESTs,
				Moderately similar to 138937 DNA/RNA-binding protein [H.sapiens], ESTs, Weakly
				similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Pancreas zinc
				finger protein, see also D1Bda10\2, hypothetical protein, MGC:7160, zinc finger protein
2735 14777 AI236	AI236565	>		260, zinc finger protein 63
				ESTs, Highly similar to P2CB_HUMAN PROTEIN PHOSPHATASE 2C BETA ISOFORM
				[H.sapiens], ESTs, Weakly similar to P2CB_HUMAN PROTEIN PHOSPHATASE 2C
				BETA ISOFORM [H.sapiens], Homo sapiens cDNA FLJ30553 fis, clone
				BRAWH2003689, highly similar to Mus musculus clone mouse1-9 putative protein
		,		phosphatase type 2C mRNA, protein phosphatase 1B (formerly 2C), magnesium-
3733 25529 NM_	NM_033096	ww		dependent, beta isoform, protein phosphatase 1B, magnesium dependent, beta isoform
				ESTs, Highly similar to PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1
				[H.sapiens], RIKEN cDNA 2810411E22 gene, RIKEN cDNA 4432411E13 gene, RIKEN
3865 18025 NM_	NM_053989	ZZ, AAA		cDNA 4930431E10 gene
3600 12638 NM_	NM_031099	L		ESTs, Highly similar to PC4210 ribosomal protein L5 [H.sapiens], ribosomal protein L5
		H, S, II, FFF,		
		General		
3600 12639 NM_	NM_031099	Alternate		ESTs, Highly similar to PC4210 ribosomal protein L5 [H.sapiens], ribosomal protein L5

	ଓଡ଼				TAIBLE SI: TAIBLE SI: THE SI
	elec.	Consenta Accor Rescapo	Model Gode	Human Homologous KnowniGene Name Human Homo	Ruman Homologous Known Gene Name Homologous Sequence Cluster Title
		,		ESTs, Highly s RELATED KIN ESTs, Modera KINASE C-RE	ESTs, Highly similar to PKL2_RAT PROTEIN KINASE C-LIKE 2 (PROTEIN-KINASE C-RELATED KINASE 2) (PAK-2) [R.norvegicus], ESTs, Moderately similar to PKL2_RAT PROTEIN KINASE C-LIKE 2 (PROTEIN-KINASE C-RELATED KINASE 2) (PROTEASE-ACTIVATED KINASE 2)
2773	14827	AI237404	g	[R.norvegicus], f Weakly similar to kinase PKNbeta	[R.norvegicus], ESTs, Weakly similar to JC7083 protein kinase [H.sapiens], ESTs, Weakly similar to PC4220 protein kinase [M.musculus], protein kinase C-like 2, protein kinase PKNbeta
				ESTs, Highly s Weakly similar	ESTs, Highly similar to PLE1_MOUSE PLECTIN 1 (PLTN) (PCN) [M.musculus], ESTs, Weakly similar to plectin [Rattus norvegicus] [R.norvegicus], KIAA1009 protein, Mus
4231	1141	X59601	UU, KKK	expressed seq	indecules, doite investe: 100000, invite, partial cas, destribulatin (OT), OT), et il,
998	22017	AA944209	, J.J.	ESTs, Highly s PIM-1 [M.muso	ESTs, Highly similar to PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE PIM-1 [M.musculus], PAS domain containing serine/threonine kinase
1271	22018	A1008309	III, JJJ, KKK	ESTs, Highly s PIM-1 [M.mus	ESTs, Highly similar to PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE PIM-1 [M.musculus], PAS domain containing serine/threonine kinase
				ESTs, Highly & RAS) [R.norve	ESTs, Highly similar to RASH_RAT TRANSFORMING PROTEIN P21/H-RAS-1 (C-H- RAS) [R.norvegicus], Harvey rat sarcoma oncogene, subgroup R, Harvey rat sarcoma
2166	4445	AI175466	z	virus oncogen homolog, cloni ras) oncogene	virus oncogene, Mus musculus, Similar to v-Ha-ras Harvey rat sarcoma viral oncogene homolog, clone MGC:19390 IMAGE:3152667, mRNA, complete cds, related RAS viral (ras) oncogene homolog, v-Ha-ras Harvey rat sarcoma viral oncogene homolog
	-			ESTs, Highly s ESTs, Highly s Moderately sin	ESTs, Highly similar to RL26_HUMAN 60S RIBOSOMAL PROTEIN L26 [H.sapiens], ESTs, Highly similar to S33713 ribosomal protein L26, cytosolic [H.sapiens], ESTs, Moderately similar to RL26 HUMAN 60S RIBOSOMAL PROTEIN L26 [H.sapiens],
4200	4200 18541 X14671	X14671	BB, CC, RR	ribosomal prot	ribosomal protein L26, ribosomal protein L26-like 1



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	8				Altomoy Dockel 44921-6038-01W0
(S)	etec ID No.	Consonia Acoor	Model Code	Human Homologous Known Gene Name	nn Homologous nn Geneinkimen Humani Homologous Sequence (Gluster IIII)
					ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus], ESTs, Highly similar to S34195 ribosomal protein L3, cytosolic [H.sapiens], ESTs,
					Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus],
463	6029	AA891037	n		ESTS, Weakly Similar to KL3 inCOSE 603 KIBOSOMAL PROTEIN L3 [incmusculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like
		·			ESTs, Highly similar to S03700 nonhistone chromosomal protein HMG-17 [H.sapiens], ESTs Weakly similar to HG17 RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-
					17 [R.norvegicus], high mobility group nucleosomal binding domain 2, high mobility
					group nucleosomal binding domain 3, high-mobility group (nonhistone chromosomal)
					protein 14, high-mobility group (nonhistone chromosomal) protein 17, thyroid hormone
1605	10533	AI058430	BBB		receptor interactor 7
					ESTs, Highly similar to S03700 nonhistone chromosomal protein HMG-17 [H.sapiens],
					ESTs, Weakly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-
					17 [R.norvegicus], high mobility group nucleosomal binding domain 2, high mobility
					group nucleosomal binding domain 3, high-mobility group (nonhistone chromosomal)
	•				protein 14, high-mobility group (nonhistone chromosomal) protein 17, thyroid hormone
2373	17349	AI179987	AAA		receptor interactor 7
				-	ESTs, Highly similar to S12207 hypothetical protein [M.musculus], ESTs, Highly similar
					to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], ESTs, Moderately
	-				similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus], RIKEN cDNA
		-			1110046J11 gene, neural precursor cell expressed, developmentally down-regulated 4,
2015	5716	AI169347	RR		neural precursor cell expressed, developmentally down-regulated gene 4a
					ESTs, Highly similar to S12207 hypothetical protein [M.musculus], ESTs, Moderately
		-			similar to T00363 hypothetical protein KIAA0674 [H.sapiens], KIAA0674 protein, RIKEN
2122	2218	AI172011	RR		cDNA 1110046J11 gene

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TABLE 3	E3			Allemey Deckel 4.1921-5018-01WO	0 P. S
	elec elec elec elec elec elec elec elec	Cee or Refee ID	Modell Code:	Human Homologotis The state of the state o	海港 的
					o
				TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA 4930547K05 gene, heterogeneous	
74	15011	AA799893	R, MM, TTT	nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A3	
1698	11596	AI071194	88	ESTs, Highly similar to S16506 hypothetical protein [H.sapiens], ESTs, Weakly similar to S16506 hypothetical protein [H.sapiens], Homo sapiens, similar to putative, clone MGC:22793 IMAGE:4773899, mRNA, complete cds, hypothetical protein El. 112748	2
				ESTs, Highly similar to S25644 Ig mu chain C region - rat (fragment) [R.norvegicus],	Ţ
				sequence Al326478, expressed sequence Al893585, immunoglobulin heavy chain 6	
2675	22609	AI234828	X, ≺	(heavy chain of IgM), immunoglobulin heavy constant mu	_
2456	11527	AI229307	22	ESTs, Highly similar to S27958 transcription factor BTF2 62K chain [H.sapiens], general transcription factor IIH, polypeptide 1 (62kD subunit)	<u>a</u>
				ESTs, Highly similar to S57449 fusca protein homolog - rat [R.norvegicus], ESTs,	
0			(() (Weakly similar to S57449 fusca protein homolog - rat [R.norvegicus], G protein pathway suppressor 1, Mus musculus, Similar to G protein pathway suppressor 1, clone	ag
2903	3815	H3190/	FFF, GGG	MGC:/191 IMAGE:34819/9, mKNA, complete cds, KIKEN cDNA 2400006A19 gene	T
				ESTs, Highly similar to S57449 fusca protein homolog - rat [R.norvegicus], ESTs, Weakly similar to S57449 fusca protein homolog - rat [R.norvegicus]. G protein pathway	<u>~</u>
3858	6357	NM_053969	S	suppressor 1, Mus musculus, Similar to G protein pathway suppressor 1, clone MGC:7191 IMAGE:3481979, mRNA, complete cds, RIKEN cDNA 2400006A19 gene	

Core Tox Core Tox	
2917 Al145614 S, UUU C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core 10544 NM_152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	an Homologous 1922
2917 A1145614 S, UUU C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core 10544 NM_152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	ESTs, Highly similar to S57449 fusca protein homolog - rat [R.norvegicus], G protein pathway suppressor 1, Homo sapiens cDNA FLJ30168 fis, clone BRACE2000750,
2917 A1145614 S, UUU C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core 10544 NM 152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM 152935 Markers A, B, E, CC,	Homo sapiens cDNA FLJ30648 fis, clone CTONG2006449, moderately similar to
2917 A1145614 S, UUU C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core General Core 10544 NM 152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM 152935 Markers A, B, E, CC,	Urosophila melanogaster 25S proteasome regulatory complex subunit p4zA mKNA, KIAA0107 gene product, Mus musculus, Similar to G protein pathway suppressor 1,
C. H. JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core 10544 NM 152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	clone MGC:7191 IMAGE:3481979, mRNA, complete cds, RIKEN cDNA 2400006A19
C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	priph
AAA, HHH, PPP, QQQ, General Core 10544 NM_152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	
10544 NM 152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	ANG accident amous functions Us distant OC and \$10000 at actionic classic at 707
10544 NM_152935 Tox Markers C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	ESTS, mignify similar to 3002 13 mas 20 protein (n.saprens), nomo saprens Conv. FLJ30361 fis. clone BRACE2007764. RIKEN cDNA 1810060K07 gene, RIKEN cDNA
C, FFF, GGG, HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	4930553D19 gene, translocase of outer mitochondrial membrane 20 (yeast) homolog
HHH, PPP, QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	
QQQ, General Core Tox 10545 NM_152935 Markers A, B, E, CC,	
10545 NM_152935 Markers A, B, E, CC,	ESTs, Highly similar to S68215 Mas 20 protein [H.sapiens], Homo sapiens cDNA
10545 NM_152935 Markers A, B, E, CC,	FLJ30361 fis, clone BRACE2007764, RIKEN cDNA 1810060K07 gene, RIKEN cDNA
	4930553D19 gene, translocase of outer mitochondrial membrane 20 (yeast) homolog
	ESTs, Highly similar to S68418 protein phosphatase 1M chain M110 isoform - rat
	[R.norvegicus], ESTs, Weakly similar to S37771 ankyrin, erythrocyte - mouse
	[M.musculus], ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110
	isoform - rat (fragment) [R.norvegicus], leukocyte receptor cluster (LRC) member 3,
	molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of
QQ, III, JJJ,	mouse, myosin phosphatase, target subunit 1, protein phosphatase 1, regulatory
1174 3773 AA998356 KKK, NNN (inhibitor) subunit 12/	(inhibitor) subunit 12A



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Seq		Centenk Ace or Passa (n	September 1	Rumen Homological	With the control of t
Î	833				CONTROL CONTROL OF THE CONTROL OF TH
					ESTS, Fighty strings to STRN_RAT Striam [K.:notvegicus], Homo sapiens conA
					2510040D07 gene, RIKEN cDNA 4930434E21 gene, RIKEN cDNA 5430411C10 gene
					platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, striatin, striatin,
2148	23157	AI172489	Q, R		calmodulin binding protein
					ESTs, Highly similar to T00065 hypothetical protein KIAA0442 [H.sapiens], Homo
					sapiens cDNA FLJ12396 fis, clone MAMMA1002758, KIAA1545 protein, hypothetical
2210	13678	AI176490	ww		protein FLJ11618
					ESTs, Highly similar to T03842 fission yeast Skb1 protein homolog [H.sapiens], Homo
			HHH, General		sapiens cDNA FLJ14831 fis, clone OVARC1001107, highly similar to Homo sapiens
2322	11660	AI178944	Alternate		protein methyltransferase (JBP1) mRNA
					ESTs, Highly similar to T08726 tubulin beta chain [H.sapiens], ESTs, Highly similar to
					TBB1_RAT TUBULIN BETA CHAIN (T BETA-15) [R.norvegicus], ESTs, Highly similar to
					TBB2_HUMAN TUBULIN BETA-2 CHAIN [H.sapiens], RIKEN cDNA 2410129E14 gene,
					RIKEN cDNA 4930447K03 gene, RIKEN cDNA 4930542G03 gene, expressed
163	17771	AA818224	AA.		sequence AI451582, expressed sequence C79445, tubulin beta-5, tubulin, beta 3
					ESTs, Highly similar to T08726 tubulin beta chain [H.sapiens], ESTs, Highly similar to
					TBB1_RAT TUBULIN BETA CHAIN (T BETA-15) [R.norvegicus], ESTs, Highly similar to
					TBB2_HUMAN TUBULIN BETA-2 CHAIN [H.sapiens], RIKEN cDNA 2410129E14 gene,
					RIKEN cDNA 4930447K03 gene, RIKEN cDNA 4930542G03 gene, Rat mRNA for beta-
					tubulin T beta15, expressed sequence AI451582, expressed sequence C79445, tubulin
4186	1700	X03369	NN, UU		beta-5, tubulin, beta 2, tubulin, beta 3, tubulin, beta polypeptide
					ESTs, Highly similar to T08726 tubulin beta chain [H.sapiens], ESTs, Highly similar to
					TBB1_RAT TUBULIN BETA CHAIN (T BETA-15) [R.norvegicus], ESTs, Highly similar to
					TBB2_HUMAN TUBULIN BETA-2 CHAIN [H.sapiens], RIKEN cDNA 2410129E14 gene,
					RIKEN cDNA 4930447K03 gene, RIKEN cDNA 4930542G03 gene, Rat mRNA for beta-
					tubulin T beta15, expressed sequence AI451582, expressed sequence C79445, tubulin
33	18361	AA799591	U, V, GG		beta-5, tubulin, beta 3, tubulin, beta, 2

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RABLE 3	જી જી				Attorney Decitet 4492/1-3038-6/1006
68 89	elec Div	<u>ලබෙනෙක්</u> රුලෙ ගැ යිමෙකල් [ම	Model Gode	Human Homologous Known Gene Name	In Homologous In Gene Name: HumaniHomologous Sequence Quster Mille
2473	16093	AI229849	T		ESTs, Highly similar to T13152 WDR1 protein [H.sapiens], ESTs, Moderately similar to T13152 WDR1 protein [H.sapiens], WD repeat domain 1
2363	14586	AI179865	רנו		ESTs, Highly similar to T17270 hypothetical protein DKFZp434N241.1 [H.sapiens], KIAA1007 protein
2288	16739	AI178151	C, H		ESTs, Highly similar to T46366 hypothetical protein DKFZp434C0118.1 [H.sapiens], F-box only protein 9, Homo sapiens cDNA FLJ32209 fis, clone PLACE6003372
263	19412	AA849222	CC, PP, UU, III, KKK, NNN		ESTs, Highly similar to T46904 hypothetical protein DKFZp761D081.1 [H.sapiens], Homo sapiens cDNA: FLJ21587 fis, clone COL06946, likely ortholog of mouse Arkadia
648	19410	AA893667	PP, UU, III, KKK		ESTs, Highly similar to T46904 hypothetical protein DKFZp761D081.1 [H.sapiens], Homo sapiens cDNA: FLJ21587 fis, clone COL06946, likely ortholog of mouse Arkadia
			E, BB, NN, PP, QQ, EEE, III,		
648	19411	AA893667	JJJ, KKK, MMM, NNN		ESTs, Highly similar to T46904 hypothetical protein DKFZp761D081.1 [H.sapiens], Homo sapiens cDNA: FLJ21587 fis, clone COL06946, likely ortholog of mouse Arkadia
					ESTs, Highly similar to T4S4_HUMAN TRANSMEMBRANE 4 SUPERFAMILY, MEMBER 4 [H.sapiens], Mus musculus, clone MGC:19127 IMAGE:4211816, mRNA,
1320	3828	A1009601	>		complete cds, transmembrane 4 superfamily member 1, transmembrane 4 superfamily member 4, transmembrane 4 superfamily member 5
					ESTs, Highly similar to THDE_RAT Thyrotropin-releasing hormone degrading ectoenzyme (TRH-degrading ectoenzyme) (TRH-DE) (TRH-specific aminopeptidase)
					(Tinyroliberinase) (Pyrogiutamyl-peptidase II) (PAP-II) [K.norvegicus], ESTS, weakly similar to AMPE MOUSE GLUTAMYL AMINOPEPTIDASE [M.musculus], ESTS, Weakly similar to PUROMYCIN-SENSITIVE AMINOPEPTIDASE [M.musculus], aminopeptidase
617	3865	AA893065	ZZ, AAA		puromycin sensitive, puromycin-sensitive aminopeptidase
4000		600000) ()		ESTs, Highly similar to TPMN_HUMAN TROPOMYOSIN, CYTOSKELETAL TYPE [H.sapiens], ESTs, Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE
4082	14121	582383	U, P, W		[M.muscuius]



TABLES	ଜ ଜ				
- - - - - - - - - - - - - - - - - - -	GLGC ID No.	<u>ිමෝඩෝබැි</u> Ae ෙග් Rම්පිලෙ [D	Model Gode	Human Nomologous Kinown Gene Name	an Homologous) Vni Genei Namer Human Homologous Sequence Gluster Title
					ESTs, Highly similar to TVHUR1 transforming protein rap1b [H.sapiens], ESTs, Weakly similar to GTP-binding protein ROC2 [M.musculus], Mus musculus, Similar to RAS-like,
					estrogen-regulated, growth-inhibitor, clone MGC:31467 IMAGE:4483442, mRNA,
1777	22700	VI013404	a		complete cds, RAP1B, member of RAS oncogene family, RAP2B, member of RAS
Ì	Т	AIC 13404	0		Ulcogelle lanilly, NAC-line, estinger Hegulared, glowin-linibud
					ESTs, Highly similar to TVHUR1 transforming protein rap1b [H.sapiens], ESTs, Weakly
					similar to GTP-binding protein ROC2 [M.musculus], Mus musculus, Similar to RAS-like,
					estrogen-regulated, growth-inhibitor, clone MGC:31467 IMAGE:4483442, mRNA,
					complete cds, RAP1B, member of RAS oncogene family, RAP2B, member of RAS
3961	16456	NM_134346	۵		oncogene family, RAS-like, estrogen-regulated, growth-inhibitor
					ESTs, Highly similar to TVHUR1 transforming protein rap1b [H.sapiens], ESTs, Weakly
					similar to GTP-binding protein ROC2 [M.musculus], Mus musculus, Similar to RAS-like,
					estrogen-regulated, growth-inhibitor, clone MGC:31467 IMAGE:4483442, mRNA,
					complete cds, RAP1B, member of RAS oncogene family, RAP2B, member of RAS
3961	16457	NM_134346	A, B, O, P, W		oncogene family, RAS-like, estrogen-regulated, growth-inhibitor
					ESTs, Highly similar to TYB4 MOUSE THYMOSIN BETA-4 [M.musculus], ESTs,
					Moderately similar to PC4259 ferritin associated protein [H.sapiens], Homo sapiens
					cDNA FLJ31414 fis, clone NT2NE2000260, weakly similar to THYMOSIN BETA-4,
3615	15052	NM_031136	BBB, CCC		thymosin, beta 4, X chromosome
					ESTs, Highly similar to TYROSINE-PROTEIN KINASE ITK/TSK [M.musculus], ESTs,
					Moderately similar to ITK MOUSE TYROSINE-PROTEIN KINASE ITKTSK
					[M.musculus], IL2-inducible T-cell kinase, Mus musculus 0 day neonate thymus cDNA,
					RIKEN full-length enriched library, clone:A430106A18:IL2-inducible T-cell kinase, full
2246	2359	AI177029	00		insert sequence, tec protein tyrosine kinase

			ESTs, Highly similar to UBP3 HUMAN UBIQUITIN CARBOXYL-TERMINAL	
			HYDROLASE 3 [H.sapiens], ESTs, Weakly similar to 158376 hypothetical protein unp -	
			mouse [M.musculus], ESTs, Weakly similar to UBP3_HUMAN UBIQUITIN CARBOXYL-	•
			TERMINAL HYDROLASE 3 [H.sapiens], Homo sapiens, clone MGC:20741	
•			IMAGE:4579283, mRNA, complete cds, Mus musculus, clone IMAGE:3711168, mRNA,	}
AA956794	Q, R		partial cds, RIKEN cDNA 4930550B20 gene, ubiquitin specific protease 3	-
	0, Р, GG, НН,			
	EEE, GGG,		ESTs, Highly similar to ULA4_HUMAN MAWD binding protein (Unknown protein 32 from	_
NM_138530 MMM	MMM		2D-page of liver tissue) [H.sapiens], MAWD binding protein	
			ESTs, Highly similar to UV EXCISION REPAIR PROTEIN PROTEIN RAD23	-
			HOMOLOG B [M.musculus], RAD23 homolog B (S. cerevisiae), RAD23b homolog (S.	-77
AI145997	S, LL		cerevisiae)	2-
			ESTs, Highly similar to Z208_HUMAN ZINC FINGER PROTEIN 208 [H.sapiens], ESTs,	
•			Moderately similar to 2208_HUMAN ZINC FINGER PROTEIN 208 [H.sapiens], ESTs,	
			Moderately similar to zinc finger protein 30 [M.musculus], ESTs, Weakly similar to zinc	
			finger protein 30 [M.musculus], Homo sapiens cDNA FLJ20562 fis, clone KAT11992,	
AI072402	FF		KRAB zinc finger protein KR18, zinc finger protein 208	
	,	-	ESTs, Moderately similar to Arg/Abl-interacting protein ArgBP2 [Rattus norvegicus]	
			[R.norvegicus], ESTs, Weakly similar to Arg/Abl-interacting protein ArgBP2 [Rattus	
			norvegicus] [R.norvegicus], RIKEN cDNA 2010203003 gene, SH3-domain protein 5	
NM_053770	⋖		(ponsin), sorbin and SH3 domain containing 1	
			ESTs, Moderately similar to Arg/Abl-interacting protein ArgBP2 [Rattus norvegicus]	
. •			[R.norvegicus], ESTs, Weakly similar to Arg/Abl-interacting protein ArgBP2 [Rattus	P(
			norvegicus] [R.norvegicus], RIKEN cDNA 2010203003 gene, SH3-domain protein 5	CT/
NM_053770	٧		(ponsin), sorbin and SH3 domain containing 1	us
			ESTs, Moderately similar to glycogenin 2 [Homo sapiens] [H.sapiens], glycogenin,	03/
NM_031043 O, P, VV	0, P, W		glycogenin 1, glycogenin 2	03:
				19

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	TABLE 3			14. Table 1.	A CHAINE AND BOOKER ALBEAT-EOSSE-ONWO BOOKER ALBEAT-EOSSE-ONWO
833 10 10 10 10 10 10 10 10 10 10 10 10 10	erec Bixo	Consental Ace or Refer D		Humen Homologous Kinowai Geael Neme	HumenThomologous The factor of the Kanal Kanal Sequence (Cluster/Title)
					ESTs, Moderately similar to hypothetical protein MGC2663 [Homo sapiens] [H.sapiens], ESTs, Moderately similar to S47073 finger protein HZF2, Krueppel-related [H.sapiens],
				1	ESTs, Weakly similar to TC17 MOUSE TRANSCRIPTION FACTOR 17 [M.musculus],
					ESTs, Weakly similar to TC17_RAT Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidnev. ischemia. and developmentally regulated
					protein-1) [R.norvegicus], expressed sequence AI875089, hypermethylated in cancer 2,
3054	1410	M96548	ww	7	zinc finger protein 354A, zinc finger protein 354B
					ESTs, Moderately similar to protein tyrosine phosphatase type IVA, member 2, isoform
				•	1; protein tyrosine phosphatase IVA; protein tyrosine phosphatase IVA2; phosphatase of
					regenerating liver 2 [Homo sapiens] [H.sapiens], protein tyrosine phosphatase 4a2,
1917	9575	AI112250	SS		protein tyrosine phosphatase type IVA, member 2
					ESTs, Moderately similar to protein tyrosine phosphatase type IVA, member 2, isoform
				•	1; protein tyrosine phosphatase IVA; protein tyrosine phosphatase IVA2; phosphatase of
					regenerating liver 2 [Homo sapiens] [H.sapiens], protein tyrosine phosphatase 4a2,
3772	9573	NM_053475	ZZ, AAA		protein tyrosine phosphatase type IVA, member 2
					ESTs, Moderately similar to RAN, member RAS oncogene family [Rattus norvegicus]
					[R.norvegicus], F-box and WD-40 domain protein 7, archipelago homolog (Drosophila),
					RAN, member RAS oncogene family, RAS-like, family 2, locus 9, RIKEN cDNA
3766	14670	NM_053439 UUU	nnn		1700009N14 gene
					ESTs, Moderately similar to rhoB gene [Rattus norvegicus] [R.norvegicus], ESTs,
					Weakly similar to rhoB gene [Rattus norvegicus] [R.norvegicus], Mus musculus, clone
					MGC:29297 IMAGE:5003249, mRNA, complete cds, RIKEN cDNA 5830400A04 gene,
3486	9541	NM_022542 W, II, QQ	W, II, QQ		ras homolog B (RhoB), ras homolog gene family, member B
		}			ESTs, Moderately similar to ribosomal protein S6 kinase, 70kD, polypeptide 2; S6
	·				kinase 2 [Mus musculus] [M.musculus], RIKEN cDNA 2610318115 gene, ribosomal
					protein S6 kinase, 70kD, polypeptide 1, ribosomal protein S6 kinase, 70kD, polypeptide
3720	3720 18899	NM_031985	LL, TT	, 1	

TABLE 3	38 38			44 - 44 - 44 - 44 - 44 - 44 - 44 - 44
නිලේ ල	erec D'No	ල්බා වෙ. Aලේම් RefSල්	ik D- Model Code	an Komologóvs vn Cene Names Rumán Homologous Sequence Cluster Tittle
			U, FF, TT, UU, DDD, SSS, UUU, General	ESTs, Moderately similar to RIKEN cDNA 1300002A08 [Mus musculus] [M.musculus],
1285	16701	AI008838	Core Tox Markers	RIKEN cDNA 1300002A08 gene, methylene tetrahydrotolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, protease, serine, 15
			K, U, FF, LL, TT, UU, HHH,	
			LLL, SSS,	Confront MA forthwester of MA 42000000000000000000000000000000000000
			Core Tox	ESTS, Moderately similar to Trinein Source 13000022400 (mus musculus) (m.musculus), RIKEN cDNA 1300002408 gene, methylene tetrahydrofolate dehydrogenase (NAD+
2338	16703	AI179300	Markers	dependent), methenyltetrahydrofolate cyclohydrolase, protease, serine, 15
				ESTs, Moderately similar to 2118320A neurodegeneration-associated protein 1 [Rattus norvegicus] [R. norvegicus], KIAA0438 gene product, Mus musculus, clone
				IMAGE:3499845, mRNA, partial cds, g1-related zinc finger protein, goliath protein,
			XX, YY, ZZ,	hypothetical protein FLJ20552, hypothetical protein LOC51255, praja 1, praja1, RING-
662	7637	AA894089	AAA	H2 motif containing, similar to RIKEN cDNA 1300002C13, zinc finger protein 364
				ESTs, Moderately similar to 2118320A neurodegeneration-associated protein 1 [Rattus
				norvegicus] (R.norvegicus), KIAA0438 gene product, Mus musculus, clone IMACE:2400045, mBNA, partial ade at related zinc finan protein, colleth protein
				Investigation of the control of the
3992	7635	NM 138896	NM 138896 K, M, ZZ, AAA	H2 motif containing, similar to RIKEN cDNA 1300002C13, zinc finger protein 364
		t .		ESTs, Moderately similar to 2118320A neurodegeneration-associated protein 1 [Rattus
				norvegicus] [R.norvegicus], KIAA0438 gene product, Mus musculus, clone
				IMAGE:3499845, mRNA, partial cds, g1-related zinc finger protein, goliath protein,
				hypothetical protein FLJ20552, hypothetical protein LOC51255, praja 1, praja1, RING-
3992	7636	NM_138896_22, AAA	77. AAA	HZ motif containing, similar to KIKEN CUNA 130000ZC13, zinc tinger protein 304
3297		20702 NM 017166 ZZ, AAA	ZZ, AAA	ESTs, Moderately similar to A40936 stathmin [H.sapiens], expressed sequence AI131641, leukemia-associated gene, stathmin 1/oncoprotein 18
		-		



/Micropy Decket 4492/1-5020-0/W/O		eakly similar to ANM1_MOUSE	i [im.musculus], rim I i incher ilus, Similar to protein arginine N-	7159, mRNA, complete cds, RIKEN	cleoproteins methyltransferase-	proteins methyltransferase-like 2 (S	-LJ10640, protein arginine N-	erevisiae)-like 3	I MITOCHONDRIAL CARRIER	4.sapiens], solute carrier family 25	or), member 10, solute carrier family	, member 10, solute carrier family 24	r 11	I MITOCHONDRIAL CARRIER	20M_HUMAN MITOCHONDRIAL 2	H.sapiens], solute carrier family 25	tor), member 10, solute carrier family	, member 10, solute carrier family 24	r 11	RIN-BINDING PROTEIN CABIN 1		N CAPPING PROTEIN ALPHA-3	IC PROTEIN 3) [M.musculus],	i 2, capping protein alpha 2, capping	
kiemoy Doeket 14.924-5038-01WO	nn Homologous nn Genein Samer Human Homologous Sequence Guster Title	ESTs, Moderately similar to ANMI_MOUSE PROTEIN ARGININE N-METHYLTRANSFERASE 1 [M.musculus], ESTs, Weakly similar to ANMI_MOUSE	PROTEIN ARGININE N-METHIL IRANSFERASE T [M.musculus], DWTT IMANSFERASE T [M.musculus], DWTT IMANSFERASE THE METHING TO BE SENTINE TO BE SENTINE OF THE METHING THE	methyltransferase 6, clone MGC:30554 IMAGE:5067159, mRNA, complete cds, RIKEN	cDNA 2410016A17 gene, neterogeneous nuclear ribonucleoprotein metriyinaristerase- like 1 (S. cerevisiae). heterogeneous nuclear ribonucleoproteins methyltransferase-like	2 (S. cerevisiae), heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S.	cerevisiae), related sequence, hypothetical protein FLJ10640, protein arginine N-	methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3	ESTs, Moderately similar to BMCP_HUMAN BRAIN MITOCHONDRIAL CARRIER DECTEIN 1 to conject ESTs Weakly similar to M20M HIMAN MITOCHONDRIAL 2-	OXOGLUTARATE/MALATE CARRIER PROTEIN IH.sapiens], solute carrier family 25	(mitochondrial carrier, adenine nucleotide translocator), member 10, solute carrier family	25 (mitochondrial carrier; dicarboxylate transporter), member 10, solute carrier family 25	(mitochondrial carrier; oxoglutarate carrier), member 11	ESTs, Moderately similar to BMCP_HUMAN BRAIN MITOCHONDRIAL CARRIER	PROTEIN-1 [H.sapiens], ESTs, Weakly similar to M2OM_HUMAN MITOCHONDRIAL 2-	OXOGLUTARATE/MALATE CARRIER PROTEIN [H.sapiens], solute carrier family 25	(mitochondrial carrier; adenine nucleotide translocator), member 10, solute carrier family	25 (mitochondrial carrier; dicarboxylate transporter), member 10, solute carrier family 25	(mitochondrial carrier; oxoglutarate carrier), member 11	ESTs, Moderately similar to CABI RAT CALCINEURIN-BINDING PROTEIN CABIN 1	R.norvegicus], calcineurin binding protein 1	ESTs, Moderately similar to CAZ3_MOUSE F-ACTIN CAPPING PROTEIN ALPHA-3	SUBUNIT (CAPZ ALPHA-3) (GERIM CELL-SPECIFIC PROTEIN 3) [M.muscuius],	capping protein (actin filament) muscle Z-line, alpha 2, capping protein alpha 2, capping	protein alpha 3
	Month of the second of the sec	<u>₩</u> ≅ 8	<u>t</u> <u>E</u>	Ē	<u>3</u> <u>¥</u>	2	8	Ĕ	<u>й</u> о	0	<u>)</u>	25	<u>u)</u>	<u> </u>	<u>a</u>	<u>0</u>	<u>E)</u>	25	(π	33	N)	Ĭ	<u> </u>	8	[pr
	Model Gode							UU					PP, QQ						99		A, B, DD, EE				
	Consent Ace or the Robeild							AF059530					NM_133418						NM_133418		AF061947				AA892842
(연)	GLGG DNo.							16762					17634						17635		18675				7148
TABLE 3								1236					3941						3941		1237				298

	Rabes				Attomery Docket 44921-5633-611Wo
Seq. (6)	@F@@ @Wo.	<u>ිලෙක නො.</u> කිලෙ ගේ ලිමේකීල් (D	Model Gode	Humani Homologous Known Genel Name	an Homologous An Genel Name Human Homologous Séquence Cluster Mile
					ESTs, Moderately similar to CNE6_MOUSE COPINE VI (NEURONAL-COPINE) (N-COPINE) IM musculus LESTs. Weakly similar to CNE3. HUMAN COPINE III
1634	24.0	A10E0204))		[H.sapiens], RIKEN cDNA 3632411M23 gene, copine 6, copine II, copine III, expressed
20	80101	A1039204	NNN NNN		Sequence Accounting the Sequence Away (NETRONAL COPINE) (N.
					COPINE) [M.musculus], ESTs, Weakly similar to CNE3_HUMAN COPINE III
					[H.sapiens], RIKEN cDNA 3632411M23 gene, copine 6, copine II, copine III, expressed
2780	18854	AI237636	000		sequence AU067659, expressed sequence AW047065
					ESTs, Moderately similar to COG2_MOUSE Coatomer gamma-2 subunit (Gamma-2
					coat protein) (Gamma-2 COP) [M.musculus], Mus musculus 0 day neonate skin cDNA,
			DDD, General		RIKEN full-length enriched library, clone:4632427M03:coatomer protein complex,
2561	19274	AI232135	Alternate		subunit gamma 1, full insert sequence, coatomer protein complex, subunit gamma 2
					ESTs, Moderately similar to CPJ3_RAT CYTOCHROME P450 2J3 (CYPIIJ3)
					[R.norvegicus], ESTs, Weakly similar to CPJ6 MOUSE CYTOCHROME P450 2J6
			CC, NN, OO,		[M.musculus], Homo sapiens cDNA FLJ14042 fis, clone HEMBA1006038, weakly
			BBB, CCC,		similar to LAMININ ALPHA-5 CHAIN, Mus musculus, Similar to CYP2J4, clone
			General		MGC:25927 IMAGE:4235131, mRNA, complete cds, RIKEN cDNA 8430436A10 gene,
4127	18038	U39943	Alternate		cytochrome P450, 2j6, cytochrome P450, 2j9, expressed sequence Al314783
					ESTs, Moderately similar to CPJ3_RAT CYTOCHROME P450 2J3 (CYPIIJ3)
					[R.norvegicus], ESTs, Weakly similar to CPJ6 MOUSE CYTOCHROME P450 2J6
					[M.musculus], Homo sapiens cDNA FLJ14042 fis, clone HEMBA1006038, weakly
			G, H, OO,		similar to LAMININ ALPHA-5 CHAIN, Mus musculus, Similar to CYP2J4, clone
			General		MGC:25927 IMAGE:4235131, mRNA, complete cds, RIKEN cDNA 8430436A10 gene,
4128	18036	U40004	Alternate		cytochrome P450, 2j6, cytochrome P450, 2j9, expressed sequence Al314783



Control Cont	TABLE 3	ନ ଜୁ				Attorneylboekeit44924isbusbeunwe
B, L, X, Y, HH, GGG, LLL, OOO, SSS, UUU, General Core Tox Markers 154 U32681 MMM BB, CC, NN, PP, QQ, EEE, 155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL		GLGC ID No.	රෙකිනෙන්? Acc or ි RolSca [D.	Modell Gode	Human Homologous Knovin Gene Name	
17401 NM 013043 Markers 17401 NM 013043 Markers 154 U32681 MMM 155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL				В, L, X, Y, ИН, GGG, LLL,		
17401 NM_013043 Markers Core Tox Core Tox NN, PP, EEE, MMM BB, CC, NN, PP, QQ, EEE, 155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL				, sss,		ESTs, Moderately similar to DIP_HUMAN DIP PROTEIN [H.sapiens], KIAA0669 gene
17401 NM_013043 Markers 154 U32681 MMM 155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL				UUU, General		product, RIKEN cDNA 0610009M14 gene, RIKEN cDNA 1810043J12 gene, 1SC-22- ike transforming growth factor beta 1 induced transcript 4_transforming growth factor
154 U32681 MMM 154 U32681 MMM 155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL	3202	17401	NM 013043	Markers		beta-stimulated protein TSC-22
154 U32681 MMM BB, CC, NN, PP, QQ, EEE, PP, QQ, EEE, MMM 18172 AI058364 EE, WW		_				ESTs, Moderately similar to DMBT1 protein, 5.8 kb transcript [H.sapiens], ESTs, Weakly
154 U32681 MMM BB, CC, NN, PP, QQ, EEE, PP, QQ, EEE, MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL						similar to crp-ductin [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to NETR
154 U32681 MMM BB, CC, NN, PP, QQ, EEE, 155 U32681 MMM 18172 AI058364 EE, WW						MOUSE NEUROTRYPSIN PRECURSOR [M.musculus], ESTs, Weakly similar to
154 U32681 MMM BB, CC, NN, PP, EEE, BB, CC, NN, PP, QQ, EEE, 155 U32681 MMM 18172 AI058364 EE, WW						T42721 CRP-ductin-alpha precursor - mouse [M.musculus], RIKEN cDNA 5430419D17
154 U32681 MMM BB, CC, NN, PP, QQ, EEE, 155 U32681 MMM 18172 AI058364 EE, WW			,	NN, PP, EEE,		gene, crp-ductin, deleted in malignant brain tumors 1, lectin, galactoside-binding,
BB, CC, NN, PP, QQ, EEE, MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL	4120	154	U32681	MMM		soluble, 3 binding protein, peptidylprolyl isomerase C-associated protein
155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL						ESTs, Moderately similar to DMBT1 protein, 5.8 kb transcript [H.sapiens], ESTs, Weakly
155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL						similar to crp-ductin [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to NETR
155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL						MOUSE NEUROTRYPSIN PRECURSOR [M.musculus], ESTs, Weakly similar to
155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL				BB, CC, NN,		T42721 CRP-ductin-alpha precursor - mouse [M.musculus], RIKEN cDNA 5430419D17
155 U32681 MMM 18172 AI058364 EE, WW 24323 AI104798 DDD, LLL				PP, QQ, EEE,		gene, crp-ductin, deleted in malignant brain tumors 1, lectin, galactoside-binding,
18172 AI058364 EE, WW 24323 AI104798 DDD, LLL	4120	155	U32681	MMM		soluble, 3 binding protein, peptidylprolyl isomerase C-associated protein
18172 AI058364 EE, WW 24323 AI104798 DDD, LLL						ESTs, Moderately similar to G02313 CDC37 homolog [H.sapiens], Hsp90-associating
DDD, LLL	1603	18172	AI058364	EE, WW		relative of Cdc37
000, LLL						ESTs, Moderately similar to GTM1_RAT Glutathione S-transferase YB1 (Chain 3) (GST
םסם, רור						M1-1) (GST class-Mu 1) [R.norvegicus], Glutathione-S-transferase, mu type 2 (Yb2),
	1881	24323	AI104798	DDD, LLL		glutathione S-transferase M4, glutathione S-transferase, mu 1

		7		
AA408365	ww		18209	554
Inrotein SRo25 nuclear protein, expressed sequence AA408210, expressed sequence				
ESTs, Moderately similar to JC7220 nuclear protein SR-25 [H.sapiens], HSVI binding		Т		
(peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	II, ZZ, AAA	AA800175	21064	98
[M.musculus], protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1, protein				
ESTs, Moderately similar to JC7136 peptidylprolyl isomerase (EC 5.2.1.8) - mouse			_	
5730434103 gene, basic transcription factor 3	ODO	AA892835	17581	282
IMAGE:2648048, mRNA, complete cds, RIKEN cDNA 1700054E11 gene, RIKEN cDNA	,			_
FACTOR BTF3, Mus musculus, basic transcription factor 3, clone MGC:6799				• •
sapiens cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION				
ESTs, Moderately similar to JC1235 transcription factor BTF3a [H.sapiens], Homo				<u>. </u>
expressed sequence AA986540, insulin, insulin I, insulin II	D, Z, AA	_	24392	3350
ESTs, Moderately similar to INS2 MOUSE INSULIN 2 PRECURSOR [M.musculus],				L.
PAT 12	JJ, KK		16182	3337
interacting protein (rabin3)-like 1, hypothetical protein FLJ22548 similar to gene trap		· ·		
musculus, clone MGC:28059 IMAGE:3708973, mRNA, complete cds, RAB3A		•••		
ESTs, Moderately similar to I57546 Rabin3 - rat [R.norvegicus], Grab protein, Mus				
ESTs, Moderately similar to I38937 DNA/RNA-binding protein [H.sapiens]	RR	AI071895	17673	1715
histocompatibility complex, class II, DR beta 5	<u></u>	AI111537	16718	1901
antigen E beta, major histocompatibility complex, class II, DR beta 1, major				
beta chain precursor (RT1.D(n)) mRNA, complete cds, histocompatibility 2, class II				
precursor (RT1.D(a)) mRNA, complete cds, Rattus norvegicus Class II MHC RT1.D(n)				
PRECURSOR [R.norvegicus], Rattus norvegicus Class II MHC RT1.D(a) beta chain				
HB2D RAT RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN, D-1 BETA CHAIN				
ANTIGEN, D-1 BETA CHAIN PRECURSOR (R.norvegicus), ESTs, Weakly similar to				
ESTs, Moderately similar to HB2D_RAT RT1 CLASS II HISTOCOMPATIBILITY				
Kinowni Gene Name Human Homologous Sequence Gluster intte	Model Gode		. WE WE	9
Human Homologous)			स्राख्य	San
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		部の名を変	ළින	
	ESTS, Moderately similar to Hazo RATRI CLASS II HISTOCOMPATIBILITY ANTICEN D. 1 BETA CHAIN PRECUESOR (R.norvegicus). ESTS, Weakly similar to Hazo RATRI CLASS II HISTOCOMPATIBILITY ANTICEN D. 1 BETA CHAIN PRECUESOR (R.norvegicus). ESTS, Weakly similar to HBZD RAT RT I CLASS II HISTOCOMPATIBILITY ANTICEN D. 1 BETA CHAIN PRECUESOR (R.norvegicus). ESTS, Weakly similar to HBZD RAT RT I CLASS II HISTOCOMPATIBILITY ANTICEN. D. 1 BETA CHAIN PRECUESOR (R.norvegicus). ESTS, Weakly similar to HBZD RAT RT I CLASS II HISTOCOMPATIBILITY ANTICEN. D. 1 BETA CHAIN PRECUESOR (R.norvegicus). ESTS, Moderately similar to 100 mRNA, complete cds, histocompatibility complex, class II, DR beta 5 ESTS, Moderately similar to 138937 DNA/RNA-binding protein (H.sapiens). ESTS, Moderately similar to 105948 beta 0. insulin, insulin II ESTS, Moderately similar to 105405 Insulin, insulin II ESTS, Moderately similar to 1057135 transcription factor BIT3a (H.sapiens). Homo sapiens cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BIT3, Muse musculus, bone MBC28059 IMAGE:370893, insulin, insulin II ESTS, Moderately similar to 107135 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus). ESTS, Moderately similar to 107136 peptidyprolyl isomerase (EC 5.2.13) - mouse IIM. musculus).	Social Kindenting Control of the Con	Cenbernk Reference Rinowin Rinowin	EGNESTRAND

0 03/004024			-779-			PC1/US03/03	194
Attorney Docket 4492/1-5038-0/1000 Attorney Document No. 1935323.1 An Homologous Here The Sequence Gives at 11119	ESTs, Moderately similar to JE0343 terf protein - rat [R.norvegicus], ESTs, Weakly similar to BUTY MOUSE BUTYROPHILIN PRECURSOR [M.musculus], ESTs, Weakly similar to JE0343 terf protein - rat [R.norvegicus], butyrophilin, subfamily 1, member A1, expressed sequence AA414909, expressed sequence AW538890, ret finger protein, tripartite motif protein 17, tripartite motif-containing 17	ESTs, Moderately similar to KTHY MOUSE THYMIDYLATE KINASE [M.musculus], Homo sapiens cDNA FLJ12070 fis, clone HEMBB1002358, thymidylate kinase	ESTS, Moderately similar to NEUROFILAMENT TRIPLET M PROTEIN [M.musculus], ESTS, Weakly similar to NFM_RAT Neurofilament triplet M protein (160 kDa neurofilament protein) (Neurofilament medium polypeptide) (NF-M) [R.norvegicus], ESTS, Weakly similar to T00365 hypothetical protein KIAA0670 [H.sapiens], ESTS, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sapiens], KIAA0888 protein, Musmusculus, Similar to sodium/calcium/potassium exchanger, clone MGC:27617	ESTs, Moderately similar to NICA_HUMAN NICASTRIN PRECURSOR [H.sapiens], nicastrin	ESTS, Moderately similar to NUCLEOLIN [M.musculus], ESTs, Weakly similar to A35804 nucleolin [H.sapiens], ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens], ESTs, Weakly similar to NUCL_RAT Nucleolin (Protein C23) [R.norvegicus], RIKEN cDNA 1200009A02 gene, eukaryotic translation initiation factor 3, subunit 4 (delta, 44 kDa), nucleolin, pigpen	ESTs, Moderately similar to P4H1_RAT Prolyl 4-hydroxylase alpha-1 subunit precursor (4-PH alpha-1) (Procollagen-proline,2-oxoglutarate-4-dioxygenase alpha-1 subunit) [R.norvegicus], Homo sapiens, clone IMAGE:3162218, mRNA, partial cds, RIKEN cDNA 4933406E20 gene, procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide, procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 11 polypeptide, procollagen-proline, 2-oxoglutarate 4-	dioxygenase (proline 4-hydroxylase), alpha polypeptide I, procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II
Model Gees		x, Y, UUU			FFF, General Core Tox Markers		Q, R, Z, AA, RR
Accomentation of the Research	Al012393	AA943116	A A 9 E 0 4 E 0	1	0		X78949
33 GLGC 10 No.	7120	24262	277	4267			23302
7731.33 Seg (9 10	1414	838	796	376	4		4265



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TABL	WABUES :				
නිලේ (ල	elec Id No	Geneenik Aee Ti Rabee (D	Model Gode	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Mile
			H, II, W, EEE, FFF, LLL,		ESTs, Moderately similar to PYRD MOUSE Dihydroorotate dehydrogenase,
			MMM, UUU,		mitochondrial precursor (Dihydroorotate oxidase) (DHOdehase) [M.musculus], RIKEN
3584	6911	NM 031027			dehydrogenase
					ESTs, Moderately similar to PYRD_MOUSE Dihydroorotate dehydrogenase, mitochondrial precursor (Dihydroorotate oxidase) (DHOdehase) fM.musculus]. RIKEN
	0		X, Y, II, W,		cDNA 2810417D19 gene, dihydroorotate dehydrogenase, dihydropyrimidine
3584	6912	NM_031027 XX, YY	XX, YY		dehydrogenase
					ESTs, Moderately similar to S12207 hypothetical protein [M.musculus], ESTs, Weakly similar to mitogen activated protein kinase kinase kinase 1 [Rattus norvegicus]
		·			[R.norvegicus], mitogen activated protein kinase kinase kinase 1, mitogen activated
			-		protein kinase kinase kinase 2, mitogen activated protein kinase kinase kinase 3,
					mitogen-activated protein kinase kinase kinase 1, mitogen-activated protein kinase
2387	1455	AI180373	≩		kinase kinase 3
					ESTs, Moderately similar to S12207 hypothetical protein [M.musculus], ESTs, Weakly
			-		similar to mitogen activated protein kinase kinase kinase 1 [Rattus norvegicus]
					[R.norvegicus], mitogen activated protein kinase kinase kinase 1, mitogen activated
					protein kinase kinase kinase 2, mitogen activated protein kinase kinase kinase 3,
					mitogen-activated protein kinase kinase kinase 1, mitogen-activated protein kinase
3847	1453	NM_053887	=		kinase kinase 3
					ESTs, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
					[R.norvegicus], ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein 1 -
					rat [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S. pombe) 1,
					clone MGC:11742 IMAGE:3969488, mRNA, complete cds, RIKEN cDNA 2810036L13
					gene, heterogeneous nuclear ribonucleoprotein L, polypyrimidine tract binding protein 1,
513	3902	AA891901	JJ, KK		polypyrimidine tract binding protein 2

mologous ne Name - Human Homologous Seguence Cluster Miller

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		ESTs. Moderately similar to S15552 polypovrimidine tract-binding protein 1 - rat
	<u>E</u>	(R.norvegicus), ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein 1
rat [R	rat [R	rat [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S. pombe) 1,
	cione iv	cione indoc. 11742 image3303400, inintra, complete cas, minera com zo rococe to gene. heterogeneous nuclear ribonucleoprotein L. polypyrimidine tract binding protein 1,
JJ, KK polypyrii	polypyrie	polypyrimidine tract binding protein 2
	ESTs, N	ESTs, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat
[R.nor	[R.norv	[R.norvegicus], ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein 1 -
rat [R.n	rat [R.n	rat [R.norvegicus], Mus musculus, Similar to regulator of differentiation (in S. pombe) 1,
clone M	clone N	clone MGC:11742 IMAGE:3969488, mRNA, complete cds, RIKEN cDNA 2810036L13
gene, h	gene, h	gene, heterogeneous nuclear ribonucleoprotein L, polypyrimidine tract binding protein 1,
NM_022516 VV polypyr	polypyr	polypyrimidine tract binding protein 2
ESTS, N	ESTS, N	ESTs, Moderately similar to S47073 finger protein HZF2, Krueppel-related [H.sapiens],
WW Zinc fin	zinc fin	zinc finger protein 191, zinc finger protein 354A, zinc finger protein 354B
JJ, KK ESTS, N	ESTS, N	ESTs, Moderately similar to T08795 hypothetical protein DKFZp586J1822.1 [H.sapiens]
ESTS, I	ESTs, I	ESTs, Moderately similar to T09123 hybrid receptor SorLA precursor - mouse
RRR [M.mus	[M.mus	[M.musculus], sortilin-related receptor, L(DLR class) A repeats-containing
ESTs,	ESTs,	ESTs, Moderately similar to T46347 hypothetical protein DKFZp434K0614.1
[H.sapi	H.sapi	[H.sapiens], Homo sapiens cDNA FLJ11663 fis, clone HEMBA1004631, homolog of
l, J mouse	esnow	mouse BMP-2 inducible kinase
ESTs,	ESTs,	ESTs, Moderately similar to T46637 transcription factor 1, neural - rat [R.norvegicus],
Homo	Ното	Homo sapiens mRNA; cDNA DKFZp434E0922 (from clone DKFZp434E0922), Mus
mnscni	muscul	musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library,
clone:2	clone:2	clone:2810003118:myelin transcription factor 1-like, full insert sequence, myelin
NM_133423 WW transcri	transcri	transcription factor 1-like
	ESTS, I	ESTs, Moderately similar to T47183 hypothetical protein DKFZp434K1822.1
ZZ, AAA [H.sapi	[H.sapi	[H.sapiens], ubiquitin specific protease 22

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3476

3905

1837

21911

7961

1545

14507

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13933

2514

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	<u>ම</u> ම	Consent		Human Homologous	main Homologious)
9	(D) No.	Rásag (D.	. Model ලින්ම	Known Gene Nemel	own Geng Name Human Homologous Sequence Cluster intile Bara
					ESTs, Moderately similar to T50638 synaptic glycoprotein SC2 [H.sapiens], ESTs,
					Weakly similar to T50638 synaptic glycoprotein SC2 [H.sapiens], expressed sequence
			S, Z, AA,		AI173355, glycoprotein, synaptic 2, steroid 5 alpha-reductase 2, steroid 5 alpha-
			General		reductase 2-like, steroid 5-alpha-reductase 2, steroid-5-alpha-reductase, alpha
3980	16922	NM_138549 Alternate	Alternate		polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
					ESTs, Moderately similar to T50638 synaptic glycoprotein SC2 [H.sapiens], ESTs,
		_			Weakly similar to T50638 synaptic glycoprotein SC2 [H.sapiens], expressed sequence
			A, B, S, Z, AA,		AI173355, glycoprotein, synaptic 2, steroid 5 alpha-reductase 2, steroid 5 alpha-
			FF, General		reductase 2-like, steroid 5-alpha-reductase 2, steroid-5-alpha-reductase, alpha
3980	25479	NM_138549 Alternate	Alternate		polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
					ESTs, Moderately similar to TALIN [M.musculus], ESTs, Weakly similar to S69890
					mitogen inducible gene mig-2 [H.sapiens], Homo sapiens cDNA: FLJ21712 fis, clone
					COL10231, Mus musculus, Similar to hypothetical protein MGC11134, clone
_					MGC:41710 IMAGE:1364225, mRNA, complete cds, chromosome 20 open reading
2084	22340	A1171276	II, KK		frame 42, lysosomal amino acid transporter 1, mitogen inducible 2, talin, talin 2
					ESTs, Moderately similar to TALIN [M.musculus], Mus musculus, Similar to hypothetical
					protein MGC11134, clone MGC:41710 IMAGE:1364225, mRNA, complete cds, talin,
122	21416	AA800962	0, x, Y		talin 2
					ESTs, Moderately similar to TROPOMYOSIN 5, CYTOSKELETAL TYPE [M.musculus],
2924 1514	1514	J02780	0, P, W		tropomyosin 4

						١
	sequence AA986709		¥	NM_031533	14633	640
,	mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2					
	glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890,					
	2B5 PRECURSOR, MICROSOMAL [M.musculus], Mus musculus, Similar to UDP					
	ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE					
	yeast)		BB, CC	AA858551	15284	37
	(UBC4/5 homolog, yeast), ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog,	-				
	6130401J04 gene, hypothetical protein FLJ11011, ubiquitin-conjugating enzyme E2E 1			-		
	UBC4/5), clone MGC:28917 IMAGE:4923869, mRNA, complete cds, RIKEN cDNA					
	musculus, Similar to ubiquitin-conjugating enzyme E2E 3 (homologous to yeast			· ·		
	similar to UBIQUITIN-CONJUGATING ENZYME E2-23 KDA (EC 6.3.2.19), Mus					
4-	21 KD UBCH6 [H.sapiens], Homo sapiens cDNA FLJ25157 fis, clone CBR08008, highly					•
-78	ESTs, Moderately similar to UBC6_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-					
	yeast)		E	AI227894	16801	404
	1, UBC4/5 homolog (yeast), ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog,					
	conjugating enzyme E2E 1 (UBC4/5 homolog, yeast), ubiquitin-conjugating enzyme E2E					
	yeast), ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5), ubiquitin-					
	hypothetical protein FLJ11011, ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog,					•
,	6.3.2.19), RIKEN cDNA 1100001F19 gene, RIKEN cDNA 1600028I17 gene,					
	CBR08008, highly similar to UBIQUITIN-CONJUGATING ENZYME E2-23 KDA (EC					
•	enzyme E2.17kB - rat [R.norvegicus], Homo sapiens cDNA FLJ25157 fis, clone				_	
	21 KD UBCH6 [H.sapiens], ESTs, Weakly similar to S53358 ubiquitin-conjugating					
	ESTs, Moderately similar to UBC6_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-					
	HumaniHomologous Sequence Clusteriii	Known GeneiName	M ळवंबी देळते	RefSed ID	_ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _	
		Rivinan Komologous		Serieming (1)	<u>@</u>	· @
			7 . W. W. A. P.		E3:	



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Company Comp		VABLES.			k de de la
17805 NM_031980 PP, QQ, TT 17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU	833 10	61.66 (D. No.	content lacor Reseque	 Wodd	· 计算程序系统
17805 NM_031980 PP, QQ, TT 17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE 285 PRECURSOR MICROSOMAL IM musculus) Mus musculus
17805 NM_031980 PP, QQ, TT 17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890,
17805 NM_031980 PP, QQ, TT 17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2
17805 NM_031980 PP, QQ, TT 17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed
17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU	3718	$\overline{}$			sequence AA986709
17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE
17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU	_				2B5 PRECURSOR, MICROSOMAL [M.musculus], Mus musculus, Similar to UDP
17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890,
17806 NM_031980 RRR 14346 NM_153314 N 14347 NM_153314 K, QQ, UU					mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2
17806 NM 031980 RRR 14346 NM 153314 N 14347 NM 153314 K, QQ, UU					family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed
14346 NM_153314 N 14347 NM_153314 K, QQ, UU	3718	17806	NM_031980		sequence AA986709
14346 NM_153314 N 14347 NM_153314 K, QQ, UU					ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE
14346 NM_153314 N 14347 NM_153314 K, QQ, UU					2B5 PRECURSOR, MICROSOMAL [M.musculus], Mus musculus, Similar to UDP
14346 NM_153314 N 14347 NM_153314 K, QQ, UU			_		glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890,
14346 NM_153314 N 14347 NM_153314 K, QQ, UU					mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2
14346 NM_153314 N 14347 NM_153314 K, QQ, UU					family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed
14347 NM 153314 K, QQ, UU	4047	14346	NM_153314		sequence AA986709
14347 NM_153314 K, QQ, UU					ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE
14347 NM_153314 K, QQ, UU			_		2B5 PRECURSOR, MICROSOMAL [M.musculus], Mus musculus, Similar to UDP
14347 NM 153314 K, QQ, UU					glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890,
14347 NM_153314 K, QQ, UU					mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2
14347 NM_153314 K, QQ, UU					family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed
	4047	14347	NM 153314	t K, QQ, UU	sequence AA986709

Alterney Docket (4921-5938-91W)	Aumani Homologous	ESTs, Moderately similar to UDB5 MOUSE UDP-GLUCURONOSYLTRANSFERASE 2B5 PRECURSOR, MICROSOMAL [M.musculus], Mus musculus, Similar to UDP glycosyltransferase 2 family, polypeptide B4, clone MGC:37823 IMAGE:5098890, mRNA, complete cds, RIKEN cDNA 1300012D20 gene, UDP glycosyltransferase 2 family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed	sequence AA986709	ESTs, Weakly similar to 2-oxoglutarate carrier [Rattus norvegicus] [R.norvegicus], solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 10, solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	ESTs, Weakly similar to 2-oxoglutarate carrier [Rattus norvegicus] [R.norvegicus], solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 10, solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11		ESTs, Weakly similar to argininosuccinate lyase [Rattus norvegicus] [R.norvegicus], argininosuccinate lyase	ESTs, Weakly similar to betaine-homocysteine methyltransferase [Rattus norvegicus] [R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930572N12:betaine-homocysteine methyltransferase, full insert sequence, betaine-homocysteine methyltransferase, betaine-homocysteine	methyltransferase 2	ESTs, Weakly similar to cadherin EGF LAG seven-pass G-type receptor [Mus musculus] [M.musculus], FAT tumor suppressor homolog 1 (Drosophila), Fta3 protein, cadherin 23 (otocadherin), calsyntenin 1, calsyntenin 2
	Wedel Gode		MM, TTT	BB, CC	W, DD, EE, BBB, CCC	A, B, I, J, L, MM, ww, BBB, KKK, OOO, TTT,	General Alternate	OO.	000	ر م
	Continui Lagor Refisa (D		NM_153314 MM,	AA859975	NM_022398		NM 021577		AF038870	NM 031819 Q, R
ନ ଜ	erec ID No.		14632	23301	23300		18727		1995	23407
TABLES	(S)		4047	407	3469		3424		1233	3698

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Seg (D	GLGC Wo.	ලෙකෑනෙයි ඵලෙ ගැ යින්පිනු [D	Model Gode	Human Homologous หีกัดพัก Gene Name HumaniHomologous Sequence Gluster ITนิอา	Store Title
3966	2643	NM_134408	Z, AA, RR	ESTs, Weakly similar to cadherin EGF LAG seven-pass G-ty musculus] [M.musculus], KIAA1828 protein, cadherin EGF LA seven-pass G-type receptor 3	ESTs, Weakly similar to cadherin EGF LAG seven-pass G-type receptor [Mus musculus] [M.musculus], KIAA1828 protein, cadherin EGF LAG seven-pass G-type receptor 1, cadherin EGF LAG seven-pass G-type receptor 3
				ESTs, Weakly similar to calcium/calmodulin-dependent serine protein kinas norvegicus] [R.norvegicus], RIKEN cDNA 2810038M04 gene, RIKEN cDNA 5430426E14 gene, calcium/calmodulin-dependent serine protein kinase, calcium/calmodulin-dependent serine protein kinase, memi	ESTs, Weakly similar to calcium/calmodulin-dependent serine protein kinase [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2810038M04 gene, RIKEN cDNA 5430426E14 gene, calcium/calmodulin-dependent serine protein kinase, calcium/calmodulin-dependent serine protein kinase (MAGLIK family) membrane
1243	20133	AF087697	×, ×	protein, palmitoylated (55 kDa), membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	protein, palmitoylated (55 kDa), membrane protein, palmitoylated 1 (55kD), membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
3447	20248	UM 022205	77	ESTs, Weakly similar to CXC chemok G protein-coupled receptor, chemokine X-C) receptor 4	ESTs, Weakly similar to CXC chemokine receptor [Rattus norvegicus] [R.norvegicus], G protein-coupled receptor, chemokine (C-X-C motif), receptor 4 (fusin), chemokine (C-X-C) receptor 4
3447	T	NM 022205	SS, EEE, MMM	ESTs, Weakly similar to CXC chemokine G protein-coupled receptor, chemokine X-C) receptor 4	ESTs, Weakly similar to CXC chemokine receptor [Rattus norvegicus] [R.norvegicus], G protein-coupled receptor, chemokine (C-X-C motif), receptor 4 (fusin), chemokine (C-X-C) receptor 4
3953	15029	NM 133583	1	ESTs, Weakly similar to development-related protein [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to NDRG family, member 4, clone IMAGE:3156802, mRNA, complete cds, N-myc downstream regulated 2, downstream regulated 3, N-myc downstream regulated 3, N-myc downstream regulated gene 1, RIKEN cf 1110025J03 gene. development-related protein	ESTs, Weakly similar to development-related protein [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to NDRG family, member 4, clone MGC:7067 IMAGE:3156802, mRNA, complete cds, N-myc downstream regulated 2, N-myc downstream regulated 3, N-myc downstream regulated gene 1, RIKEN cDNA
3953		- NM 133583	 	ESTs, Weakly similar to development-related protein [Rattus norvegicus] [R. norvegicus], Mus musculus, Similar to NDRG family, member 4, clone IMAGE:3156802, mRNA, complete cds, N-myc downstream regulated 2, downstream regulated 3, N-myc downstream regulated gene 1, RIKEN cf 1110025.103 gene.	ESTs, Weakly similar to development-related protein [Rattus norvegicus] [R. norvegicus], Mus musculus, Similar to NDRG family, member 4, clone MGC:7067 IMAGE:3156802, mRNA, complete cds, N-myc downstream regulated 2, N-myc downstream regulated 3, N-myc downstream regulated gene 1, RIKEN cDNA 1110025,103 gene. development-related protein
502		AA891810		ESTs, Weakly similar to g1-related zinc finge Homo sapiens, clone IMAGE:3956746, mRN, protein, similar to RIKEN cDNA 1300002C13	ESTs, Weakly similar to g1-related zinc finger protein [Mus musculus] [M.musculus], Homo sapiens, clone IMAGE:3956746, mRNA, partial cds, g1-related zinc finger protein, similar to RIKEN cDNA 1300002C13

TABLE 3	ල ම	A STATE OF S			AKOTAN DOCKEI AKEN-EUB-OAWO
Sed (0)	GLGC D'No.	ල්බාවෙබ්. Ae ෙෙි Rake ල	 	Rumen Homologous (Feet R	nae Guster Miler
502	8969	AA891810	Σ.	ESTs, Wea Homo sapit protein, sim	ESTs, Weakly similar to g1-related zinc finger protein [Mus musculus] [M.musculus], Homo sapiens, clone IMAGE:3956746, mRNA, partial cds, g1-related zinc finger protein, similar to RIKEN cDNA 1300002C13
				ESTs, Wea expression protein, GA protein like	ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus], GABA(A) receptor-associated protein, GABA(A) receptor-associated protein like 1, GABA(A) receptor-associated protein like 2, GABA(A) receptor-associated protein-like 2, GABA(A) receptor-associated protein-like 2, GABA(A) receptors
1803	2967	A1102520	EEE, MMM	associated p protein-like 1	associated protein like 3, gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1
1803	2969	Al102520	EEE, MMM	ESTs, Wea expression protein, GA protein like associated protein-like	ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus], GABA(A) receptor-associated protein, GABA(A) receptor-associated protein like 1, GABA(A) receptor-associated protein like 2, GABA(A) receptor-associated protein-like 2, GABA(A) receptor-associated protein-like 3, gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1, gamma-aminobutyric acid receptor associated protein
		·		ESTs, Wea expression protein, GA protein like associated	ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus], GABA(A) receptor-associated protein, GABA(A) receptor-associated protein like 1, GABA(A) receptor-associated protein like 2, GABA(A) receptor-associated protein-like 2, GABA(A) receptor-associated protein like 3, gamma-aminobutyric acid (GABA(A)) receptor-associated
3514	24458	NM_022706	L, LL	protein-like	protein-like 1, gamma-aminobutyric acid receptor associated protein
				ESTS, Wea [Mus musca 1600029D2	ESTs, Weakly similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon [Mus musculus] [M.musculus], RIKEN cDNA 0610038H21 gene, RIKEN cDNA 1600029D21 gene, gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon, tight
3546	15779	NM_024163	RR	junction pro	junction protein 4 (peripheral)
	12243	AI070133	RR	ESIS, Wea histone ace	ESTS, Weakly Sittiliar to Tilstoffe acetyfitransferase [wids filusculus] [w.t.filusculus], histone acetyltransferase, monocytic leukemia zinc finger protein-related factor
1317	11322	AI009492	CC, UUU	ESTs, Wea	ESTs, Weakly similar to hypothetical protein [Homo sapiens] [H.sapiens]

B. XX, YY ESTS, Weakly similar to isopentenyl-diphospha ESTS, Weakly similar to isopentenyl-diphospha R. norvegicus], Mus musculus, Similar to isopenchorspha R. norvegicus], Mus musculus, Similar to isopenchorspha ESTS, Weakly similar to isopentenyl-diphospha ESTS, Weakly similar to isopentenyl-diphospha ESTS, Weakly similar to isopenchoryl-diphospha ESTS, Weakly similar to the indiphosphate isomerase 2, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 2, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 2, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 2, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphate isomerase 2, isopentenyl-diphosphate isomerase 2, isopentenyl-diphosphate isomerase 3, isopentenyl-diphosphatenyl-dipho	TABLE 3	ශ ස	19 - 19 - 19 - 19 - 19 - 19 - 19 - 19 -			
7 1058 AF003835 B, XX, YY D 7691 Al236611 Y 1 1205 Al013107 D, V D 15904 Al013971 QQ	Sed (D	eleë Bro	Ace or Refee (10).	ූ . ග	Human Homologous Feet Khowai Khomer	
7 1058 AF003835 B, XX, YY D 7691 AI236611 Y 1205 AI013107 D, V D 15904 AI013971 QQ					ESTs, 1	Weakly similar to isopentenyl-diphosphate delta isomerase [Rattus norvegicus]
7 1058 AF003835 B, XX, YY D 7691 AI236611 Y AI236611 Y AI013107 D, V D 504 AI013971 QQ A8819643 K					[R.norv	egicus], Mus musculus, Similar to isopentenyl-diphosphate delta isomerase,
7 1058 AF003835 B, XX, YY D 7691 AI236611 Y AI205 AI013107 D, V D 15904 AI013971 QQ					clone N	IGC:8139 IMAGE:3589498, mRNA, complete cds, diphosphate dimethylallyl
7691 AI236611 Y 1205 AI013107 D, V 15904 AI013971 QQ	1217	1058	AF003835	B, XX, YY	diphos	phate isomerase 2, isopentenyl-diphosphate delta isomerase
1 1205 AI013107 D, V 1 15904 AI013971 QQ 15668 AA819643 K					ESTs,	Weakly similar to isopentenyl-diphosphate delta isomerase [Rattus norvegicus]
1 1205 AI013107 D, V 1 15904 AI013971 QQ 15668 AA819643 K					[R.norv	egicus], Mus musculus, Similar to isopentenyl-diphosphate delta isomerase,
1 1205 AI013107 D, V 1 15904 AI013971 QQ 15668 AA819643 K					clone N	AGC:8139 IMAGE:3589498, mRNA, complete cds, diphosphate dimethylallyl
1 1205 AI013107 D, V 9 15904 AI013971 QQ 1568 AA819643 K	2740	7691	AI236611	٨	soudip	shate isomerase 2, isopentenyl-diphosphate delta isomerase
1 1205 AI013107 D, V 3 15904 AI013971 QQ 15668 AA819643 K					ESTs,	Weakly similar to kinesin family member 3C [Rattus norvegicus] [R.norvegicus],
1 1205 AI013107 D, V 9 15904 AI013971 QQ 15668 AA819643 K					Kinesin	family member 3B, kinesin family member 3C, kinesin family member 3b, kinesin
3 15904 AI013971 QQ 15668 AA819643 K	1441	1205	AI013107	۵, ۷	family r	nember 3c
15904 AI013971 QQ					ESTs,	Weakly similar to L1 cell adhesion molecule [Mus musculus] [M.musculus],
15904 AI013971 QQ					ESTs,	Weakly similar to A41060 neural cell adhesion molecule L1 precursor
9 15904 AI013971 QQ 15668 AA819643 K					[H.sapi	ens], ESTs, Weakly similar to S36126 neural cell adhesion molecule L1 - rat
15904 AI013971 QQ					[R.norv	egicus], L1 cell adhesion molecule, L1 cell adhesion molecule (hydrocephalus,
15904 AI013971 QQ					stenosi	s of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and
15904 AI013971 QQ 15668 AA819643 K					adduct	ed thumbs) syndrome, spastic paraplegia 1), close homolog of L1, neuronal cell
15668 AA819643 K	1469	15904	AI013971	aa	adhesik	on molecule
15668 AA819643 K					ESTs,	Weakly similar to MAP/microtubule affinity-regulating kinase 3; ELKL motif
15668 AA819643 K					kinase	2 long form [Mus musculus] [M.musculus], ESTs, Weakly similar to A53621 AMP-
15668 AA819643 K					activate	ed protein kinase - rat [R.norvegicus], ESTs, Weakly similar to PUTATIVE
15668 AA819643 K					SERIN	E/THREONINE-PROTEIN KINASE EMK [M.musculus], G-protein-coupled
15668 AA819643 K					recepto	or induced protein GIG2, Homo sapiens, clone MGC:13661 IMAGE:4286367,
15668 AA819643 K					mRNA	complete cds, SNF related kinase, SNF1-like kinase, phosphoprotein regulated
	224		AA819643	K	by mito	genic pathways, protein kinase, AMP-activated, alpha 2 catalytic subunit

7 LL D, U Se D Se D		ABLES .				
3880 AA893247 LL 3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE	(Seg		(CONTENT AGG OF	100		Homologous-Seguence Gluster/III(Ia)
3880 AA893247 LL 3882 AI010191 D, U 16104 NM_031058 D 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE			21 -	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ESTs, Weakly similar to MAP/microtubule affinity-regulating kinase 3; ELKL motif
3880 AA893247 LL 3882 AI010191 D, U 16104 NIM_031058 D 23178 NIM_022395 D, SS 22105 AI175221 RR 16561 NIM_031020 DD, EE					kinase	kinase 2 long form [Mus musculus] [M.musculus], MAP/microtubule affinity-regulating
3880 AA893247 LL 3882 AI010191 D, U 16104 NM_031058 D 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE					kinase	kinase 3, Mus musculus, clone MGC:36574 IMAGE:5098034, mRNA, complete cds,
3880 AA893247 LL 3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE					PAS do	PAS domain containing serine/threonine kinase, serine/threonine kinase 22C
3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE	630	3880	AA893247	Tr	(spermi	ogenesis associated)
3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE					ESTs, \	ESTs, Weakly similar to MAP/microtubule affinity-regulating kinase 3; ELKL motif
3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE			•		kinase	kinase 2 long form [Mus musculus] [M.musculus], MAP/microtubule affinity-regulating
3882 AI010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 AI175221 RR 16561 NM_031020 DD, EE					kinase	kinase 3, Mus musculus, clone MGC:36574 IMAGE:5098034, mRNA, complete cds,
3882 Al010191 D, U 16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE					PAS do	PAS domain containing serine/threonine kinase, serine/threonine kinase 22C
16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE	1343	3882	AI010191	D, U	spermi	ogenesis associated)
16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE					ESTs, \	ESTs, Weakly similar to mismatch repair protein [Rattus norvegicus] [R.norvegicus],
16104 NM_031058 D 16106 NM_031058 T 23178 NM_022395 D, SS 22105 A175221 RR 16561 NM_031020 DD, EE					mutS h	mutS homolog 2 (E. coli), mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli),
16104 NM 031058 D 16106 NM 031058 T 23178 NM 022395 D, SS 22105 Al175221 RR 16561 NM 031020 DD, EE					mutS h	mutS homolog 3 (E. coli), mutS homolog 4 (E. coli), mutS homolog 5 (E. coli), mutS
16106 NM_031058 T 23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE	3593	16104	NM_031058		olomou	g 6 (E. coli)
16106 NM_031058 T 23178 NM_022395 D, SS 22105 A1175221 RR 16561 NM_031020 DD, EE					ESTs, \	ESTs, Weakly similar to mismatch repair protein [Rattus norvegicus] [R.norvegicus],
16106 NM_031058 T 23178 NM_022395 D, SS 22105 A1175221 RR 16561 NM_031020 DD, EE					mutS h	mutS homolog 2 (E. coli), mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli),
16106 NM 031058 T 23178 NM 022395 D, SS 22105 A1175221 RR 16561 NM 031020 DD, EE					mutS h	mutS homolog 3 (E. coli), mutS homolog 4 (E. coli), mutS homolog 5 (E. coli), mutS
23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE	3593	16106	NM_031058	Ţ	olomou	g 6 (E. coli)
23178 NM_022395 D, SS 22105 Al175221 RR 16561 NM_031020 DD, EE					ESTs, \	ESTs, Weakly similar to mitochondrial processing peptidase beta [Rattus norvegicus]
22105 A1175221 RR 16561 NM 031020 DD, EE					[R.norv	[R.norvegicus], RIKEN cDNA 3110004O18 gene, peptidase (mitochondrial processing)
23178 NM_022395 D, SS 22105 A1175221 RR 16561 NM_031020 DD, EE					beta, ut	beta, ubiquinol-cytochrome c reductase core protein 1, ubiquinol-cytochrome c
22105 A1175221 RR 16561 NM 031020 DD, EE	3468		NM_022395		reducta	se core protein I
22105 AI175221 RR 16561 NM 031020 DD, EE		1.			ESTs, \	ESTs, Weakly similar to mitochondrial ribosomal protein L16 [Homo sapiens]
16561 NM 031020 DD, EE	2162	22105	A1175221	RR	[H.sapie	ens], mitochondrial ribosomal protein L16
16561 NM 031020 DD, EE					ESTs, \	ESTs, Weakly similar to p38 mitogen activated protein kinase [Rattus norvegicus]
16561 NM 031020 DD, EE						[R.norvegicus], mitogen activated protein kinase 14, mitogen-activated protein kinase
	3583		NM_031020	DD, EE	11, mitc	gen-activated protein kinase 14

TABLES	ଞ୍ଚ				Attorney Docket 4/92/1-5033-01WM ************************************
Seq. (10	(C)	keenemi Keeor Kekeelo	ලානු ලනුගු	Human Hemologous Known Gene Name	Human Homologous Sequence Chister IIIIe
2603	40.00	2000	} L		ESTs, Weakly similar to p38 mitogen activated protein kinase [Rattus norvegicus] [R.norvegicus], mitogen activated protein kinase
2002	70001	NW 031020	E, 1, DD	- W	11, mitogen-activated protein kinase 14 ESTs, Weakly similar to p38 mitogen activated protein kinase [Rattus norvegicus]
3583	16564	NM_031020	E, W, TT	<u> </u>	[R.norvegicus], mitogen activated protein kinase 14, mitogen-activated protein kinase 11, mitogen-activated protein kinase 14
3719	15265	NM 031981	Q, R	<u>ш</u> б	ESTs, Weakly similar to p47 [Homo sapiens] [H.sapiens], RIKEN cDNA 3110003A22 gene
3719	15266	NM 031981	Q R	шб	ESTs, Weakly similar to p47 [Homo sapiens] [H.sapiens], RIKEN cDNA 3110003A22 gene
3719	15267	NM_031981	ww	ш ŏ	ESTs, Weakly similar to p47 [Homo sapiens] [H.sapiens], RIKEN cDNA 3110003A22 gene
3396	5264	NM 019340	JJ, KK	ш <u>с.</u> б	ESTs, Weakly similar to regulator of G-protein signaling 3 [Rattus norvegicus] [R.norvegicus], GTP-rho binding protein 1, hypothetical protein FLJ22938, regulator of G protein signaling 3
3796	21445	NM 053587 W.	W, BB	<u>a o o m</u>	ESTs, Weakly similar to \$100 calcium-binding protein A9 (calgranulin B); intracellular calcium-binding protein (MRP14) [Rattus norvegicus] [R.norvegicus], \$100 calcium binding protein A13, \$100 calcium binding protein A7 (psoriasin 1), \$100 calcium binding protein A9 (calgranulin B)
				ш ю ю <u>с</u> ठ <u>с</u>	ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-101; serine/arginine repetitive matrix protein 1 [Mus musculus] [M.musculus], ESTs, Weakly similar to A35938 profilaggrin [H.sapiens], ESTs, Weakly similar to A55817 cyclindependent kinase p130-PITSLRE - mouse [M.musculus], Mus musculus, Similar to hypothetical protein MGC13125, clone MGC:38070 IMAGE:5252666, mRNA, complete cds, expressed sequence A1480556, expressed sequence AW742389, glucocorticoid-induced gene 1, serine arginine-rich pre-mRNA splicing factor SR-A1, serine/arginine repetitive matrix 1, serine/serinine-rich
3410	24066	NM_019384	UU		2, interacting protein

			·			
Attenney Decket 44921-5038-011W0 In Homologous Homologous Sequence (cluster title)	ESTs, Weakly similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus norvegicus] [R.norvegicus], KIAA0446 gene product, Mus musculus, Similar to CG4995 gene product, clone MGC:7958 IMAGE:3584570, mRNA, complete cds, RIKEN cDNA 1300006L01 gene, expressed sequence AW491445, hypothetical protein FLJ13044, solute carrier family 25 (carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carrier), member 18, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 13, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 13, solute carrier family 25 (mitochondrial carrier), member 13, solute carrier family 25, mitochondrial carrier), member 18, solute carrier family 25, member 13 (citrin)	ESTs, Weakly similar to syntenin [Rattus norvegicus] [R.norvegicus], syndecan binding protein, syndecan binding protein (syntenin), syndecan binding protein (syntenin) 2	ESTs, Weakly similar to v-ral simian leukemia viral oncogene homolog B (ras related) [Rattus norvegicus] [R.norvegicus], v-ral simian leukemia viral oncogene homolog B (ras related), v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	ESTs, Weakly similar to 1313184B alpha1 antitrypsin [H.sapiens], ESTs, Weakly similar to A29035 thyroid hormone-regulated proteinase inhibitor - rat (fragment) [R.norvegicus]	ESTs, Weakly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus], Mus musculus, clone MGC:12070 IMAGE:3708271, mRNA, complete cds, RIKEN cDNA 1110018G07 gene, RIKEN cDNA 2810411E22 gene, RIKEN cDNA 4432411E13 gene, RIKEN cDNA 4930431E10 gene, expressed	sequence AW212605, upstream regulatory element binding protein 1
Humen Homologous Knovan Gene Name						
Model Gode	GGG, HHH, General Alternate	0, R	0, P, W	U, BB, EEE, MMM		д, В
Consent Consent Ace or Resco (D	A1045151	NM_031986	NM_053821	A1137506		U08214
ES GLGC ID No.	5711	19768	20421	22598		2686
MARIN See (D	1581	3721	3835	1955		4094

RABLE 8	ଞ୍ଚ			. Altomay Docket 44921-5038-01000
ි. ලිල් ලි	erec D No.	Cemen Ace or Refseq	13. D= (Node) මෙරෙ	Humani Homologous Knowni Genei Namesi Humani Homologousi Sec
				ESTs, Weakly similar to 2019405A upstream regulator element-binding protein [Rattus
				norvegicus] [R.norvegicus], Mus musculus, clone MGC:12070 IMAGE:3708271, mRNA,
				complete cds, RIKEN cDNA 1110018G07 gene, RIKEN cDNA 2810411E22 gene,
				RIKEN cDNA 4432411E13 gene, RIKEN cDNA 4930431E10 gene, expressed
4132	2685	U47312	a, R, PP, aa	sequence AW212605, upstream regulatory element binding protein 1
				ESTs, Weakly similar to 2122252A Lasp-1 protein [H.sapiens], LIM and SH3 protein 1,
3578	8815	NM_030991	<u>×</u>	RIKEN cDNA 1200007O21 gene
				ESTs, Weakly similar to 2122252A Lasp-1 protein [H.sapiens], LIM and SH3 protein 1,
3729	8817	NM_032613	NM 032613 L, W, AA, CC	RIKEN cDNA 1200007O21 gene
				ESTs, Weakly similar to 2204387A peroxisome assembly factor 2 [Rattus norvegicus]
				R.norvegicus), ESTs, Weakly similar to TRANSITIONAL ENDOPLASMIC RETICULUM
_				ATPASE [M.musculus], RIKEN cDNA 4833413G10 gene, expressed sequence
				Al195026, peroxisomal biogenesis factor 6, peroxisome biogenesis factor 1, valosin
3882	921	NM_057125 KKK	KK	containing protein
				ESTs, Weakly similar to A26882 pIL2 hypothetical protein - rat [R.norvegicus], ESTs,
				Weakly similar to AF191020 1 E2IG5 [H.sapiens], RIKEN cDNA 2310056P07 gene,
3310	18445	NM_017220	F, L	RIKEN cDNA 9430073N08 gene, hypothetical protein, estradiol-induced
				ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR
_			E, Y, MM,	[M.musculus], Mus musculus GPI-anchored alpha-2 macroglobulin-related protein
912	1798	AA945569	NNN, TTT	mRNA, complete cds, alpha-2-macroglobulin
				ESTs, Weakly similar to A39321 mucin - rat [R.norvegicus], mucin 17, mucin 3,
3038	1138	M76740	RR, SS	intestinal, mucin 3B, silver
				ESTs, Weakly similar to A39321 mucin - rat [R.norvegicus], mucin 17, mucin 3,
3038	25446	M76740	D, SS	intestinal, mucin 3B, silver
				ESTs, Weakly similar to A46506 leukocyte activation antigen M6 [H.sapiens], basigin
3815	5798	NM_053719	T	(OK blood group), embigin

NABLE 3	ଜୁଲ				**************************************
	elec:	<u>Centent</u> Ace or Refeet [D];	Model Gode	Human Homologous Known Gene Namer Human Homologousi Sequence Glust	
				ESTs, Weakly similar to A46661 leukotriene B4 omega-hydroxylase [H.sapiens], ESTs,	omega-hydroxylase [H.sapiens], ESTs,
· · · · · · ·			II, III, JJJ, KKK, General	Weakly similar to CYP4B1 [M.musculus], RIKEN cDNA A230105L22 gene, cytochrome P450 Suhfamily IV B. polypeptide 1, cytochrome P450	V cDNA A230105L22 gene, cytochrome
4048	1753	NM 153318		subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase), expressed sequence AW108534, expressed sequence AW11961	ega hydroxylase), expressed sequence pressed sequence
2506	20055	AI230762	V. EEE. MMM	ESTs, Weakly similar to A53742 calponin, acidic - rat [R.norvegicus], Homo sapiens, clone IMAGE:4669781, mRNA, partial cds	c - rat [R.norvegicus], Homo sapiens,
				ESTs, Weakly similar to A54691 octamer-binding protein NonO - mouse [M.musculus],	g protein NonO - mouse [M.musculus],
				ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPLICING FACTOR [H.sapiens]. RIKEN cDNA 9030402K04 gene. non-POU-domain-containing, octamer	SOCIATED SPLICING FACTOR on-POU-domain-containing, octamer
1060	8430	AA964033	I I	binding protein, splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	rich (polypyrimidine tract binding protein
				ESTs, Weakly similar to A54691 octamer-binding protein NonO - mouse [M.musculus],	g protein NonO - mouse [M.musculus],
	_			ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPLICING FACTOR	SOCIATED SPLICING FACTOR
				[H.sapiens], RIKEN cDNA 9030402K04 gene, non-POU-domain-containing, octamer	on-POU-domain-containing, octamer
1232	8426	AF036335	JJ, KK, HHH	binding protein, splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	rich (polypyrimidine tract binding protein
				ESTs, Weakly similar to A54691 octamer-binding protein NonO - mouse [M.musculus],	g protein NonO - mouse [M.musculus],
				ESTS, Weakly similar to PSF_HUMAN PTB-ASSOCIATED SPLICING FACTOR IfH.sapiens], RIKEN cDNA 9030402K04 gene, non-POU-domain-containing, octamer	SOCIALED SPLICING FACTOR on-POU-domain-containing, octamer
				binding protein, splicing factor proline/glutamine rich (polypyrimidine tract binding protein	rich (polypyrimidine tract binding protein
1232	8427	AF036335	В, ННН	associated)	
				ESTs, Weakly similar to A54691 octamer-binding protein NonO - mouse [M.musculus], ESTs, Weakly similar to PSF HUMAN PTB-ASSOCIATED SPLICING FACTOR	g protein NonO - mouse [M.musculus], SOCIATED SPLICING FACTOR
				[H.sapiens], RIKEN cDNA 9030402K04 gene, non-POU-domain-containing, octamer	on-POU-domain-containing, octamer
1330	8431	A1009761		binding protein, spilicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	rich (polypyrimidine tract binding protein

							-79	95-								
Attorney Docket 44921-5038-010VO	IS Numani Homologous Seguence Gustar intle	ESTs, Weakly similar to A54854 Ras GTPase activating protein-related protein	[H.sapiens]	ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05	gene, calpain, small subunit 1, programmed cell death 6, sorcin	ESTs, Weakly similar to A55190 transitional endoplasmic reticulum ATPase (EC 3.6.1) [Validated] - rat [R.norvegicus], ESTs, Weakly similar to TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE [M.musculus], Homo sapiens spermatogenesis	associated factor (SPAF) mRNA, complete cds, RIKEN cDNA 4833413G10 gene, RIKEN cDNA 4933439B08 gene, expressed sequence Al195026, katanin p60 (ATPase-	containing) subunit A1, nuclear VCP-like, peroxisome biogenesis factor 1,	sperinarogenesis associated factor, valosin containing protein, valosin-containing protein	ESTs, Weakly similar to A55190 transitional endoplasmic reticulum ATPase (EC 3.6.1) [validated] - rat [R.norvegicus], ESTs, Weakly similar to TRANSITIONAL	ENDOPLASMIC RETICULUM ATPASE [M.musculus], Homo sapiens spermatogenesis associated factor (SPAF) mRNA, complete cds, RIKEN cDNA 4833413G10 gene.	RIKEN cDNA 4933439B08 gene, expressed sequence Al195026, katanin p60 (ATPase-	containing) subunit A1, nuclear VCP-like, peroxisome biogenesis factor 1,	protein	ESTs, Weakly similar to A55571 chloride conductance inducer Mat-8 [H.sapiens], FXYD domain-containing ion transport regulator 3, FXYD domain-containing ion transport	regulator 4
	Human Komologous Known Genel Name															
	्रीक्रियी (स्थान) स्थान	General	Alternate		Κ, ૮		· .		z				_	L		F
	ල්කෑකෙ Xee ග RajSeq (p		AA800671		AA892921				NM_053864					NM_053864		L41254
ଜ	GLGC BNG.		17997		3438				18357					18358		695
		_	_		-T				3843							

430	Control of the Contro	AND AND PROPERTY OF THE PROPER	
elec do No,		Model Gode	Numen Homologous Known Gene Neme: Human Homologous Sequence Gluster Mile
			interacting protein) [M.musculus], RIKEN cDNA 4921513J16 gene, beclin 1 (coiled-coil,
		PP, QQ, DDD,	myosin-like BCL2 interacting protein), beclin 1 (coiled-coil, myosin-like BCL2-interacting
15269	NM_053739	ННН	protein)
		w, cc,	ESTs, Weakly similar to C2F1_HUMAN CYTOCHROME P450 2F1 [H.sapiens],
		General Core	cytochrome P450 monooxygenase CYP2T1, cytochrome P450, 2f2, cytochrome P450,
1099	NM_019303	Tox Markers	subfamily IIF, polypeptide 1
			ESTs, Weakly similar to C35826 hypothetical 13K protein A [H.sapiens], X-linked
			protein, brain expressed X-linked 2, nerve growth factor receptor (TNFRSF16)
16018	3 NM_053401	GG, ZZ, AAA	associated protein 1, reduced expression 3
			ESTs, Weakly similar to CAH5_RAT Carbonic anhydrase VA, mitochondrial precursor
		00, General	(Carbonate dehydratase VA) (CA-VA) [R.norvegicus], carbonic anhydrase 11, carbonic
		Core Tox	anhydrase 5a, mitochondrial, carbonic anhydrase 5b, mitochondrial, carbonic anhydrase
24883	3 NM_019293 Markers	Markers	VA, mitochondrial, carbonic anhydrase VB, mitochondrial
			ESTs, Weakly similar to CATB MOUSE CATHEPSIN B PRECURSOR [M.musculus],
20944	4 NM_022597	W, EEE, MMM	cathepsin B
			ESTs, Weakly similar to CATZ_HUMAN Cathepsin Z precursor (Cathepsin X)
4491	AA818798	0, P, V, W	(Cathepsin P) [H.sapiens], cathepsin Z, expressed sequence AU019819
			ESTs, Weakly similar to CATZ_HUMAN Cathepsin Z precursor (Cathepsin X)
4490	AA851184	O, P, W, HHH	(Cathepsin P) [H.sapiens], cathepsin Z, expressed sequence AU019819
			ESTs, Weakly similar to CO5 MOUSE COMPLEMENT C5 PRECURSOR [M.musculus],
10378	3 AI233300	노	complement component 5, hemolytic complement
			ESTs, Weakly similar to CO9 MOUSE COMPLEMENT COMPONENT C9 [M.musculus],
			Mus musculus, Similar to complement component 8, alpha polypeptide, clone
		YY, PPP,	MGC:29381 IMAGE:5052412, mRNA, complete cds, RIKEN cDNA 4930439B20 gene,
230	AA819870	000	complement component 8, beta polypeptide

TABLE 9	(주)				**************************************
) (1)	@L@@ ID No.	Composition (Composition Composition Compo	Model Gode	Kumen Homologous Kinown Genei Neme Kinown Genei Neme	
				ESTs, Weakly similar to CO9 MOUSE (ESTs, Weakly similar to CO9 MOUSE COMPLEMENT COMPONENT C9 [M.musculus],
			H, K, DD, EE,	Mus musculus, Similar to complement component 8, alpha polypeptide, clone	component 8, alpha polypeptide, clone
			UUU, General	MGC:29381 IMAGE:5052412, mRNA, c	MGC:29381 IMAGE:5052412, mRNA, complete cds, RIKEN cDNA 4930439B20 gene,
4107	228	U20194	Alternate	complement component 8, beta polypeptide	ptide
				ESTs, Weakly similar to CO9 MOUSE (ESTs, Weakly similar to CO9 MOUSE COMPLEMENT COMPONENT C9 [M.musculus],
		#	S, Z, AA, BBB,	Mus musculus, Similar to complement component 8, alpha polypeptide, clone	component 8, alpha polypeptide, clone
_			CCC, PPP,	MGC:29381 IMAGE:5052412, mRNA, c	MGC:29381 IMAGE:5052412, mRNA, complete cds, RIKEN cDNA 4930439B20 gene,
4107	229	U20194	QQQ, RRR	complement component 8, beta polypeptide	ptide
				ESTs, Weakly similar to COXG MOUSE	ESTs, Weakly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE
				VIB [M.musculus], Homo sapiens, hypo	VIB [M.musculus], Homo sapiens, hypothetical gene LOC125965, clone MGC:33640
944	20832	AA946040	F	IMAGE:4827471, mRNA, complete cds	
				ESTs, Weakly similar to COXG MOUSE	ESTs, Weakly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE
				VIB [M.musculus], Homo sapiens, hypo	VIB [M.musculus], Homo sapiens, hypothetical gene LOC125965, clone MGC:33640
1857	20833	AI104035	SS	IMAGE:4827471, mRNA, complete cds	
				ESTs, Weakly similar to CPI3_RAT CO	ESTs, Weakly similar to CPI3_RAT CONTRAPSIN-LIKE PROTEASE INHIBITOR 3
				PRECURSOR (CPI-23) (SERINE PRO:	PRECURSOR (CPI-23) (SERINE PROTEASE INHIBITOR 1) (SPI-1) [R.norvegicus],
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
		_	A, F, G, V,	member 4, serine (or cysteine) proteina	member 4, serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,
			SSS, General	pigment epithelium derived factor), men	pigment epithelium derived factor), member 1, serine protease inhibitor 2, serine
940	1562	AA893552	Alternate	protease inhibitor 2, related sequence 1	
			F, FFF,	ESTs, Weakly similar to CYP4B1 [M.musculus], cytochrome P450 CYP4F13,	usculus], cytochrome P450 CYP4F13,
			General	cytochrome P450, subfamily IV B, polyp	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVF,
4126	255	U39206	Alternate	polypeptide 2, expressed sequence AI7	polypeptide 2, expressed sequence AI787289, expressed sequence AW108534
			N, EEE, HHH,	ESTs, Weakly similar to CYP4B1 [M.m.	ESTs, Weakly similar to CYP4B1 [M.musculus], RIKEN cDNA 1810054N16 gene,
			MMM, PPP,	cytochrome P450, subfamily IVF, polypo	cytochrome P450, subfamily IVF, polypeptide 14 (leukotriene B4 omega hydroxylase),
			QQQ, General	cytochrome P450, subfamily IVF, polypo	cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF,
3411	20716	3411 20716 NM_019623 Alternate	Alternate	polypeptide 8, expressed sequence AW	polypeptide 8, expressed sequence AW108534, expressed sequence AW111961

Containing Con		ଜୁ			$ imes_{ m in} imes_{ m in} imes_{ m in}$	Anomey Decket (ACEN-Siss-61W)
1797 NM_013105 K, L, TT, DDD 21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4940 NM_022526 U, BBB 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, CC	Sed	99,79 98,89	Centent.		Humani Romologous	
1797 NM_013105 K, L, TT, DDD 21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_022526 U, BBB 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, CCC, RRR, SSS SSO	ا	(ID) (NO)	Kerseq W		vni Genernamera	
1797 NM_013105 K, L, TT, DDD 21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS CCC, RRR, CCC, R					ESTs, Weakly similar to cytochrome P450 3A13 [M.mus	sculus], Mus musculus mRNA for
21915 NM_013105 K, L, TT, DDD 21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS CCC, RRR, CCC,					cytochrome P450, CYP3A, complete cds, cytochrome F	450, steroid inducible 3a11,
21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NIM_024392 U, RRR, SSS CCC, RRR, CCC,		1797	NM_013105	K, L, TT, DDD	cytochrome P450, subfamily IIIA (niphedipine oxidase),	polypeptide 3
21915 NM_138910 Z, AA, OO 21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_025526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR,					ESTs, Weakly similar to DAD1_HUMAN Defender agair	nst cell death 1 (DAD-1)
21916 NM_138910 OO 4941 AA851650 CCC 4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS CCC, RRR, C		21915	NM_138910		[R.norvegicus], defender against cell death 1	
21916 NIM_138910 OO 4941 AA851650 CCC 4940 NIM_022526 U, BBB U, EE, XX, YY, 9929 NIM_024392 RRR, SSS 9931 NIM_024392 U, RRR, SSS CCC, RRR, CCCC, RRR, CCCC, RRR, CCC, RRR, CCC,					ESTs, Weakly similar to DAD1_HUMAN Defender agair	nst cell death 1 (DAD-1)
4941 AA851650 CCC 4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NIM_024392 U, RRR, SSS CCC, RRR,			NM_138910		[R.norvegicus], defender against cell death 1	
4941 AA851650 CCC 4940 NIM_022526 U, BBB U, EE, XX, YY, 9929 NIM_024392 RRR, SSS 9931 NIM_024392 U, RRR, SSS U, FR, LL, CCC, RRR, CCC, RRR, SSS					ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	CIATED PROTEIN 1
4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FR, LL, CCC, RRR, CCC, RRR, SSS		4941	AA851650	သသ	[H.sapiens], death-associated protein	
4940 NM_022526 U, BBB U, EE, XX, YY, 9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR,					ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	CIATED PROTEIN 1
9929 NIM_024392 RRR, SSS 9931 NIM_024392 U, RRR, SSS U, FR, LL, CCC, RRR, CCC, RRR, SSS		4940	NM_022526		[H.sapiens], death-associated protein	
9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					ESTs, Weakly similar to DHB4 MOUSE ESTRADIOL 17	' BETA-DEHYDROGENASE 4
9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FR, LL, CCC, RRR, CCC, RRR, SSS					[M.musculus], ESTs, Weakly similar to DHB4_HUMAN	ESTRADIOL 17 BETA-
9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					DEHYDROGENASE 4 [H.sapiens], RIKEN cDNA 11100	329G07 gene, RIKEN cDNA
9929 NM_024392 RRR, SSS 9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR,				U, EE, XX, YY,	1700010M22 gene, RIKEN cDNA 3110069K09 gene, hy	droxysteroid (17-beta)
9931 NIM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NIM 024392 SSS		9929	NM_024392		dehydrogenase 4	
9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					ESTs, Weakly similar to DHB4 MOUSE ESTRADIOL 17	BETA-DEHYDROGENASE 4
9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					[M.musculus], ESTs, Weakly similar to DHB4_HUMAN	ESTRADIOL 17 BETA-
9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					DEHYDROGENASE 4 [H.sapiens], RIKEN cDNA 11100)29G07 gene, RIKEN cDNA
9931 NM_024392 U, RRR, SSS U, FF, LL, CCC, RRR, 25070 NM 024392 SSS			_		1700010M22 gene, RIKEN cDNA 3110069K09 gene, hy	droxysteroid (17-beta)
U, FF, LL, CCC, RRR, 25070 NM 024392 SSS		9931	NM_024392		dehydrogenase 4	
U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					ESTs, Weakly similar to DHB4 MOUSE ESTRADIOL 17	BETA-DEHYDROGENASE 4
U, FF, LL, CCC, RRR, 25070 NM 024392 SSS					[M.musculus], ESTs, Weakly similar to DHB4_HUMAN	ESTRADIOL 17 BETA-
25070 NM 024392 SSS				U, FF, LL,	DEHYDROGENASE 4 [H.sapiens], RIKEN cDNA 11100)29G07 gene, RIKEN cDNA
25070 NM 024392 SSS					1700010M22 gene, RIKEN cDNA 3110069K09 gene, hy	/droxysteroid (17-beta)
	3555	25070	NM_024392	SSS	dehydrogenase 4	****

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Attenney Bocket (** 221-2020-00)Wolfman (No. 1926223.1) Hemologous Mumeni Homologous Sequence Cluster III (e. 1926)	ESTs, Weakly similar to DUS5_RAT Dual specificity protein phosphatase 5 (MAP-kinase phosphatase CPG21) [R.norvegicus], ESTs, Weakly similar to 149365 protein tyrosine phosphatase - mouse [M.musculus], Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 0710001B24 gene, RIKEN cDNA 2310043K02 gene, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 5, expressed sequence BB104621, hypothetical protein MGC1136, protein tyrosine phosphatase, non-receptor type 16	ESTs, Weakly similar to FA7 MOUSE COAGULATION FACTOR VII PRECURSOR [M.musculus], coagulation factor IX, coagulation factor X, proline-rich Gla (G-carboxyglutamic acid) polypeptide 1, protein Z, vitamin K-dependent plasma glycoprotein	ESTs, Weakly similar to FGD1 MOUSE PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [M.musculus], Mus musculus actin-binding protein frabin-alpha mRNA, complete cds, RIKEN cDNA 5830461L01 gene, faciogenital dysplasia (Aarskog-Scott syndrome), faciogenital dysplasia homolog	ESTs, Weakly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus], Homo sapiens clone HQ0582, expressed sequence Al303526, fibrinogen, A alpha polypeptide, fibrinogen, alpha polypeptide, polypeptide	ESTs, Weakly similar to FIBULIN-1, ISOFORM C PRECURSOR [M.musculus], Homo sapiens cDNA FLJ23816 fis, clone HSI02685, Homo sapiens cDNA FLJ32009 fis, clone NT2RP7009498, weakly similar to FIBULIN-1, ISOFORM A PRECURSOR, Mus musculus mRNA for CRTAC1-B protein (CRTAC1 gene), RIKEN cDNA 5730592L21 gene, fibulin 5
Humein Höin Khowin Gen	,				
Model Gode	O	General Core Tox Markers	a, R, PPP, aaa	E, V, W, Z, AA, BB, CC, OO, PP, SS, UU, EEE, III, KKK, LLL, MMM,	တ
A - 14	NM 133578	AI229192	AA866482	AA875097	AA957736
三3 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	1183	6604	16013	20701	24135
7735LE 3 Seq (91 (0) (0)	3952	2451	424	435	1039

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Human Homologous Sequence (இயக்கோயாடி)
ESTs, Weakly similar to JC4647 KW8 protein - rat [R.norvegicus], ESTs, Weakly similar to JC4688 neuro D-related factor - mouse [M.musculus], basic helix-loop-helix domain
ESTs, Weakly similar to JC4647 KW8 protein - rat [R.norvegicus], ESTs, Weakly s to JC4688 neuro D-related factor - mouse [M.musculus], basic helix-loop-helix don containing, class B, 4, hypothetical protein FLJ14708, neurogenic differentiation 2, neurogenic differentiation 4, oligodendrocyte lineage transcription factor 2
intaining, class B surpoenic differer
containing, cras neurogenic diff
neurogenic differentiation 4, oligodendrocyte lineage transcription factor 2
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A1007666 EE
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Alforney Dockel 4/92/1-5038-0/10/00 The Document No. 1935223.1 Human Honologous Scauence Gluster III 18	ESTs, Weakly similar to KEAP_RAT Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus], Kelch-like ECH-associated protein 1, Mus musculus, Similar to chromosome 16 open reading frame 44, clone MGC:37805 IMAGE:5098064, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ11078, clone MGC:38024 IMAGE:5151231, mRNA, complete cds, RIKEN cDNA 1200009K10 gene, kelch-like ECH-associated protein 1	ESTs, Weakly similar to LBP MOUSE LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR [M.musculus], bactericidal/permeability-increasing protein, cholesteryl ester transfer protein, plasma, lipopolysaccharide binding protein, phospholipid transfer protein	ESTs, Weakly similar to LCB1_HUMAN SERINE PALMITOYLTRANSFERASE 1 [H.sapiens]	ESTs, Weakly similar to MCAT_Human Mitochondrial Carnitine/acylcarnitine carrier protein, ESTs, Weakly similar to PM34_mouse peroxisomal membrane protein PMP34, ESTs, Weakly similar to TXTP_human tricarboxylate transport protein precursor, similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20, clone MGC:35539 IMAGE:5200129, Mus musculus, Similar to hypothetical protein FLJ20551, clone MGC:18873 IMAGE:4235245, RIKEN cDNA 1300019P08 gene, expressed sequence AM108044, ornithine transporter 2, solute carrier family 25 (mitochondrial carrier), member 18, solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 1, solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15, uncoupling protein 2, mitochondrial ESTs, Weakly similar to methyl-CpG binding protein MBD2 [H.sapiens], methyl-CpG binding domain protein 2 ESTs, Weakly similar to ML64_HUMAN MLN 64 PROTEIN [H.sapiens], RIKEN cDNA 4933429L05 gene, hypothetical protein MGC3251
Human Homologous Known Gene Neme				
Model Gode	PP, QQ	9	£.	ww BBB RRR
(1997) 1997	AI145037	AI171583	AA892380	AA957999 AA946379 AA944269
් මේ දිරි	14259	18837	8159	23541 19044 22392
TABLE 8 Seq (C) TO (D)	1977	2097	559	1042

MABLE 3	ලි ම				Alicancy Docket (4,1921-5038-01WO)
ල ල	elec D No.	Censent	Modal Gode	Human Homologous Known Gene Name Human Homologous Sequence Guster, IIIIe:	S GUSIEF MUSE
				ESTs, Weakly similar to NHPX_I	ESTs, Weakly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like
				nuclear protein 2 homolog 1) ([U	nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27)
				[R.norvegicus], NHP2 non-histor	[R.norvegicus], NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae), RIKEN
			General	CDNA 2410130M07 gene, nucle	cDNA 2410130M07 gene, nucleolar protein family A, member 2 (H/ACA small nucleolar
1408	3417	AI012337	Alternate	RNPs), sperm specific antigen 1	
				ESTs, Weakly similar to NHPX_	ESTs, Weakly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like
				nuclear protein 2 homolog 1) ([U	nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27)
			MM, TTT,	[R.norvegicus], NHP2 non-histor	[R.norvegicus], NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae), RIKEN
			General Core	cDNA 2410130M07 gene, nuclei	cDNA 2410130M07 gene, nucleolar protein family A, member 2 (H/ACA small nucleolar
2167	3418	A1175475	Tox Markers	RNPs), sperm specific antigen 1	
				ESTs, Weakly similar to OL15 M	ESTs, Weakly similar to OL15 MOUSE OLFACTORY RECEPTOR 15 [M.musculus],
				Homo sapiens cDNA FLJ32992	Homo sapiens cDNA FLJ32992 fis, clone THYMU1000098, Homo sapiens olfactory-like
_				receptor mRNA, complete cds, F	receptor mRNA, complete cds, RIKEN cDNA 4933431119 gene, RIKEN cDNA
1230	4292	AF034896	Z, AA	4933433E02 gene, olfactory receptor 15	eptor 15
				ESTs, Weakly similar to OL15 M	ESTs, Weakly similar to OL15 MOUSE OLFACTORY RECEPTOR 15 [M.musculus],
				RIKEN cDNA 4933431119 gene,	RIKEN cDNA 4933431119 gene, RIKEN cDNA 4933433E02 gene, olfactory receptor 15,
3034	20207	M64378	RR.	olfactory receptor 49, olfactory receptor sdolf	eceptor sdolf
				ESTs, Weakly similar to PDK4_	ESTs, Weakly similar to PDK4_MOUSE [PYRUVATE DEHYDROGENASE
	_			[LIPOAMIDE]] KINASE ISOZYM	[LIPOAMIDE]] KINASE ISOZYME 4, MITOCHONDRIAL PRECURSOR (PYRUVATE
				DEHYDROGENASE KINASE IS	DEHYDROGENASE KINASE ISOFORM 4) [M.musculus], pyruvate dehydrogenase
3787	15829	NM 053551	ZZ, AAA	kinase 4, pyruvate dehydrogenase kinase, isoenzyme 4	ise kinase, isoenzyme 4
		1			

TABLE 3	<u> </u>				274F ==
68 69 60	GLEC DNo.	CONTENTY Acc or Refised [D	Model Code:	Human Homologous Knowni Genei Name	
				ESTS, HSD)	ESTs, Weakly similar to PE2R_RAT 20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD) (HSD1) [R.norvegicus], Mus musculus, Similar to hydroxysteroid (17-beta)
				dehyd	dehydrogenase 5, clone MGC:37825 IMAGE:5098938, mRNA, complete cds, aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-
			A, B, P,	hydro	hydroxysteroid dehydrogenase), aldo-keto reductase family 1, member C2 (dihydrodiol
			General Core	dehyd	dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type
			Tox Markers,	(11), at	III), aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase,
-			General	type II	type II), expressed sequence AW146047, expressed sequence AW557061,
7886	25	E06822	Alternate	hydro	hydroxysteroid (17-beta) dehydrogenase 5
				ESTS,	ESTs, Weakly similar to PE2R_RAT 20-alpha-hydroxysteroid dehydrogenase (20-alpha-
				(QSH)	HSD) (HSD1) [R.norvegicus], Mus musculus, Similar to hydroxysteroid (17-beta)
				dehyd	dehydrogenase 5, clone MGC:37825 IMAGE:5098938, mRNA, complete cds, aldo-keto
				reduct	reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-
				hydro	hydroxysteroid dehydrogenase), aldo-keto reductase family 1, member C2 (dihydrodiol
				dehyd	dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type
					III), aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase,
			General	type II	type II), expressed sequence AW146047, expressed sequence AW557061,
3974	61	NM_138510) Alternate	hydro	hydroxysteroid (17-beta) dehydrogenase 5
				ESTs,	ESTs, Weakly similar to PK3G_RAT Phosphatidylinositol 3-kinase C2 domain-
				contai	containing gamma polypeptide (Phosphoinositide 3-Kinase-C2-gamma) (PtdIns-3-
_				kinase	kinase C2 gamma) (PI3K-C2gamma) [R.norvegicus], Homo sapiens cDNA FLJ12591
				fis, clo	fis, clone NT2RM4001313, moderately similar to PHOSPHATIDYLINOSITOL 3-KINASE
				VPS3	VPS34-LIKE (EC 2.7.1.137), phosphatidylinositol 3-kinase, C2 domain containing, alpha
				polype	polypeptide, phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide,
			II, General	dsoud	phosphoinositide-3-kinase, class 2, beta polypeptide, phosphoinositide-3-kinase, class
3852	4588	NM_053923	Alternate	2, gan	gamma polypeptide
				ESTs,	ESTs, Weakly similar to plasmin [H.sapiens], lipoprotein, Lp(a), plasminogen,
3775	9307	NM_053491 N, XX, YY	N, XX, YY	plasm	plasminogen-like

			<i></i>					
Altionney Docket 44924-5093-04W@	an Komologovs nn Gene Name Human Homologovs Sequence @vster Title	ESTs, Weakly similar to plasmin [H.sapiens], lipoprotein, Lp(a), plasminogen,	ESTS, Weakly similar to PSG1 MOUSE PROSTATIC SECRETORY GLYCOPROTEIN PRECURSOR [M.musculus], RIKEN cDNA 2310065D10 gene, serine protease inhibitor, Kazal type 3	ESTs, Weakly similar to R11A_HUMAN Ras-related protein Rab-11A (RAB-11) (24KG) (YL8) [R.norvegicus], RAB11A, member RAS oncogene family, RAB11a, member RAS oncogene family, expressed sequence AW496496	ESTs, Weakly similar to R11A_HUMAN Ras-related protein Rab-11A (RAB-11) (24KG) (YL8) [R.norvegicus], RAB11A, member RAS oncogene family, RAB11a, member RAS oncogene family, RAB25, member RAS oncogene family, expressed sequence AW496496	ESTs, Weakly similar to R11A_HUMAN Ras-related protein Rab-11A (RAB-11) (24KG) (YL8) [R.norvegicus], RAB11A, member RAS oncogene family, RAB25, member RAS oncogene family, expressed sequence AW496496	ESTs, Weakly similar to R6RT37 ribosomal protein L37, cytosolic [validated] - rat [R.norvegicus], RIKEN cDNA 1500002F19 gene, RIKEN cDNA 3110005M08 gene, ribosomal protein L37	ESTs, Weakly similar to RBM3 MOUSE PUTATIVE RNA-BINDING PROTEIN 3 [M.musculus], Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310074E15:RNA binding motif protein 3, full insert sequence, RNA binding motif protein, X chromosome, RNA binding motif protein, X chromosome retrogene, cold inducible RNA binding protein, cold inducible RNA-binding protein
	Rum Rodal Godo Kro	GGG, HHH, PPP, QQQ, UUU, General	ממון מון		۵	7.	F, T, U, FFF	C, G, H, General Core Tox Markers
	<u>මොඩෙබැ</u> ? ි Aමේගෙ Rakseg [D] [[D POESSON	152936	859		M75153 F	NM_031106_F	AI013911
	elec D'No.	25442	1	1		240	20807	7299
TABLE 3	Seq (D	3776				3035	3604	1466

	8 8 8	***			Altonioy Docket 4/924-5088-04WO
Seg 10	elec Id No.	esaesak Accor Resse D	Model Gode	Humen Homologous Known Gene Name	in Homologous ni Genei Namen Human Homologous Sequence @uster title
					ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0
					(nnKNP DV) (AU-rich element KNA-binding protein 1) [K.norvegicus], iwus musculus, clone MGC:36467 IMAGE:5359082, mRNA, complete cds, RIKEN cDNA 4933434H11
					gene, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear
					ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD), heterogeneous
					nuclear ribonucleoprotein D-like, high-glycine/tyrosine protein type I E5, musashi
2144	23390	AI172328	6, 666		homolog 2 (Drosophila)
					ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0
					(hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus], Mus musculus,
					clone MGC:36467 IMAGE:5359082, mRNA, complete cds, RIKEN cDNA 4933434H11
					gene, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear
					ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD), heterogeneous
					nuclear ribonucleoprotein D-like, high-glycine/tyrosine protein type I E5, musashi
3559	23387	NM_024404	<u>ш</u>		homolog 2 (Drosophila)
					ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0
					(hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus], Mus musculus,
					clone MGC:36467 IMAGE:5359082, mRNA, complete cds, RIKEN cDNA 4933434H11
					gene, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear
					ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD), heterogeneous
					nuclear ribonucleoprotein D-like, high-glycine/tyrosine protein type I E5, musashi
3559	23388	NM_024404	ပ		homolog 2 (Drosophila)
					ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0
	:		,		(hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus], Mus musculus,
				٠	clone MGC:36467 IMAGE:5359082, mRNA, complete cds, RIKEN cDNA 4933434H11
					gene, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear
					ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD), heterogeneous
i i	000	707700			nuclear ribonucleoprotein D-like, high-glycine/tyrosine protein type I E5, musashi
3228	79907	NM_024404	IMIM, 1 1 1		แดกเดย ๔ (มเจริงมาแส)

TABLE 3	ි ග				Altoniay Docket 4/921-5099-01000 The first of the Comment No. 199532.1
	GLGG ONO	Kemenar Aee or Refseq ID	Model Gode	Human Homologous Known Genet Name	an Homologous Frith Fr
					ESTs, Weakly similar to RP3A_RAT Rabphilin-3A [R.norvegicus], Mus musculus, clone IMAGE:3963643, mRNA, partial cds, RIKEN cDNA 6530413F01 gene, cDNA sequence AJ430384, membrane bound C2 domain containing protein, rabphilin 3A, rabphilin 3A-
1223	1308	AF022774	HH		like (without C2 domains)
					ESTs, Weakly similar to S10A MOUSE S-100 PROTEIN, ALPHA CHAIN [M.musculus], S100 calcium binding protein A1, S100 calcium binding brotein A1, S100 calcium binding br
3713	1475	NM_031971	A, B, Q		calcium binding protein P, S100Z protein, expressed sequence Al266795
			HH 44 7		ESTs, Weakly similar to S19586 N-methyl-D-aspartate receptor glutamate-binding chain rat [R.norvegicus], RIKEN cDNA 1110025J15 gene, RIKEN cDNA 2310061B02 gene, RIKEN cDNA 29000021 20 gene, RIKEN cDNA 29000021 20 gene.
4044	20784	NM_153308			mRNA, complete cds
					ESTs, Weakly similar to S21054 DNA-directed RNA polymerase [H.sapiens], Homo sapiens, Similar to RIKEN cDNA 4930521123 gene, clone MGC:26816 IMAGE:4811804,
1550	926	AI044259	Z, AA		mRNA, complete cds, lymphocyte antigen 64, polymerase (RNA) II (DNA directed) polypeptide A (220kD)
					ESTs, Weakly similar to S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) -
					rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial
					lcds, Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding Iorotein. RIKEN cDNA 1600017E01 gene. RIKEN cDNA 4930529O08 gene.
					dihydrolipoamide branched chain transacylase (E2 component of branched chain keto
269	11992	AA892485	MM, TTT		acid dehydrogenase complex; maple syrup urine disease), dihydrolipoamide branched chain transacylase E2, pyruvate dehydrogenase complex, component X
	<u>.</u>				ESTs, Weakly similar to S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat (fragment) [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial cds. Pyruyate dehydrogenase complex. Ilpoyl-containing component X: E3-binding
					protein, RIKEN cDNA 1600017E01 gene, RIKEN cDNA 4930529O08 gene,
					dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease), dihydrolipoamide branched
2844	2020	D10655	UU, WW		chain transacylase E2, pyruvate dehydrogenase complex, component X

1392 2516 AI011843 W [M.musculus], RIKEN cDNA 2310050L06 gene, selenoprotein R, selenoprotein X, 1

2 (VALINE-	us clone	us, clone tRNA	us, clone tRNA (sapiens],	us, clone tRNA sapiens], Lsapiens],	us, clone tRNA sapiens], sapiens], !Sapiens],	us, clone tRNA sapiens], [Sapiens], [AA1253 [Sapiens],	us, clone tRNA sapiens], Lsapiens], LSapiens], LSapiens], LSapiens], LSapiens],	us, clone tRNA sapiens], sapiens], sapiens], sapiens], sapiens], sapiens],	us, clone tRNA sapiens], sapiens], sapiens], sapiens], sapiens], sapiens],	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Sapiens], EN CDNA	us, clone tRNA sapiens], sapiens], sapiens], sapiens], sapiens], sapiens], sapiens],	us, clone tRNA sapiens], sapiens], sapiens], sapiens], sapiens], sapiens], sapiens],	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Sapiens], Ren cDNA nsketolase	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Sapiens], Rev CDNA nsketolase nsketolase	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Sapiens], Sapiens]	us, clone tRNA sapiens], Isapiens], Isapiens	us, clone tRNA sapiens], Lsapiens], Lsapiens	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Lsapiens], Rev CDNA nsketolase nsketolase nsketolase	us, clone tRNA sapiens], Lsapiens], Lsapiens], Lsapiens], Sapiens], Sapiens]	us, clone tRNA sapiens], s	us, clone tRNA Isapiens], Isapien	us, clone tRNA Isapiens], Isapien
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Consent	AI070511 G		A1045768																			
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	ก็เห็ <mark>omologous</mark> ก็เติกติโทลัพย ใน <mark>บุพลัก ห็อที่ค</mark> ับก็อโดยอุงธ์ Seqบ็ยกอยุโดมระคาแน้ย	expressed sequence AA408768, transthyretin, transthyretin (prealbumin, amyloidosis type I)	expressed sequence AA986766, organic cationic transporter-like 4, reduced in osteosclerosis transporter, solute carrier family 22 (organic anion transporter), member 8		expressed sequence AI046660, kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	expressed sequence Al195532, liver mitochondrial glutaminase	expressed sequence Al255394, phosphatidylethanolamine N-methyltransferase	expressed sequence Al323765, histocompatibility 2, class II antigen E alpha, major histocompatibility complex, class II, DR alpha	expressed sequence Al323765, histocompatibility 2, class II antigen E alpha, major histocompatibility complex, class II, DR alpha	expressed sequence Al324259, ras homolog 9 (RhoC), ras homolog gene family, member C	expressed sequence Al413471, hypothetical protein FLJ11838						expressed sequence Al462446, protein tyrosine phosphatase, non-receptor type 2
	Nodel Godo Known Gene N	zz, uuu	Σ	L, GG, EEE, GGG, KKK, LLL, MMM, UUU, General	Core Tox Markers	GG, W, GGG	EE, JJ, KK	x, 00	M, X, 00	EEE, MMM	C, KKK	B, W, BB, CC, DD, EE, J.J.	NN, 00, PP,	HHH, III, KKK, NNN, General	Core Tox	Markers,	General Alternate
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ଉ	elec D No	5052	12682		17324	293	24718	19255	19256	17333	4703						16809
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tome .																	

	Ser Title	expressed sequence AI845868, histocompatibility 2, class II antigen A, beta 1, major	histocompatibility complex, class II, DO beta, major histocompatibility complex, class II,		horin I	expressed sequence AU022220, stearoyl-CoA desaturase (delta-9-desaturase), stearoyl-Coenzyme A desaturase 3	expressed sequence AU022220, stearoyl-CoA desaturase (delta-9-desaturase),	earoyl-coenzyme A desaturase 3	n B1, plexin B2, plexin B3	n B1, plexin B2, plexin B3	expressed sequence AV066530, guanylate cyclase activator 2B (uroguanylin),			alin 2 (oncogene 24p3)	inamide nucleotide transhydrogenase	fatty acid binding protein 5 (psoriasis-associated), fatty acid binding protein 5, epidermal	n FLJ20604	n FLJ20604	Fc fragment of IgG, low affinity IIb, receptor for (CD32), Fc receptor, IgG, low affinity IIb,	cds, expressed sequence Al528646,	ranslocation associated 2		FGF receptor activating protein 1, Mus musculus, Similar to FGF receptor activating	88752, mRNA, complete cds	:80)	N cDNA 4930571K23 gene	
	rn Homologous vni Genei Name Humani Homologousi Sequencei Gluster Titlie	expressed sequence AI845868, histoc	histocompatibility complex, class II, DC	DQ beta 1	expressed sequence AU018702, ribophorin	expressed sequence AU022220, stearoyl-CoA desaturase (delta-9-desases a stearoyl-Coenzyme A desaturase 3	expressed sequence AU022220, stear	stearoyl-Coenzyme A desaturase 1, stearoyl-coenzyme A desaturase 3	expressed sequence AU042020, plexin B1, plexin B2, plexin B3	expressed sequence AU042020, plexin B1, plexin B2, plexin B3	expressed sequence AV066530, guan	guanylate cyclase activator 2b (retina)		expressed sequence AW212229, lipocalin 2 (oncogene 24p3)	expressed sequence BB168308, nicotinamide nucleotide transhydrogenase	fatty acid binding protein 5 (psoriasis-a	fatty acid synthase, hypothetical protein FLJ20604	fatty acid synthase, hypothetical protein FLJ20604	Fc fragment of IgG, low affinity IIb, rec	Mus musculus FCRL mRNA, complete cds, expressed sequence Al528646,	immunoglobulin superfamily receptor translocation associated 2	ferredoxin reductase	FGF receptor activating protein 1, Mus	protein 1, clone MGC:8108 IMAGE:3588752, mRNA, complete cds	filamin A, alpha (actin binding protein 280)	FK506 binding protein 4 (59kD), RIKEN cDNA 4930571K23 gene	
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	epoo jepoy		X, Y, NN, OO,		, FF			××××	m	РРР, ООО	ļ.	HH	E, V, W, BB, CC W FFF	III, JJJ, MMM	000	NN, 00	I, J, BB,	<u>></u>		V, X, Y, LL,	ZZ, AAA, LLI	3 D		၁	0, P		717171 7171 11
11 256 2 15 15	kënem kë er Reksq 🗈			M36151	NM_013067	AA819905		NM_139192	AA801346	AI136372		AA818875		AA946503	AA891872	AI175875	AI009273	NM_017332			X73371	NM_024153		U57715	A1009460	AI012177	
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TABLE 8:	නි _{මෙල්} ල			3021	3211	237		4010	126	1930		191		961	510	2177	1309	3343			4258	3541		4147	1315	1401	ļ

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Gelege Accor Company Human Human	Hume Nodel Godes Know	Hume Nodel Godes Know	HWinein Known	nn Homologous ***	
13091 AI136977 T, W, JJ, KK		T, W, JJ, KK		FK506 binding protein 4 (59kD), RIKEN cDNA 4930571K23 gene	
13092 AI231547 JJ, UU, KKK		T, W, DD, EE, JJ, UU, KKK		FK506 binding protein 4 (59kD), RIKEN cDNA 4930571K23 gene	
21603 AI177742 PPP, QQQ		PPP, QQQ		FK506 binding protein 8 (38 kDa), FK506 binding protein 8 (38kD), RIKEN cDNA 6330408J23 gene	۲ _A
		E, JJ, KK		folylpolyglutamate synthase, folylpolyglutamyl synthetase	
6549 AI176002 JJ		JJ		folylpolyglutamate synthase, folylpolyglutamyl synthetase	
13731 NM_012755 P	-	Ь		FYN oncogene related to SRC, FGR, YES, Fyn proto-oncogene	
				FYVE zinc finger phosphatase, Mus musculus, clone IMAGE:3668035, mRNA, partial	, partial x X-linked
13296 AI011020 YY		<u></u>		myotubular myopathy gene 1, myotubular myopathy 1	
20276 NM_022216 SS		SS		G protein-coupled receptor 20, pyrimidinergic receptor P2Y, G-protein coupled, 4	, 4
				GABA(A) receptor-associated protein, GABA(A) receptor-associated protein like 1	ke 1,
				GABA(A) receptor-associated protein like 2, GABA(A) receptor-associated protein-like	tein-like
				 SABA(A) receptors associated protein like 3, gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1, gamma-aminobutyric acid receptor associated 	(BA(A))
5968 A1170692 TT	41170692 · TT	<u> </u>		protein	-
				GABA(A) receptor-associated protein, GABA(A) receptor-associated protein like 1.	(e 1,
				GABA(A) receptor-associated protein like 2, GABA(A) receptor-associated protein-like (GABA(A) receptors associated protein like 3, gamma-aminohiltyric acid (GABA(A))	(BA(A))
				receptor-associated protein-like 1, gamma-aminobutyric acid receptor associated	ted
17566 AI232301 M		M		protein	
				gap junction membrane channel protein alpha 4, gap junction protein, alpha 4, 37kD	37kD
12736 Al233972 JJJ		լի		(connexin 37)	
23989 AI179953 PP		dd		gap junction protein, beta 2, 26kD (connexin 26)	
8, РР, QQ, 23987 X51615 ННН	, PP, HHH	В, РР, QQ, ННН		gap junction protein. beta 2. 26kD (connexin 26)	
21212]

	VABLE 8				Altomey Docket (1921-5099-01000) The Comment No. 1995323.1
	elec Idono	Consent Aec or: Rokaq (D	ik ii. Meelel Goele	Known Gere Neme Human H	Ա <mark>տաքույ Homologows (1982 - 1982)</mark> Known, Gene Name – հ uman i H omologo ws/Sequence/Glüster, մինք
				GASZ, G _€ MGC:369	GASZ, Gasz, Mus musculus, Similar to hypothetical protein DKFZp564O043, clone MGC:36949 IMAGE:4946879, mRNA, complete cds, Mus musculus, Similar to
				regulatory IMAGE:41	regulatory factor X-associated ankyrin-containing protein, clone MGC:13787 IMAGE:4190691, mRNA, complete cds, RIKEN cDNA 4933400N19 gene, kinase D-
2355	16656	AI179634	λ.	interacting protein	interacting substance of 220 kDa, regulatory factor X-associated ankyrin-containing protein
3940	19099	NM_133417	H	GCIP-inter	GCIP-interacting protein p29, Homo sapiens, clone IMAGE:4042910, mRNA, partial cds
2944	1336	L01267	РРР, ааа	general tra	general transcription factor IIF, polypeptide 2 (30kD subunit)
1747	9399	AI072812	General Core Tox Markers	alioma-am	alioma-amplified sequence-41
2534	22379	A1231448	X, Y, Z, RR, XX	o ascorilo	direase phosphate isomerase alirease phosphate isomerase 1 complex
2681	Т	1	Z, AA, NNN	d esoonid	glucose phosphate isomerase, glucose phosphate isomerase 1 complex
			E, DD, UU, III,		
			NNN, General		
1489	7451	A1029450	Alternate	glutamyl-p	glutamyi-prolyi-tRNA synthetase
2667	16781	AI234527	M, GG, TT	glutathion	glutathione S-transferase A4, glutathione S-transferase, alpha 4
4242			X, GG, II, XX,	9,99	7 - 1 - 1 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2
3763	6774	NM 053410	- 00	glutatiiloin	gludatiiolie S-uaristerase A4, gludatiiolie S-uaristerase, aipira 4 divceronephosphate O-acyltransferase
		I		Glycogen	Glycogen synthase 2 (liver), Mus musculus, clone MGC:29379 IMAGE:5051685,
				mRNA, co	mRNA, complete cds, glycogen synthase 1 (muscle), glycogen synthase 1, muscle,
2054	T	\neg	PP, QQ, YY	glycogen	glycogen synthase 3, brain
9 <u>8</u>	\neg	AA859804	۵	GM2 gang	GM2 ganglioside activator protein
1845		A1103602	999	GM2 gang	GM2 ganglioside activator protein
1925		AI112979	999	GM2 gang	GM2 ganglioside activator protein
2518	2299	AI231094	999	GM2 gang	GM2 ganglioside activator protein

					- Altomay Doctet 41921-5038-01W0 Altomay Document No. 1955828.1
	@@ @@ @@	<u>ලෙක:කෙයැ</u> /යමෙන් යිමේකු (D		iman Homologous town Gene Name	HumaniHomologous Seguence Glusterfillile);
					GRB2-related adaptor protein, GRB2-related adaptor protein 2, NCK adaptor protein 1,
0				SH3	SH3 domain protein 3, Sh3 domain YSC-like 1, growth factor receptor bound protein 2,
978	23542	AA955389	A	grow	growth factor receptor-bound protein 2, monocytic adaptor
	-			GRB	GRB2-related adaptor protein, GRB2-related adaptor protein 2, SH3 domain protein 3,
				Sh3 (Sh3 domain YSC-like 1, growth factor receptor bound protein 2, growth factor receptor-
3568	18023	NM_030846	S	unoq	bound protein 2, monocytic adaptor
				GRB	GRB2-related adaptor protein, GRB2-related adaptor protein 2, SH3 domain protein 3,
			N, MM, PPP,	Sh3 (Sh3 domain YSC-like 1, growth factor receptor bound protein 2, growth factor receptor-
3568	18728	NM_030846	QQQ, TTT	noq	bound protein 2, monocytic adaptor
		_		G-rid	G-rich RNA sequence binding factor 1, expressed sequence AA407306, heterogeneous
				nucle	nuclear ribonucleoprotein F, heterogeneous nuclear ribonucleoprotein H1,
				heter	heterogeneous nuclear ribonucleoprotein H1 (H), heterogeneous nuclear
3913	16267	NM_080896	P, Q, R	ribon	ribonucleoprotein H2
			A, E, BB, CC,		
			DD, EE, NN,	GRO	GRO1 oncogene, GRO2 oncogene, pro-platelet basic protein, pro-platelet basic protein
			00, PP, EEE,	(inclu	(includes platelet basic protein, beta-thromboglobulin, connective tissue-activating
				bepti	peptide III, neutrophil-activating peptide-2), small inducible cytokine B subfamily (Cys-X-
3567	1221	NM_030845		Cys),	Cys), member 9
			N, Z, AA, JJ,		
3876	16043	NM_057100 KK, UUU	KK, UUU	grow	growth arrest specific 6, growth arrest-specific 6
3687	14184	NM_031776 V, UU	V, UU	gnan	guanine deaminase
3687	14185	NM_031776 V, NN	V, NN	gnan	guanine deaminase
				ana	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2,
				gnau	guanine nucleotide binding protein, alpha inhibiting 2, guanine nucleotide binding
447	15887	AA875225	PP, QQ	prote	protein, alpha inhibiting 3
			O, P, X, NN,	gnan	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2,
			00, W. ZZ,	dnan	guanine nucleotide binding protein, alpha inhibiting 2, guanine nucleotide binding
447	15888	AA875225	AAA	prote	protein, alpha inhibiting 3

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Sed.''	erec. Dio	<u>©entenit</u> <u>Aegor</u> Rakso D	Model Gode	ran Homologous The first the first that the first
				guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2, guanine nucleotide binding protein, alpha inhibiting 2 guanine nucleotide binding
3586	15886	NM_031035	ZZ, AAA	gramme maccarde primarily process, apria minimarily 4, gramme mareourde binding protein, alpha inhibiting 3
2390	7460	A1180413	N, HH, TT, XX,	H factor (complement)-like 1, H factor (complement)-like 2, complement factor H related
4203	7459	X15551	. _{>}	Hactor (complement)-like 1, H factor (complement)-like 2, complement factor H related 3
				H factor (complement)-like 3, H factor 1 (complement), Mus musculus, clone
				 MGC:30368 IMAGE:5135798, mRNA, complete cds, coagulation factor XIII, beta
2045	2570	V1470244	000	subunit, complement component factor h, complement factor H-related 4, expressed
2407	Т	A1 703 14	הריי, מממ	sequence Ai 19469b, seizure related gene b
		_		 H2A histone family, member C, H2A histone family, member D, H2A histone family,
				 member I, H2A histone family, member L, H2A histone family, member N, H2A histone
		-		 family, member O, Homo sapiens, clone MGC:21597 IMAGE:4511035, mRNA,
				 complete cds, Mus musculus, similar to H2A histone family, member O, clone
1954	18943	AI137495	F, II	 MGC:36202 IMAGE:5055276, mRNA, complete cds, expressed sequence R75370
				H4 histone family, member D, H4 histone family, member H, H4 histone family, member
				 H4 histone family, member J, H4 histone family, member K, Mus musculus, H4
			_	histone family, member A, clone MGC:30488 IMAGE:4205460, mRNA, complete cds,
3204	6121	NM_022686	GG	histone 4 protein
3505	20507	NM_022687	F	hairy and enhancer of split 3, (Drosophila), hairy homolog (Drosophila)
				hemopoietic cell phosphatase, protein tyrosine phosphatase, non-receptor type 13,
3851	8152	NM_053908	\neg	 protein tyrosine phosphatase, non-receptor type 6
			B, S, GGG,	
			PPP, aga,	
			General	
1214	23417	AB022209	Alternate	heterogeneous nuclear ribonucleoprotein F
3898	8820	NM 080399	S' TTF	 HIF-1 responsive RTP801, Homo sapiens, Similar to RIKEN cDNA 1700037B15 gene, clone MGC:9960 IMAGE:3877854. mRNA. complete cds

ABLE 3				Attorney Doctret (4921-5088-011WO)
. (७) ↔	GLGG Ake or BOG Ake or DNo RASE D	Model Gode	From Salaman	n Homologous n Genei Name Human Homologous Sequence @luster Till the
18	23282 U90725	FF	high	high density lipoprotein binding protein (vigilin)
3381	AA892993	X, CCC, SSS, UUU	deid	high mobility group 20 B. high-mobility group 20B
14608	®	n	HLA	HLA-B associated transcript 5
		F, LLL, SSS,		
8036	AI230884	กกก	HMB	HMBA-inducible
			Hom	Homo sapiens cDNA FLJ10203 fis, clone HEMBA1004930, moderately similar to 26S
3816	3 AI233729	K, Q, UUU	ATP	ATPase, 5
			Hom	Homo sapiens cDNA FLJ11845 fis, clone HEMBA1006674, Mus musculus, Similar to
			hypo	hypothetical protein FLJ10350, clone MGC:27585 IMAGE:4489521, mRNA, complete
		KK, HHH,	cds,	cds, Mus musculus, Similar to neurofilament, heavy polypeptide (200kD), clone
		General Core	MGC	MGC:32399 IMAGE:5037953, mRNA, complete cds, nucleolar protein 5A (56kD with
4944	AA924405	Tox Markers	KKE	KKE/D repeat)
		R, BB, CC, JJ,	Hom	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05
		KK, General	gene	gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5R.2, diaphorase
17530	10 NM 138877	Alternate	(NAC	(NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
			Hom	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05
		General	gene	gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5R.2, diaphorase
17531	31 NM_138877	Alternate	(NAE	(NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
			Hom	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05
	_	FFF, General	dene	gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5R.2, diaphorase
17532	32 NM_138877		(NAC	(NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
		I, J, FFF,	Hom	Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05
			euee	gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5R.2, diaphorase
17533	33 NM 138877	Alternate	(NAC	(NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)

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		The Control of the Co			Homo sapiens cDNA FLJ14413 fis, clone HEMBA1004670, RIKEN cDNA 1500005G05
			KK, General		gene, cytochrome b5 reductase 1 (B5R.1), cytochrome b5 reductase b5R.2, diaphorase
	25039 NI	NM_138877	Alternate		(NADH) (cytochrome b-5 reductase), diaphorase 1 (NADH)
	_				Homo sapiens cDNA FLJ14666 fis, clone NT2RP2003000, weakly similar to TUMOR
					NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, Homo sapiens cDNA FLJ30639
					fis, clone CTONG2002803, Homo sapiens polymerase delta-interacting protein 1
	•				mRNA, complete cds, MSTP028 protein, tumor necrosis factor, alpha-induced protein 1
	-	AA943494	MM, TTT		(endotheliat)
	<u> </u>				Homo sapiens cDNA FLJ14828 fis, clone OVARC1000915, highly similar to Homo
2124 764	7642 AI	AI172045	C, MM, TTT		sapiens histone deacetylase 5 mRNA, histone deacetylase 5, histone deacetylase 9
3798 208	20896 NI	NM_053592	U, NNN		Homo sapiens cDNA FLJ25344 fis, clone TST01087, RIKEN cDNA 5031412106 gene
·					Homo sapiens cDNA FLJ30086 fis, clone BNGH41000002, moderately similar to
1636 8315	·. ·	AI059389	SSS, UUU		ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4)
					Homo sapiens cDNA FLJ30116 fis, clone BRACE1000042, weakly similar to PROTEIN
					PHOSPHATASE 2C ABI2 (EC 3.1.3.16), Homo sapiens cDNA FLJ30553 fis, clone
,		•			BRAWH2003689, highly similar to Mus musculus clone mouse1-9 putative protein
					phosphatase type 2C mRNA, Homo sapiens cDNA FLJ32332 fis, clone
					PROST2005121, weakly similar to PROBABLE PROTEIN PHOSPHATASE 2C
			Q, R, General		T23F11.1 (EC 3.1.3.16), KIAA0015 gene product, expressed sequence AI481720,
366 6440	•	AA859130	Alternate		protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
	-				Homo sapiens cDNA FLJ30116 fis, clone BRACE1000042, weakly similar to PROTEIN
					PHOSPHATASE 2C ABI2 (EC 3.1.3.16), Homo sapiens cDNA FLJ30553 fis, clone
-	•				BRAWH2003689, highly similar to Mus musculus clone mouse1-9 putative protein
					phosphatase type 2C mRNA, Homo sapiens cDNA FLJ32332 fis, clone
					PROST2005121, weakly similar to PROBABLE PROTEIN PHOSPHATASE 2C
	-				T23F11.1 (EC 3.1.3.16), KIAA0015 gene product, expressed sequence AI481720,
4035 6439		NM_147209	n		protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
					Homo sapiens cDNA FLJ30813 fis, clone FEBRA2001523, ubiquintin c-terminal
372 1151	15149 A	AA859327	PPP, 000		hydrolase related polypeptide, ubiquitin specific protease 10

	<u> </u>				9) Docket 4/82/1-6088-011WO
	GLGC ID No.	CONSTANT Logo Or Refised (D	Nodel Gode	Human Homologous Auman Homologous VnovniGeneName Human Homologous Sequence Gluster mile)	
326	19158	AA851953	L.		
				Homo sapiens cDNA FLJ30934 fis, clone FEBRA2007017, moderately similar to Homo	imilar to Homo
2665	17537	AI234497	W	sapiens TRAF4-associated factor 2 mRNA, sorting nexin 6	
				Homo sapiens cDNA FLJ31164 fis, clone KIDNE1000104, weakly similar to SYNTAXIN	r to SYNTAXIN
3522	15697	NM_022939	PP, QQ, UU	7, expressed sequence AU041521, syntaxin 12, syntaxin 16, syntaxin 7	
450	15410	AA875268		Homo sapiens cDNA FLJ31499 fis, clone NT2NE2005441, weakly similar to	ar to
	2	20.00	222 (111)	Hone to the control of CTATES for the control of th	3
				Homo sapiens cDNA FLJ3176Z its, clone N1ZRIZU07734, weakly straiter to INTESTINAL MEMBRANE A4 PROTEIN, hypothetical protein BC010116. hypothetical	r to 5. hvpothetical
1453	22592	AI013740	o, P, uuu	protein BC013109	
				Homo sapiens cDNA FLJ31775 fis, clone NT2RI2008115, biphenyl hydrolase-like	olase-like
2702	11164	AI235739	A, B	(serine hydrolase; breast epithelial mucin-associated antigen)	
				Homo sapiens cDNA FLJ32122 fis, clone PEBLM1000144, moderately similar to Trg,	imilar to Trg,
				KIAA1058 protein, erythroid differentiation regulator, expressed sequence AA959601	e AA959601,
4250	602	X68101	ZZ, AAA	expressed sequence R75174	
				Homo sapiens cDNA FLJ32122 fis, clone PEBLM1000144, moderately similar to Trg,	imilar to Trg,
		_		KIAA1058 protein, R.norvegicus trg mRNA, RIKEN cDNA 1200017A24 gene, erythroid	gene, erythroid
1819	11655	AI102881	T	differentiation regulator, expressed sequence AA959601, expressed sequence R75174	uence R75174
				Homo sapiens cDNA FLJ32237 fis, clone PLACE6004966, Human transposon-like	poson-like
4012	22595	NM_139253	K	element mRNA	
				Homo sapiens cDNA FLJ32400 fis, clone SKMUS2000317, weakly similar to Drainin,	ar to Drainin,
994	12427	AA955771	⊢	KIAA0608 protein, KIAA1322 protein	
379	23340	AA859519	BBB, CCC	Homo sapiens cDNA FLJ32971 fis, clone TESTI2008847	
379	23341	AA859519	၁၁၁	Homo sapiens cDNA FLJ32971 fis, clone TESTI2008847	
				Homo sapiens cDNA: FLJ21205 fis, clone COL00328, integral inner nuclear membrane	lear membrane
2692	11264	AI235493	НН	protein	
			MM, TTT,	Homo sapiens cDNA: FLJ21251 fis, clone COL01259, Homo sapiens, Similar to	imilar to
			General	activated p21cdc42Hs kinase, clone MGC:15139 IMAGE:4302390, mRNA, complete	IA, complete
2891	21864	H31144	Alternate	cds	

			T	,		
Altomay Deckel (1921-5018-6018-601W) Michaelegous Comment Homologous Sequences (Cluster Mile),	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970, RIKEN cDNA 4933436C10 gene, nudix (nucleoside diphosphate linked moiety X)-type motif 3, nudix (nucleotide diphosphate linked moiety X)-type motif 3	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970, RIKEN cDNA 4933436C10 gene, nudix (nucleoside diphosphate linked moiety X)-type motif 3, nudix (nucleotide diphosphate linked moiety X)-type motif 3	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970, RIKEN cDNA 4933436C10 gene, nudix (nucleoside diphosphate linked moiety X)-type motif 3, nudix (nucleotide diphosphate linked moiety X)-type motif 3	Homo sapiens cDNA: FLJ22845 fis, clone KAIA5195, Mus musculus, Similar to cytochrome P450, 2d10, clone MGC:18824 IMAGE:4207630, mRNA, complete cds, cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing), polypeptide 6	Homo sapiens cDNA: FLJ22845 fis, clone KAIA5195, Mus musculus, Similar to cytochrome P450, 2d10, clone MGC:18824 IMAGE:4207630, mRNA, complete cds, cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing), polypeptide 6	Homo sapiens cDNA: FLJ22845 fis, clone KAIA5195, RIKEN cDNA 1300006E06 gene, cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing), polypeptide 6
ໄປທາກອາກ Homologiqus ເຮັບກໍ່ສາການ Homologiqus Kikidowni Gental						
Model Gode	M, DD, SS, TT, FFF, General Core Tox Markers, General Alternate	E, DD, JJ, KK, MM, UU, FFF, KKK, NNN, TTT, General Alternate	N, GG, JJ, KK, General Alternate	PP, QQ, EEE, FFF, MMM	j	'n, T
eensens Ree or Reseq (D	NM_053598	NM_053598	NM 053598	AB008424	NM_153313	18730 NM_012730 N, TT
33 9166 10 No.	11830	18795	23192	16304	1130	18730
TABU See	3801	3801	3801	1206	4046	3128

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88 (D	@F@G @D No:	Centenia Vec or Refeeq (D	model Gode:	enilī Jajsnīja japuanbas snagojojomahjurimnij jaman adajumahjumamnij Human Homologojo Human Homologojojojojojojojojojojojojojojojojojoj	
2056	3013	A1170532	۵	Homo sapiens mRNA; cDNA DKFZp566P2346 (from clone DKFZp566P2346), RIKEN cDNA 1700019B01 gene, golgi autoantigen, golgin subfamily a, 4	DKFZp566P2346), RIKEN y a, 4
1393	4286	AI011920	>	Homo sapiens PNAS-29 mRNA, complete cds, WD repeat domain 1	domain 1
2897	17913	H31707	BB, CC	Homo sapiens, clone IMAGE:3940519, mRNA, partial cds, hypothetical protein DKFZp7620076	hypothetical protein
2540	19271	A1231566	Щ	Homo sapiens, clone MGC:18164 IMAGE:4155088, mRNA, complete cds	complete cds
				Homo sapiens, clone MGC:24603 IMAGE:4245508, mRNA, complete cds, hypothetical	complete cds, hypothetical
			General	protein DKFZp564F013, putative homeodomain transcription factor, putative	n factor, putative
829	12247	AA942812	Alternate	homeodomain transcription factor 1	
4293	8664	Z75029	Q, ZZ, AAA	Homo sapiens, clone MGC:25063 IMAGE:4480702, mRNA, complete cds	complete cds
			III, JJJ, Geograf Cero		
2371	22569	AI179979	Tox Markers	Homo sapiens, clone MGC:26636 IMAGE:4825619, mRNA, complete cds	complete cds
				Homo sapiens, clone MGC:32124 IMAGE:4877960, mRNA, complete cds, RIKEN	complete cds, RIKEN
				cDNA 1110060M21 gene, RIKEN cDNA 4631434O19 gene, progesterone receptor	progesterone receptor
527	16836	AA892005	BBB, CCC	membrane component 1, progesterone receptor membrane component 2	component 2
				Homo sapiens, Similar to protein kinase NYD-SP25, clone MGC:26757	AGC:26757
1847	13317	AI103637	>	IMAGE:4828082, MKNA, complete cas, KIKEN cDNA 2810411623 gene, tumor protein D52-like 2	411623 gene, tumor protein
				Homo sapiens, Similar to RIKEN cDNA 4930513O09 gene, clone MGC:33185	clone MGC:33185
				IMAGE:5269882, mRNA, complete cds, Mus musculus, Similar to hypothetical protein	ilar to hypothetical protein
				DKFZp761J139, clone MGC:11924 IMAGE:3599595, mRNA, complete cds, RIKEN	A, complete cds, RIKEN
			٠	cDNA 4930513O09 gene, cellular nucleic acid binding protein, zinc finger protein 9 (a	in, zinc finger protein 9 (a
3498	20959	NM_022598	D	cellular retroviral nucleic acid binding protein)	
				Homo sapiens, Similar to RIKEN cDNA 4930513009 gene, clone MGC:33185	clone MGC:33185
				IMAGE:5269882, mRNA, complete cds, Mus musculus, Similar to hypothetical protein	ilar to hypothetical protein
				DKFZp761J139, clone MGC:11924 IMAGE:3599595, mRNA, complete cds, RIKEN	A, complete cds, RIKEN
	1	1		cDNA 4930513O09 gene, cellular nucleic acid binding protein, zinc finger protein 9 (a	in, zinc finger protein 9 (a
3498	20960	NM_022598		cellular retroviral nucleic acid binding protein)	

(A) (B) (C)		 	, , ,						 _
Milomey Docket 44924-5038-01W0 Miloment No. 1035328.1 Milomey Docket 44924-5038-01W0 Miloment No. 1035328.1 Miloment No. 1035328.1 Miloment Medical Medical Miloment Medical Medic	Homo sapiens, Similar to solute carrier family 6 (neurotransmitter transporter, GABA), member 13, clone MGC:24068 IMAGE:4594185, mRNA, complete cds, Homo sapiens, clone MGC:24098 IMAGE:4612245, mRNA, complete cds, Mus musculus, Similar to solute carrier family 6 (neurotransmitter transporter, GABA), member 13, clone MGC:28956 IMAGE:4240641, mRNA, complete cds, expressed sequence AA589632	Homo sapiens, Similar to transcription factor EB, clone IMAGE:3944945, mRNA, partial cds	HSPC142 protein HTGN20 protein trans-polici pertuorit protein 1 trans-polici pertuorit protein 2	HTGN29 protein, trans-golgi network protein 1, trans-golgi network protein 2 HTGN29 protein, trans-golgi network protein 1, trans-golgi network protein 2 Human DNA sequence from cDNA 16pHQG;19 from chromosome 16p13.3	Human putative ribosomal protein S1 mRNA, RIKEN cDNA 9130413I22 gene, T-cell activation protein, hypothetical protein BC006130	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1, hydroxysteroid dehydrogenase-4, delta<5>-3-beta, hydroxysteroid dehydrogenase-5, delta<5>-3-beta	Hydroxysteroid dehydrogenase, 11 beta type 1, Mus musculus, Similar to hydroxysteroid 17-beta dehydrogenase 11, clone MGC:30360 IMAGE:5132342, mRNA, complete cds, Mus musculus, clone MGC:6908 IMAGE:2655855, mRNA, complete cds, hydroxysteroid (11-beta) dehydrogenase 1, hydroxysteroid 11-beta dehydrogenase 1, retinal short-chain dehydrogenase/reductase retSDR2	hypothetical protein hypothetical protein hypothetical protein	hypothetical protein BC008246, inorganic pyrophosphatase, pyrophosphatase (inorganic)
Model Gede	11. 11. 12.	MM, UU, TTT	SS HH	nn nn	ННН	K, GGG	Q Q	WW, FFF C, FFF	L, BB, CC, NNN, OOO, General Alternate
Consent	M95762	AA946421 AA924716	AI104376	X53565 AA893749	AA799550	NM_012584	AI236972	AI639411 AI639411	AA891800
<u> </u>	729	18383	21922	1899 4554	16959	17292	21091	2434 2435 7087	11966
	3052	952	1869	4217 652		3086	2760	2824 2824 2400	501

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			000, General	hypothetical protein BC0082	hypothetical protein BC008246, inorganic pyrophosphatase, pyrophosphatase	
201	18128	AA891800	Alternate	(inorganic)		
442	15339	AA875171	nn	hypothetical protein CAB56184	184	
442	15340	AA875171	XX, YY	hypothetical protein CAB56184	184	
981	23561	AA955477	E	hypothetical protein FLJ10074	74	
545	22903	AA892250	P, W	hypothetical protein FLJ10514	14	
			General Core			
	٠		General	hypothetical protein FL.1106	hypothetical protein FL 110613, hypothetical protein FL 112595, nucleolar GTPase	
1652	8132	A1060050	Alternate	putative nucleotide binding protein, estradiol-induced	orotein, estradiol-induced	
211	7208	AA819337	ш	hypothetical protein FLJ10856	56	-82
			General			
740	20797	AA924310	Alternate	hypothetical protein FLJ20419	19	
			LL, PPP,			
			aaa, RRR,			
83	22918	AA800243	UUU	hypothetical protein FLJ20871 similar to FSP27	71 similar to FSP27	
			III, JJJ, KKK,			
· 			000, General			
			Core Tox			
			Markers,			
			General			
222	22867	AA892353	Alternate	hypothetical protein FLJ22353	53	
2014	20891	AI169337	А. В. ННН	hypothetical protein HSPC111	11	
929	3879	AA893237	T, DDD	hypothetical protein MBC3205	05	
1789	21691	AI102027	L	hypothetical protein MGC10540	540	
1348		AI010295	Γ	hypothetical protein MGC13010	010	
45		AA799633		hypothetical protein MGC13016	016	
3946	19613	NM_133544	Q, R, XX	hypothetical protein MGC14	hypothetical protein MGC14697, upregulated during skeletal muscle growth 5	

TABLES	E3				
20 20 20 20 20 20 20 20 20 20 20 20 20	etec One	<u> (consenia</u> Ace or Rofseq D	्रिक्टबी (इंट्रिंट)	Huma Know	ก Nomologous กิเษียกติ Name Human Homologous Sequence Gluster, Imile
			C, ZZ, AAA,		
661	2192	 AA894086	Alternate	<u></u>	hypothetical protein MGC17552
1296	2193	AI009062	DD, EE, WW	4	hypothetical protein MGC17552
824	9942	AA942697	SS	4	hypothetical protein MGC3133
4022	23251	NM_145085	PP, QQ	ų	hypothetical protein MGC3265, prenylcysteine lyase
92	17206	AA800296	Z, AA	£	hypothetical protein MGC5378, poly(A) polymerase beta (testis specific)
784	12386	AA925450	TIT	ji.	immunoglobulin superfamily, member 4, nectin 3
348	12729	AA858677	×		immunoglobulin superfamily, member 8
3026	1586	M57728	BBB, CCC	įį	inositol polyphosphate-5-phosphatase, 72 kDa
3448	20266	NM_022212	D, SS		insulin receptor-related receptor
			I, J, W, MM,		
			General Core		
3227	16982	NM_013144	Tox Markers		insulin-like growth factor binding protein 1
				.=	interferon gamma receptor 2, interferon gamma receptor 2 (interferon gamma
1093	2492	AA964866	w, aa	t	transducer 1)
3827	25625	NM_053783	PP, QQ		interferon gamma receptor, interferon gamma receptor 1
1111	2809	AA996471	A, B, II	ſ	JM11 protein
				7	JM5 protein, Mus musculus, Similar to hypothetical protein FLJ10055, clone
1388	15033	AI011754	SSS, UUU	V	MGC:36416 IMAGE:5322999, mRNA, complete cds, RIKEN cDNA 0610008N23 gene
			L, FFF, HHH,		
63	16730	AA799766	000	<u></u>	JTV1 gene
			W, BB, CC,		
464	5384	AA891041	QQ, III, NNN		Jun-B oncogene, jun B proto-oncogene
3430	20161	NM 021836			lin B oncodene iin B aroto-oncodene
24.48				2 .3	and office debates, just a protection alabatest
110	_	020020	D, NNN		Julicini Prancigionii

TABLE 9	138 138				Altorney Dockel 44.921-505-01000 Pocument No. 1995828.1
- 8 9 9	GLEC D No.	<u>නොඩොන් කි</u> උදලේගේ දැන්හිලෝ ල්	Modell Gode:	Human Homologous Khowa GeneName	ம்seே ரிமிக்
606	7683	AA945320	ZZ, AAA	karyopher	karyopherin (importin) alpha 3, karyopherin alpha 3 (importin alpha 4)
2495	7416	AI230458	MM, TTT	KDEL (Ly:	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
1427	17132	AI012648	KKK	KIAA0022	KIAA0022 gene product, RIKEN cDNA 1110055L24 gene
2690	18484	AI235349	Z	KIAA0184 protein	f protein
1607	10069	AI058503	111, JJJ	KIAA0247	KIAA0247 gene product
2388	12556	AI180376	Щ	KIAA0310	KIAA0310 gene product
		_	General		
762	23440	AA924881	Alternate	KIAA0365	KIAA0365 gene product
			General		
2736	15398	AI236566	Alternate	KIAA0375	KIAA0375 gene product, nesca protein
1403	16783	AI012215	JJ, QQ, ННН	KIAA0376	KIAA0376 protein, p10-binding protein, ring finger protein 40
				KIAA0553	KIAA0553 protein, MDN1, midasin homolog (yeast), O-linked N-acetylglucosamine
				(GlcNAc)	(GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl
			JJ, KK, MM,	transferas	transferase), PC326 protein, TPR-containing, SH2-binding phosphoprotein, death
715	3944	AA900688	ш	inducer-ot	inducer-obliterator-1, expressed sequence AF013969
				KIAA0553	KIAA0553 protein, MDN1, midasin homolog (yeast), O-linked N-acetylglucosamine
				(GicNAc)	(GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl
				transferas	transferase), PC326 protein, TPR-containing, SH2-binding phosphoprotein, death
2915		H33842	JJJ	inducer-ok	inducer-obliterator-1, expressed sequence AF013969
4029	18457	S45812	XX, YY	KIAA0601	KIAA0601 protein, monoamine oxidase A
3964	21166	NM_134406	nn	KIAA0602	KIAA0602 protein, hypothetical protein FLJ20748
82	3915	AA800029	N	KIAA0916 protein	3 protein
2521	14303	AI231159	PP, QQ	KIAA1049 protein) protein
1452	7274	AI013715	l n	LAG1 long	LAG1 longevity assurance homolog 1 (S. cerevisiae), bone morphogenetic protein 5
209	6237	AA819288	H, S	latexin, rei	atexin, retinoic acid receptor responder (tazarotene induced) 1
			CCC, RRR,		
2140		AI172286	SSS	leucine-ric	leucine-rich PPR-motif containing
342	10517	AA858600	KKK, NNN	leucine-ziț	leucine-zipper-like transcriptional regulator, 1

	<u>ଅ</u>				A BOOKER 4492A-5099-0AWO
Sec. [1]	OLGC ONO	<u>රෙක:නෙයි.</u> Ace රිර Reliseg (D	ं ^क ित्व । Model Goe	Human Homologous Known Gene Neme	en Hömölögöus an Gene Nemer HumenHömölögöus Sequence Glusser Mile
3571	9594	NM_030855	RR		ligase I, DNA, ATP-dependent, ligase III, DNA, ATP-dependent, ligase IV, DNA, ATP-dependent
4195	672	X13722	77		low density lipoprotein receptor, low density lipoprotein receptor (familial hypercholesterolemia)
1292	410	AI008974	UU, OOO, General Alternate		low density lipoprotein receptor-related protein associated protein 1, low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
2567	409	AI232268	99		low density lipoprotein receptor-related protein associated protein 1, low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
2605	17240	AI233054	N, QQ, XX, YY		low molecular mass ubiquinone-binding protein (9.5kD)
2775	21653	AI237535	Q, R, DD, EE, CCC		LPS-induced TNF-alpha factor
4140	21654	U53184	Q, R, W		LPS-induced TNF-alpha factor
					Lysosomal-associated multispanning membrane protein-5, lysosomal-associated protein transmembrane 4A, lysosomal-associated protein transmembrane 4B, lysosomal-
3783	14199	NM_053538	О, Р		associated protein transmembrane 5
1462	7316	AI013883	> -		makorin, ring finger protein, 1
6761		20150	III BBB		Handilli, Illig illigal protein,
			CCC, LLL, RRR. SSS.		
2592	3860	AI232703	ຸດດດ		malonyl-CoA decarboxylase
3092	382	NM_012599	FF, RRR		mannose binding lectin, liver (A), mannose-binding lectin (protein C) 2, soluble (opsonic defect)
3789	22919	NM_053556	RR		maternal G10 transcript
1686	514	AI070584	KKK		matrix metalloproteinase 14 (membrane-inserted)
2034	3909	AI169903	О, Р		MD-2 protein, lymphocyte antigen 96

								830	-													
Altomacy Docket 44921-5058-01000 Homologous Homen's Common Sequence Cluster Title	microsomal glutathione S-transferase 3	mitochondrial ribosomal protein L24	mitochondrial ribosomal protein L49	mitochondrial ribosomal protein L49 mitochondrial ribosomal protein L53	mitochondrial ribosomal protein L53	mitochondrial ribosomal protein S16	mitochondrial ribosomal protein S25	mitochondrial ribosomal protein S33	mitogen activated protein kinase 1, mitogen-activated protein kinase 1, nemo like kinase	mitogen activated protein kinase 9, mitogen-activated protein kinase 9	mitogen activated protein kinase 9, mitogen-activated protein kinase 9	MLL septin-like fusion, septin 9	molybdenum cofactor synthesis 2	molybdenum cofactor synthesis 2	monokine induced by gamma interferon, small inducible cytokine B subfamily (Cys-X-	Cys motif), member 13 (B-cell chemoattractant), small inducible cytokine B subfamily	(Cys-X-Cys), member 10, small inducible cytokine subfamily B (Cys-X-Cys), member	10, small inducible cytokine subtamily B (Cys-X-Cys), member 11	MORF-related gene 15	MORF-related gene 15, RIKEN cDNA 1700060H10 gene, testis expressed gene 189	mucosal vascular addressin cell adhesion molecule 1	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833401P12:peroxiredoxin 4, full insert sequence, peroxiredoxin 4
Hume Knowy																						
jegos jepogi	A, B, X, Y, GG, NN, OO, GGG		S, EEE, MMM	۵ ۷	L	99	MM	XX, YY, CCC	PPP, QQQ	33	A, B, L	WW, KKK	W, DDD, LLL	Q, R, WW, LLL				M	000	PP, QQ	D, Z, AA	L
is consent Coco One One Coco	AA892234	AA892843	A1172185	AI235362 AA926098	AI172214	AI230278	AI169648	AA858695	NM_053842			NM_031837	AA851017	AA851017				ĝ	AI137864	AI179883	NM_019317	NM_053512
	8317	17923	11416	3545 20866	20867	23628	18343	12829	17299	24766	24767	10176	3924	3925	•			808	12654	17224	24757	7219
	541	669	2133	2691 812	2135	2488	2025	349	3837	3341	3341	3704	299	299			9	4000	1962	2364	3394	3777

	NBUE 30			Attomey Docket 44921-5033-011W0	-01000 5020.1
 	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Cemental Light of Referred (D**)	Model Gode	13.16.240.4	
2698	1462	AI235585	~	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810054L16:kidney-derived aspartic protease-like protein, full insert sequence, cathepsin D. cathepsin D. (lysosomal aspartyl protease)	, oce,
3662	20765	NM 031643		Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:300002B10:mitogen activated protein kinase kinase 5, full insert sequence, mitogen activated protein kinase kinase 1, mitogen-activated protein kinase kinase	
3662	20767	NM_031643	۵	Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000002B10:mitogen activated protein kinase kinase 5, full insert sequence, mitogen activated protein kinase kinase 1, mitogen-activated protein kinase kinase	- 0 -
504	7050	AA891824	SS	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110005M20:serine/arginine-rich protein specific kinase 2, full insert sequence, Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011B22:signal sequence receptor, delta, full insert sequence, serine/threonine kinase 23	,
1792	7051	AI102055	ZZ, AAA	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110005M20:serine/arginine-rich protein specific kinase 2, full insert sequence, Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011B22:signal sequence receptor, delta, full insert sequence, serine/threonine kinase 23	, j
3434	19824	NM_021750	A, B, JJ, HHH, General Alternate	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015E02:deoxyribonuclease II alpha, full insert sequence, cysteine sulfinic acid decarboxylase-related protein 2	ig
3434	19825	NM_021750	B, I, J, JJ, HHH, General Alternate	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015E02:deoxyribonuclease II alpha, full insert sequence, cysteine sulfinic acid decarboxylase-related protein 2	je Si
1127	3112	AA997122	NN, 00	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN cDNA 5930436K22 gene, adrenomedullin receptor, protein phosphatase	z
426	22781	AA874926	V, RR, SS	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN cDNA 5930436K22 gene, protein phosphatase	Z

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原 96	erec Id No.	<u>නොහොය.</u> ක්රෙමේ RefSeg (D	Medal Goda	Numern Homologous
029	22783	AA894207	SS	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN cDNA 5930436K22 gene, protein phosphatase
2526	22791	A1231230	SS	Mus musculus dual specificity phosphatase T-DSP10 mRNA, complete cds, RIKEN cDNA 5930436K22 gene, protein phosphatase
3800	21708	PP, 053596 WW	PP, QQ, UU, WW	Mus musculus endothelin converting enzyme-2 mRNA, complete cds, endothelin converting enzyme 1, expressed sequence AW322500, mel transforming oncogene-like 1
3800	21709	NM_053596	MM, PP, UU, III, JJJ, TTT, UUU	Mus musculus endothelin converting enzyme-2 mRNA, complete cds, endothelin converting enzyme 1, expressed sequence AW322500, mel transforming oncogene-like 1
3868	24430	NM_053996 Z, AA	Z, AA	Mus musculus glycine transporter type 2 (Glyt2) mRNA, complete cds, glycine transporter 1, homolog of rat orphan transporter v7-3, solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
2964	1795	L24207	K, L, N, O, P, X, NN, OO, PP, TT, LLL, UUU	Mus musculus mRNA for cytochrome P450, CYP3A, complete cds, cytochrome P450, steroid inducible 3a11, cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3
2964	1796	L24207	K, L, M, N, X, TT	Mus musculus mRNA for cytochrome P450, CYP3A, complete cds, cytochrome P450, steroid inducible 3a11, cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3
3221	1793	NM_013105	K, L, M, N, FF, TT, DDD, UUU	Mus musculus mRNA for cytochrome P450, CYP3A, complete cds, cytochrome P450, steroid inducible 3a11, cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3
3221	1794	NM_013105	K, L, M, N, TT, DDD, LLL, UUU	Mus musculus mRNA for cytochrome P450, CYP3A, complete cds, cytochrome P450, steroid inducible 3a11, cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 3

_	cation channel, subtaining m, member 2, transfert receptor protein 4			AI234013	140/0	
	receptor potential cation channel, subfamily C, member 5, transient receptor potential		L	1004645		
	receptor 1, transient receptor potential cation channel, subfamily C, member 4, transient					_
	Mus musculus, clone IMAGE:3986429, mRNA, TRP ion channel TRPM8, cold/menthol					
	dehydrogenase-6, delta<5>-3-beta		D	AB000199	⋖	1962 A
	delta<5>-3-beta, hydroxysteroid dehydrogenase-3, delta<5>-3-beta, hydroxysteroid					
	hydroxysteroid dehydrogenase-1, delta<5>-3-beta, hydroxysteroid dehydrogenase-2,					
	cds, hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1,				_	
	hydroxysteroid dehydrogenase/delta5-delta4 isomerase (3beta-HSD) mRNA, complete				_	
	Mus musculus, clone IMAGE:3491119, mRNA, partial cds, Rattus norvegicus 3beta-					
	sequence Al326910, retinal S-antigen		W	NM_012911 VV		16581
	cds, RIKEN cDNA 1200006117 gene, arrestin 3, retinal, arrestin, beta 2, expressed					
	Mus musculus, Arrestin, beta 2, clone MGC:6525 IMAGE:2651372, mRNA, complete					•
	sequence Al326910, retinal S-antigen		Λ	AI013765	_	16584
	cds, RIKEN cDNA 1200006117 gene, arrestin 3, retinal, arrestin, beta 2, expressed					
	Mus musculus, Arrestin, beta 2, clone MGC:6525 IMAGE:2651372, mRNA, complete					
	induced factor 2 (TALE family homeobox)		a, w	AI178025		19184
	induced transcription factor 2-like, TGFB-induced factor (TALE family homeobox), TGFB					
	5430405H02 gene, RIKEN cDNA 5730599009 gene, TG interacting factor, TGF(beta)-					
	Mus musculus testis expressed homeobox mRNA, complete cds, RIKEN cDNA					
	chitinase 3-like 3, chitobiase, di-N-acetyl-		Z, AA	M95768		1624
	cDNA 2210401K11 gene, RIKEN cDNA 4921536I21 gene, chitinase 1 (chitotriosidase),				_	
	Similar to di-N-acetylchitobiase, clone IMAGE:4038549, mRNA, partial cds, RIKEN					
	Mus musculus secreted protein precursor Ym2 mRNA, complete cds, Mus musculus,					
	domain associated protein 2		D	NM_053341		15791
	protein 1, regulator of G-protein signalling 19 interacting protein 1, semaF cytoplasmic				_	
	GIPC2, expressed sequence AU021850, regulator of G-protein signaling 19 interacting				_	
	Mus musculus mRNA for PDZ-domain protein Gipc3, complete cds, PDZ domain protein				_	
	m Genoiname Human Homologous Sequence Gluster Mile	Knox	Model Gode	Refse (D.*		D No.
		Human Homologous		Ace or		10.
				द्राच्या इस्ता हर	-	1
	A STATE OF THE STA			ા માંગ્રામાં કે કે માંગ્રામાં માના માના માના માના માના માના માના	2012	ව
		THE REAL PROPERTY AND ADDRESS OF THE PARTY O	A MARK THE	Section of the section of	þ	

TABLE S	ලි				Aitomay Dockat 44921-5088-01W0 r. Bocumant No. 1985828.1
Sed Des	erec Das	<u>eeneent</u> Aee er Ræseg (D	(१९८०) (एन्ट्रन्	Human Homologous Known Gene Name	nen Homotogous Reference R
3553	23489	NM_024375	RR		Mus musculus, clone IMAGE:4224368, mRNA, partial cds, growth differentiation factor 10
3294	2967	NM_017158	H		Mus musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA 2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29, cytochrome P450, 2c38, cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19, expressed sequence Al159681, expressed sequence Al662255
3294	2968	NM_017158_MM,	MM, TTT		Mus musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA 2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29, cytochrome P450, 2c38, cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19, expressed sequence A1159681, expressed sequence A1662255
3294	2969	NM_017158 N,	'n, T		Mus musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA 2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29, cytochrome P450, 2c38, cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19, expressed sequence A159681, expressed sequence A1662255
3294	2970	NM_017158	N, HH, SS		Mus musculus, clone MGC:25860 IMAGE:4195655, mRNA, complete cds, RIKEN cDNA 2010301M18 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29, cytochrome P450, 2c38, cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19, expressed sequence Al159681, expressed sequence Al662255
4144	669	U55765	D, E, BB, GG, NN, III, JJJ, RRR		Mus musculus, clone MGC:25863 IMAGE:4196269, mRNA, complete cds, Mus musculus, clone MGC:37860 IMAGE:5100400, mRNA, complete cds, serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10, serine protease inhibitor 1-1

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Altomey, Decket, 44921-5018-01W0 s	S Human Homologous:Seguence:©fuster.Title		(peroxisomal 3-oxoacyl-Coenzyme A molase), nydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Mus musculus, Similar to aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase), clone MGC:25814 IMAGE:4162788, mRNA, complete cds, aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	Mus musculus, Similar to aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase), clone MGC:25814 IMAGE:4162788, mRNA, complete cds, aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	Mus musculus, Similar to aminopeptidase B, clone MGC:29229 IMAGE:5041005, mRNA, complete cds, expressed sequence AI894167, leukotriene A4 hydrolase	Mus musculus, Similar to aminopeptidase B, clone MGC:29229 IMAGE:5041005, mRNA, complete cds, expressed sequence AI894167, leukotriene A4 hydrolase	Mus musculus, Similar to aspartyl-tRNA synthetase, clone MGC:6719 IMAGE:3586278, mRNA, complete cds, asparaginyl-tRNA synthetase, asparatyl-tRNA synthetase tRNA synthetase	Mus musculus, Similar to complement component 1, s subcomponent, clone MGC:19094 IMAGE:4196654, mRNA, complete cds, Mus musculus, Similar to complement component 1, s subcomponent, clone MGC:28492 IMAGE:4166254,	mRNA, complete cds, complement component 1, s subcomponent, protein C
	Humen Homologous Known Genel Name	·								
	Model Gode		U, FP, XX, YY, BBB, RRR, SSS	EEE, MMM	ጽ	NN, 00	KK, PP, QQ	W	T, U, JJ, KK, WW, BBB, GGG, PPP,	QQQ, RRR
	ප්තෑනබැ Ref පිදෙ [D		D16479	NM_138884	NM 138884	AA858552	S87522	NM 053799		AA799803
ଜ	elec Id No.		1728	14964	14965	13523	13520	25594		20998
TABLES			2850	3989	3989	338	4084	3828		29

		-030-			
Attorney Docket 4/92/1-5033-6/1W6 Bocument No. 1935328.0 Internologous Reneinand Human Homologous Sequence Cluster Mile	Mus musculus, Similar to hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit, clone IMAGE:4953760, mRNA, partial cds, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Mus musculus, Similar to hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit, clone IMAGE:4953760, mRNA, partial cds, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Mus musculus, Similar to hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit, clone IMAGE:4953760, mRNA, partial cds, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Mus musculus, Similar to hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hydratase (trifunctional protein), alpha subunit, clone IMAGE:4953760, mRNA, partial cds, RIKEN cDNA 130002P22 gene, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Mus musculus, Similar to hypothetical protein FLJ20551, clone MGC:18873 IMAGE:4235245, mRNA, complete cds, RIKEN cDNA 1300019P08 gene, expressed sequence AW108044, ornithine transporter 2, uncoupling protein 2 (mitochondrial, proton carrier), uncoupling protein 2, mitochondrial
Human Reneliamol			·		
र इंट जिल्ला <u>खें</u>	I, J, U, FF, XX, YY, RRR	U, Z, AA, XX, BBB, CCC, RRR, SSS	ww, BBB, CCC	G, U, FF, LL, XX, YY, BBB, CCC, FFF, RRR, SSS, UUU, General Alternate	, ν.
Consentant	NM_130826	NM_130826	WW,	NM_133606	NM_019354 M, VV
E 3 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	16767	16768	16769	17758	3775
	3929	3929	3929	3958	3399

	Wells 3				
	GLGC D No:	<u>ිලිබාවෙබැ.</u> Ae ෙෆේ් Rakseg (D	Model Gode	Kinown Gene Name: Hum	rnikomologous An intermedia An intermedia
				Mus	Mus musculus, Similar to hypothetical protein MGC3178, clone MGC:28887
				1700	1700015E05 gene, RIKEN cDNA 2700053F16 gene, RIKEN cDNA 4921506J03 gene,
			I, J, K, FF,	expre	expressed sequence Al987846, expressed sequence AL023058, expressed sequence
572	15154	AA892532	000	C778	C77895, protein disulfide isomerase-related protein
				Mus	Mus musculus, Similar to hypothetical protein MGC3178, clone MGC:28887
				IMAG	IMAGE:4911455, mRNA, complete cds, RIKEN cDNA 1700015E05 gene, RIKEN cDNA
				2700	2700053F16 gene, RIKEN cDNA 4921506J03 gene, calcium binding protein, intestinal,
				expre	expressed sequence Al987846, protein disulfide isomerase related protein (calcium-
3839	19018	NM_053849	C, FF	pindi	binding protein, intestinal-related)
				Mus	Mus musculus, Similar to microsomal glutathione S-transferase 2, clone MGC:41409
				IMAG	IMAGE:1511631, mRNA, complete cds, arachidonate 5-lipoxygenase-activating protein,
1004	22576	AA955983	G, H, NNN	leuko	leukotriene C4 synthase, microsomal glutathione S-transferase 2
				Mus	Mus musculus, Similar to mitochondrial ribosomal protein L33, clone MGC:35714
180	4245	AA818692	GG, RR	IMAG	MAGE:5365357, mRNA, complete cds, mitochondrial ribosomal protein L33
				Mus	Mus musculus, Similar to N-arginine dibasic convertase 1, clone MGC:25477
				IMAG	IMAGE:4486176, mRNA, complete cds, expressed sequence AI875733, insulin
3190	9917	NM_012993	JJ, КК, ННН	degra	degrading enzyme, nardilysin (N-arginine dibasic convertase)
				Mus	Mus musculus, Similar to N-arginine dibasic convertase 1, clone MGC:25477
				IMAG	IMAGE:4486176, mRNA, complete cds, expressed sequence AI875733, insulin
3190	9918	NM_012993	JJ, KK	degra	degrading enzyme, nardilysin (N-arginine dibasic convertase)
				Mus	Mus musculus, Similar to protein C receptor, endothelial, clone MGC:41156
				IMAG	IMAGE:1054063, mRNA, complete cds, protein C receptor, endothelial, protein C
1950	9166	AI137406	BB, CC	recet	receptor, endothelial (EPCR)
				Mus	Mus musculus, Similar to serine dehydratase, clone MGC:37901 IMAGE:5102037,
			C, MM, FFF,	HRN	mRNA, complete cds, expressed sequence AU040765, serine dehydratase, serine
3826	24778	NM_053962	ШТ	racemase	nase

TABLE 3	<u>ළ</u> ිනි				Atomay Docket 4/921-5038-01Wo
See	839 GLGC GLGC GLGC	<u>නොහොයි රුමෙන් ලිමේනීම් ලි</u>	Model Code	Humen Komologous Kaown Genei Neme Kaown Genei Neme	Human Homologous Sequence Cluster Mile
					Mus musculus, Similar to serine dehydratase, clone MGC:37901 IMAGE:5102037, mRNA, complete cds, expressed sequence AU040765, serine dehydratase, serine
3856	24779	NM 053962	NM_053962 C, MM, TTT	racemase	
				Mus musculus, Sir mRNA, complete o	Mus musculus, Similar to serine dehydratase, clone MGC:37901 IMAGE:5102037, mRNA, complete cds, expressed sequence AU040765, serine dehydratase, serine
3856	25321	NM_053962	MM, FFF, TTT	racemase	
				Mus musculus, Sii IMAGE:1314987, 1	Mus musculus, Similar to single-stranded DNA binding protein, clone MGC:41439 IMAGE:1314987, mRNA, complete cds, single-stranded DNA binding protein, single-
3051	3424	M94557	Ą, B	stranded DNA binding protein 1	ding protein 1
				Mus musculus, Sir	Mus musculus, Similar to solute carrier family 22 (organic anion transporter), member 7,
_			X, ∀,	clone MGC:18877	clone MGC:18877 IMAGE:4236556, mRNA, complete cds, expressed sequence
			General	Al648912, solute of	Al648912, solute carrier family 22 (organic anion transporter), member 6, solute carrier
2970	31	L27651	Alternate	family 22 (organic	family 22 (organic anion transporter), member 7
			M, U, GGG,		
			000, PPP,		
			QQQ, General		
			Core Tox	Mus musculus, Sii	Mus musculus, Similar to solute carrier family 22 (organic anion transporter), member 7,
			Markers,	clone MGC:18877	clone MGC:18877 IMAGE:4236556, mRNA, complete cds, expressed sequence
			General	Al648912, solute of	Al648912, solute carrier family 22 (organic anion transporter), member 6, solute carrier
2970	32	L27651	Alternate	family 22 (organic	family 22 (organic anion transporter), member 7
				Mus musculus, Si	Mus musculus, Similar to solute carrier family 22 (organic cation transporter)-like 2,
			C, T, TT, EEE,	clone MGC:25980	clone MGC:25980 IMAGE:4242162, mRNA, complete cds, solute carrier family 22
4170	1602	U76379	MMM	(organic cation tra	(organic cation transporter), member 1
				Mus musculus, Sii	Mus musculus, Similar to solute carrier family 22 (organic cation transporter)-like 2,
				clone MGC:25980	clone MGC:25980 IMAGE:4242162, mRNA, complete cds, solute carrier family 22
4264	1603	X78855	F	(organic cation tra	(organic cation transporter), member 1

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Sag	BLGG.	(ලොඩොාරු \\ලේග් ^{ල්ල්} සිමහින 0	ा किया विक्रिय	Klumen Komologows K Klumen Komologows K	an Homologous Marin Homologous Seguence (duster-Title
					Mus musculus, Similar to splicing factor, arginine/serine-rich 7 (35kD), clone MGC:38287 IMAGE:5342587, mRNA, complete cds, Mus musculus, clone MGC:36924 IMAGE:4945988, mRNA, complete cds, RIKEN cDNA 1210001E11 gene, splicing
1382	16112	AI011706	ပ	# # B	factor, arginine/serine-rich 3, splicing factor, arginine/serine-rich 3 (SKp2U), splicing factor, arginine/serine-rich 4, splicing factor, arginine/serine-rich 5, splicing factor, arginine/serine-rich 5 (SRp40, HRS)
			S, General Core Tox		
		•	Markers,	2	Mus musculus, Similar to spondin 1a, clone MGC:18859 IMAGE:4221758, mRNA,
3977	21439	NM_138533	General Alternate	0 2	complete cds, RIKEN cDNA 2310045I24 gene, t-spondin, hypothetical protein MGC10724, properdin P factor, complement
			0 <	_	Mus musculus, similar to src homology three (SH3) and cysteine rich domain, clone
			KK, WW, FFF,	<u> </u>	RIKEN cDNA 2610301F02 gene, alpha-spectrin 1, erythroid, nesprin-1, spectrin, alpha,
		7	GGG, HHH,	v .	erythrocytic 1 (elliptocytosis 2), spectrin, alpha, non-erythrocytic 1 (alpha-fodrin), src
1241	20741	AF084186	PPP, QQQ	u .	homology three (SH3) and cysteine rich domain
3454	160	NM 022245		<u> </u>	Mus musculus, Similar to sulfite oxidase, clone MGC:28458 IMAGE:4160277, mRNA, complete cds, RIKEN cDNA 0610009N12 gene, cytochrome b-5
			K, GG, PP,	_	Mus musculus, Similar to sulfite oxidase, clone MGC:28458 IMAGE:4160277, mRNA,
3454	762	NM_022245		S	complete cds, RIKEN cDNA 0610009N12 gene, cytochrome b-5
			G, I, J, 000, PPP, QQQ,		
			General Core		
			Tox Markers, General	<u> </u>	Mus musculus, Similar to sulfite oxidase, clone MGC:28458 IMAGE:4160277, mRNA, complete cds. RIKFN cDNA 1810044022 dene. RIKFN cDNA 2810034.118 dene. sulfite
3613	14970	NM_031127	Alternate	0	oxidase
120	10320	AA800855	BB, CC		myeloid leukemia factor 2
369	18140	AA859240	JJ, KK	u	myo-inositol 1-phosphate synthase A1

(Sed	CLGC ONS	<u> (ट्रिकार्स्सम्) </u> Acc or RefSeq (D	Modal Goda	Human Homologous Known Gene Name Human Homologous Sequence Glusier mile	
				myxovirus (influenza virus) resistance 1,	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse),
4213	517	X52713	RR	myxovirus (influenza virus) resistance 2	
3855	14591	NM_053961	DD, EE, NNN	N-acetyl galactosaminidase, alpha, N-acetylgalactosaminidase, alpha-	cetylgalactosaminidase, alpha-
3840	16362	NM_053853	ن ان ≼	N-acetyltransferase 1 (arylamine N-acetyltransferase)	yltransferase)
				NADH dehydrogenase (ubiquinone) 1 alt	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, NADH dehydrogenase
2479	17672	AI230074	N, PPP, QQQ	(ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	JkD, MWFE)
1876	18509	AI104528	LL, RRR	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17)	eta subcomplex, 6 (17kD, B17)
			WW, BBB,	NADH dehydrogenase (ubiquinone) 1, sı	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, NADH dehydrogenase
2211	22823	AI176491	၁၁၁	(ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	(6kD, KFYI)
2709	22717	AI235948	Σ	Nidogen (entactin), nidogen (enactin), nidogen 1	idogen 1
2544	17297	AI231785	S	Niemann Pick type C2, Niemann-Pick disease, type C2	isease, type C2
3056	1508	M97662	M	Nit protein 2, expressed sequence Al195023, nitrilase 1, ureidopropionase, beta	5023, nitrilase 1, ureidopropionase, beta
			A, B, General		
-			Core Tox		
1135	16883	AA997345	Markers	Nit protein 2, RIKEN cDNA 1190017B19 gene) gene
3767	4621	NM_053463	JJ, KK	nucleobindin, nucleobindin 1	
3767	4622	NM 053463		nucleobindin, nucleobindin 1	
2457	2615	AI229318	Α, Ω	nucleolar cysteine-rich protein	
829	24369	AA944011	I	nucleotide binding protein 2, nucleotide t	nucleotide binding protein 2, nucleotide binding protein 2 (MinD homolog, E. coli)
2389	24368	AI180392	G, H, ZZ	nucleotide binding protein 2, nucleotide t	nucleotide binding protein 2, nucleotide binding protein 2 (MinD homolog, E. coli)
				OB-receptor gene related protein (OB-R	OB-receptor gene related protein (OB-RGRP), RIKEN cDNA 1520402O14 gene, leptin
711	6483	AA900461	RR	receptor gene-related protein, leptin receptor overlapping transcript-like 1	eptor overlapping transcript-like 1
				odorant receptor S1 gene, olfactory rece	odorant receptor S1 gene, olfactory receptor 41, olfactory receptor, family 6, subfamily
1246	20236	AF091570	Z, AA, RR	A, member 1	
				origin recognition complex, subunit 5 homolog (S. cerevisiae), origin recognition	molog (S. cerevisiae), origin recognition
1582	5712	AI045154	XX, YY	complex, subunit 5-like (yeast)	
2505	15551	A1230759	A, B, Z, AA, RR	ornithine decarboxylase antizvme 2	
2007				and more indicated times accordate relating signal transducer	sociated calcium signal transducer 1
2835	14332	AJ001044	=	מפי-ווייין, ימוויין די ואייין איייין איייין איייין	סטומונים כמוסיווו פופוים וומופסחכם

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Seq. (ச <u>ப</u> ின் நல்	ජෙබෑඩබැ ඵූදෙ දෙ ශී්රෙන් D	Medal Goda	700 700 700 700	aan He <mark>mologous </mark>
3395	16330	NM_019331	S	pairec propre 4	paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein), proprotein convertase subtilisin/kexin type 3, proprotein convertase subtilisin/kexin type 4
				pairec	paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein), proprotein convertase subtilisin/kexin type
3395	16331	NM_019331	S, W	4	
292	22721	AA850781	^	peptic	peptidylprolyl isomerase D (cyclophilin D)
3880	15391	NM_057114	U, LLL	perox	peroxiredoxin 1
3484	9240	NM_022540	E, 888, CCC	xood	peroxiredoxin 3
3484	9241	NM_022540	KK	perox	peroxiredoxin 3
				perox	peroxisomal biogenesis factor 11A, peroxisomal biogenesis factor 11B, peroxisomal
3774	4290	NM_053487	BBB	biogei	biogenesis factor 11a, peroxisomal biogenesis factor 11b
			XX, YY, BBB,		
96	17187	AA800315	၁၁၁	perox	peroxisomal farnesylated protein
885	22452	AA944542	L, T, KKK	perox	peroxisomal membrane protein 4, peroxisomal membrane protein 4 (24kD)
2293	1050	AI178219	۸	dsoud	phosphatidylinositol glycan, class L
				dsoyd	phosphatidylinositol-4-phosphate 5-kinase, type II, beta, phosphatidylinositol-4-
3899	15764	NM_080480	K	dsoyd	phosphate 5-kinase, type II, gamma
1713	11125	AI071867	Z	dsoud	phosphatidylserine synthase 1, phosphatidylserine synthase 2
2484	15862	AI230228	ZZ, AAA	dsoyd	phosphoserine aminotransferase
2132	1957	AI172143	KKK	phytai	phytanoyl-CoA hydroxylase, phytanoyl-CoA hydroxylase (Refsum disease)
			LLL, SSS,		
2185	7022	A1176041	תחח	Pirin,	Pirin, RIKEN cDNA 2310042L19 gene
4	19472	AA799616	ໄດ, ບບ	pituita	pituitary tumor-transforming 1 interacting protein
				platek	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit, platelet-activating
1166	14149	AA998172	99	factor	factor acetylhydrolase, isoform lb, beta subunit (30kD)
- 1	16073	AI231489		poly(r	poly(rC) binding protein 3
1128	23930	AA997182	Ш	mylod	polymerase (RNA) II (DNA directed) polypeptide H

	3.8 3.8				Attorney Docket 44921-5033-01W0
Sed	9 9 9 9 9 9 9		Consent Ace or Refse ID Model Code	Umic Pioto	in Romologous (Fig. 1) The Company of the Company o
3969	2802	NM 134449	1		polymerase I and transcript release factor, serum deprivation response, serum deprivation response (phosphatidylserine binding protein)
2181	23311		Z, AA	prol	proline arginine-rich end leucine-rich repeat protein
534	19469	AA892112	V, NN, EEE, MMM	prol	proline dehydrogenase, proline dehydrogenase (oxidase) 1
2618	19470	AI233266	GGG, HHH	pro	proline dehydrogenase, proline dehydrogenase (oxidase) 1
1552	5451	AI044322	DD, EE	prot	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
356	6403	AA858879	A, B, G, H, S, PPP, QQQ	prot	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
2627	18900	A1233570	X, Y, LLL, SSS, UUU	prot	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
				Pro	Protein kinase C. type I (gamma type). RIKEN cDNA 1200003E11 gene. Rattus
	•			Nou	norvegicus Munc13-3 mRNA, complete cds, copine III, copine IV, protein kinase C,
377	6342	AA859458	Z, AA	gamma	ma
477	21952	AA891537	UU, ZZ, AAA	prot	protein predicted by clone 23733
2509	17720	AI230778	٦' ٦	prot	protein-tyrosine sulfotransferase 2, tyrosylprotein sulfotransferase 2
3943	21703	NM_133525	JJ, KK	pute	putative c-Myc-responsive
				RAE	RAB10, member RAS oncogene family, RAB12, member RAS oncogene family, RAB32,
			L, 000,	mer	member RAS oncogene family, RAB38, member RAS oncogene family, RIKEN cDNA
			General	281	2810011A17 gene, Rab38, member of RAS oncogene family, expressed sequence
4027	24657	NM_145774	Alternate	AAE	AA536966, expressed sequence AW107754
				RAE	RAB11a, member RAS oncogene family, RAB28, member RAS oncogene family,
3860	18798	NM_053978	HH	exp	expressed sequence AW496496
3507	20303	A 0 209200 MN	a C	RA	RAB31, member RAS oncogene family, RAB5A, member RAS oncogene family, RAB5C member RAS oncogene family
	303	100770 ININI	2 2	2	ליייות אייטעטייט טייט ויטטייט יין ייין יין יין אייטטעטייט ויטטעטייט אייט אייטעטייט אייט אייט אייט א
			E, K, L, KKK, NNN, 000,		
					1
3349	20778	NM 019124	Alternate	rab	rabaptın 5, rabaptın-5

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) (1) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	GLGC BNG	<u>ලොකෙකි.</u> Aලෙගෙ Rමහිලෙගි	Model Gode	Humen Homologous Known Gene Nemo	an Romologows Vn Gene Name Humani Homologows Sequence Gluster Title
4023	9845	NM 145672	EEE, MMM		Rattus norvegicus CXC chemokine RTCK1 (Rtck1) mRNA, complete cds, interleukin 8
					Rattus norvegicus kallistatin mRNA, complete cds, serine (or cysteine) proteinase
			XX, YY, PPP,		inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1,
2372	6455	AI179984	aaa		serine protease inhibitor 2
				9	Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17
		_			(sodium/hydrogen exchanger), member 2, expressed sequence Al649385, solute carrier
4017	4949	NM_139338	D		family 34 (sodium phosphate), member 1
					RCE1 homolog, prenyl protein protease (S. cerevisiae), Ras and a-factor-converting
1947	21520	AI137332	1		enzyme 1 homolog (S. cerevisiae)
2842	1515	D10233	0, P		renin binding protein
374	15160	AA859346	S		ribonuclease P (38kD)
3511	17809	NM_022699	0, P, XX, YY		ribosomal protein L30
			S, JJ, KK, FFF, GGG,		
			General		
596	1867	AA850940	Alternate		ribosomal protein L4
					RIKEN cDNA 0610010113 gene, cystathionase (cystathionine gamma-lyase), expressed
3269	18452	NM_017074	L, 00, UU		sequence Al098105
L			L, NN, 00, III,		RIKEN cDNA 0610010113 gene, cystathionase (cystathionine gamma-lyase), expressed
3269	18453	NM_017074			sequence Al098105
			C, K, W, BB, CC, NN, OO,		
			GGG, III, JJJ,		RIKEN cDNA 0610025K21 gene, aflatoxin B1 aldehyde reductase, aldo-keto reductase
3962	23321	NM_134407	LLL		family 7, member A2 (aflatoxin aldehyde reductase)
3066	23322	NIM 12407	L, BB, CC, NN,		RIKEN cDNA 0610025K21 gene, aflatoxin B1 aldehyde reductase, aldo-keto reductase
2902	_	MINI 134407	3		ומוווון זי וויפוווטפו רצ (מוומוטאוו מוספון)עם ופענימשפן

290US AMERICAN	RIKEN cDNA 0610025K21 gene, aldo-keto reductase family 7, member A2 (aflatoxin	RIKEN cDNA 0610038004 gene, secreted phosphoprotein 2, 24kD	RIKEN cDNA 0610038O04 gene, secreted phosphoprotein 2, 24kD	RIKEN cDNA 0610038O04 gene, secreted phosphoprotein 2, 24kD	RIKEN cDNA 0610040H15 gene, RIKEN cDNA 2210409E12 gene, transcription elongation factor B (SIII), polypeptide 2 (18kD, elongin B)	RIKEN cDNA 1110007F23 gene, angiopoietin 2, angiopoietin-like 3, angiopoietin-like 4, ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin), ficolin (collagen/fibrinogen domain containing) 1, ficolin B	RIKEN cDNA 1110014L17 gene, RIKEN cDNA 1810008K16 gene, RIKEN cDNA 2400003B06 gene, transmembrane trafficking protein	RIKEN cDNA 1110014L17 gene, RIKEN cDNA 1810008K16 gene, RIKEN cDNA 2400003B06 gene, transmembrane trafficking protein	RIKEN cDNA 1110019K23 gene, methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate cyclohydrolase, methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase,	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	RIKEN cDNA 1110033E03 gene, phosphate cytidylyltransferase 2, ethanolamine RIKEN cDNA 1110033E03 gene, phosphate cytidylyltransferase 2, ethanolamine
	N. DOUGH										
	G, K, S, X, JJ, KK, NN, DDD, EEE, GGG,	LL, EEE, MMM, UUU	0, P, YY	BBB, CCC	S LL	<u>u</u> .	0, P, FF	>		MM, TTT	KKK, NNN T, XX, KKK
Centent		AA858573	AI043655	U19485	NM 031129	_ AA944481	57	NM_053467		J05519	NM 053568 NM 053568
ABLES COMPANDED TO COMPAND COMPANDED TO COMPAND COMPAN	9	18001	18002	17999	6525	14763	23274	23276		1549	21940 21941
		340	1529	4104	3614	882	3769	3769		2934	3792 3792

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in Romologious In Gene Nemes Human (Romologious)Sequence Quister Mille.	RIKEN cDNA 1300002P07 gene, RIKEN cDNA 1810009C16 gene, alcohol dehydrogenase 3 complex, alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	RIKEN cDNA 1300003A17 gene, RIKEN cDNA 3222402004 gene, expressed sequence C76800, hypothetical protein DKFZp761B2423, myeloid/lymphoid or mixed-lineage leukemia, nucleolar and coiled-body phosphoprotein 1, nucleolar and coiled-body phosphoprotein 1, nucleolar and coiled-body phosphoprotein 1, nucleolar and coiled-body coiled-body phosphoprotein 1, nucleolar and coiled-body c	RIKEN cDNA 1300003A17 gene, RIKEN cDNA 3222402O04 gene, expressed	sequence C76800, hypothetical protein DKFZp761B2423, myeloid/lymphoid or mixed- lineage leukemia, nucleolar and coiled-body phosphoprotein 1, nucleolar and coiled-	body phosphprotein 1	RIKEN cDNA 1300003A17 gene, RIKEN cDNA 3222402004 gene, expressed sequence C76800, hypothetical protein DKFZp761B2423, myeloid/lymphoid or mixed-	lineage leukemia, nucleolar and coiled-body phosphoprotein 1, nucleolar and coiled-	body phosphprotein 1	RIKEN cDNA 1300007J06 gene, RIKEN cDNA 2310022B03 gene, expressed sequence AU014768, glutamic pyruvate transaminase (alanine aminotransferase) 2, glutamic-	pyruvate transaminase (alanine aminotransferase)	RIKEN cDNA 1300007J06 gene, RIKEN cDNA 2310022B03 gene, expressed sequence AU014768, glutamic pyruvate transaminase (alanine aminotransferase) 2, glutamic-	pyruvate transaminase (alanine aminotransferase)				RIKEN cDNA 1300011D16 gene, attractin, testis intracellular mediator protein	RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, ornithine	aminotransferase, ornitnine aminotransferase (gyrate atropny)
Hybrane	_					 -	ore	ers					, S,			ore	×	
Model Godo	M, U	>			SS	C, AAA,	General Core	Tox Markers	HH, XX, General	Alternate		Σ	A, B, F, G, S,	FFF, GGG, III,	JJJ, 000,	General Core Tox Markers	A, B, F, H, X	Ι, τιτ
Constant Accor ^E Refeq ID	NM_134329	A A 9020040	2005		NM_022869			NM_022869		NM_031039		NM_031039				AA859645	10000	AA893325
38 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	19706	74790	272.00		24283			24284		21094		21096				11635	9,9	4242
	3960	009	3		3517			3517		3587		3587			,	389		633

TABLES	ල පු				Market Construction (Norman Docks) 4482A 5038-010VO
Šeg 10	GLEG ID No.	ලිකිසිබැ ශිලේන් RakSeg (D	Model Gode	in in the properties of the second se	
3050	25457	1402207	100V	RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, ornithine	2900006B13 gene, ornithine
1801	15218	AI102495	PPP 000	RIKEN cDNA 1300019121 gene, nucleoside phosphorvlase	sphorylase
				RIKEN cDNA 1500002F19 gene, RIKEN cDNA 3110005M08 gene, ribosomal protein	3110005M08 gene, ribosomal protein
884	12228	AA944536	ZZ, AAA	L37	
2241	10310	A1176961	А, В, Н	RIKEN cDNA 1500031N16 gene, mitochondrial ribosomal protein L12	ribosomal protein L12
351	6380	AA858758	FF, LL	RIKEN cDNA 1500031019 gene, hypothetical protein MGC12335	rotein MGC12335
3230	90806	NM 013218	1	RIKEN cDNA 1700018L02 gene, adenylate kinase 3 alpha like, expressed sequence	se 3 alpha like, expressed sequence
5535	20020	012C10_WW	Ē.	+1 JOOCIA	
1097	2542	AA965035	Ŧ	RIKEN cDNA 1700030G05 gene, basic leucine zipper nuclear factor 1 (JEM-1)	zipper nuclear factor 1 (JEM-1)
27	21120	AA799526	S	RIKEN cDNA 1700043E15 gene. small nuclear ribonucleoprotein D3 polypeptide (18kD)	ibonucleoprotein D3 polypeptide (18kD)
4153	1547	_	MM, TTT	RIKEN cDNA 1810009H17 gene, cell growth regulatory with ring finger domain	lulatory with ring finger domain
				RIKEN cDNA 1810026B04 gene, dicarbonyl/L-xylulose reductase, hydroxysteroid (17-	/lulose reductase, hydroxysteroid (17-
				beta) dehydrogenase 8, hypothetical protein BC014057, hypothetical protein FLJ14431,	014057, hypothetical protein FLJ14431,
2094	17529	A1171460	ww	oxidoreductase UCPA	
312	883	AA851347	O, P	RIKEN cDNA 2010006G21 gene, RIKEN cDNA 2810425K19 gene, sorting nexin 5	2810425K19 gene, sorting nexin 5
1496	16840	AI029733	Q, R	RIKEN cDNA 2010100012 gene, chromosome 20 open reading frame 52	20 open reading frame 52
				RIKEN cDNA 2200008F12 gene, expressed sequence Al324147, lectin, galactoside-	uence Al324147, lectin, galactoside-
3957		NM_133599	XX	binding, soluble, 2 (galectin 2)	
1175	24094	AA998435	XX	RIKEN cDNA 2210412K09 gene, hypothetical protein HSPC177	otein HSPC177
				RIKEN cDNA 2310003C10 gene, protein phosphatase 4, catalytic subunit, protein	natase 4, catalytic subunit, protein
3955	24352	NM_133589	 	phosphatase 6, catalytic subunit	
				RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 2, calmodulin-like 3, centrin	calmodulin 2, calmodulin-like 3, centrin
	_		General	1, centrin, EF-hand protein, 1, centrin, EF-hand protein, 2, expressed sequence	protein, 2, expressed sequence
1090	24233	AA964756	Alternate	Al327027, expressed sequence AL024000, troponin C, fast skeletal, troponin C2, fast	onin C, fast skeletal, troponin C2, fast
				RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose	ntiation related protein, adipose
428	16167	AA874941	င	differentiation-related protein	

**************************************	Humani Homologousi Sequences (Surster VIII)	RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose differentiation-related protein	RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose differentiation-related protein	RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose	differentiation-related protein RIKEN cDNA 240009B11 gene, chromosome 11 open reading frame 13	RIKEN cDNA 2410001H17 gene, hypothetical protein FLJ21749	RIKEN cDNA 2410017117 gene, RIKEN cDNA 2410137M14 gene, RIKEN cDNA	5430410E06 gene, histocompatibility 2, blastocyst, histocompatibility 2, class II, locus Mb2, hypothetical protein DKFZp547I014, major histocompatibility complex, class II, DM		RIKEN cDNA 2410045101 gene, SNRPN upstream reading frame, small nuclear	polypeptide N, small nuclear ribonucleoprotein polypeptides B and B1	RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	DIVEN ADMA 2640004647 apple likely ortholog of mouse life such reneat protein	RIKEN CDNA 26100001E17 gelle, incely of included in highest choice processing the control of the		RIKEN cDNA 2610008L04 gene, quinoid dihydropteridine reductase	RIKEN cDNA 2610009E16 gene, parathymosin, prothymosin alpha	RIKEN cDNA 2610009E16 gene, parathymosin, prothymosin alpha	RIKEN cDNA 2610016A03 gene, polyamine N-acetyltransferase	RIKEN cDNA 2610101M19 gene, phosphoribosyl pyrophosphate synthetase-associated protein 2
	romologous Senal Némo Senal Némo		RIKEN CE differentia	RIKEN CE	Alken c	RIKEN CE	RIKEN C	5430410E Mb2, hypo	beta	RIKEN CE	polypeptic	RIKEN cE 7, proteas	70 101	RIKEN C		RIKEN C	RIKEN CE	RIKEN C	RIKEN CL	RIKEN cC protein 2
	Gode Known Go							z Z					eral	XX XX	YY, III,	ø	eral e			
1974 P. 45 T.	Model (ပ	ပ	3	> X	2		O. P. V.	00		ZZ, AAA	\$	G, General	Allerinate	1	Alternate	N, General Alternate		М	ш
	Consent	AA893280	A1030932	70001714	AI178104	AI175019			AI171966		M29293	AA997406	NIM 000549	NM 022390		NM_022390	NM 031975	NM_031975	AI138020	NM_057131
3.8	GLGG TO No.	16168	16169	2,7	13389	15557			20783		1580	3172	11000	13479		13480	16257	17556	13157	15151
	ි. ම ම	631	1523		2078	2154			2118		3009	1137	2407	3466		3466	3715	3715	1966	3883

TABLES	ন্ত্র জু				ng 18 18 18 18 18 18 18 18 18 18 18 18 18
	GLEE ID No.	<u>පේඛ-ළැබැ </u> <u>Ace ලේ</u> R3(පිමේ [D	ගින්න් ලිවෙය	Human Homologous Known Gene Name: Human H	
410	4222	AA860024	KK	RIKEN C	RIKEN cDNA 2610301D06 gene, eukaryotic translation elongation factor 1 gamma
3206	14423	NM 013053	a C	RIKEN CI	RIKEN cDNA 2700028P07 gene, tyrosine 3-monooxygenase/tryptophan 5-
				RIKEN C	RIKEN cDNA 2810401C16 gene, programmed cell death 8 (apoptosis inducing factor),
483	22858	AA891591	D	programn	programmed cell death 8 (apoptosis-inducing factor)
178	6236	AA818627	K, L, UU	RIKEN of 1, insulin	RIKEN cDNA 2900053111 gene, growth response protein (CL-6), insulin induced gene 1, insulin induced protein 2
3346	16382	NM 017343	>	RIKEN CL	RIKEN cDNA 2900073G15 gene, myosin regulatory light chain
79	2098	AA799995	a, R, aaa	RIKEN C	RIKEN cDNA 3100001N19 gene, ribosomal protein L14
2374	2099	AI180015	R	RIKEN CL	RIKEN cDNA 3100001N19 gene, ribosomal protein L14
3524	3524 18107	NM 022949	General Alternate	RIKENC	RIKEN cDNA 3100001N19 gene giposomal protein I 14
	· .			RIKEN C	RIKEN CDNA 3110021P21 gene, expressed sequence Al314976, syntaxin binding
1649	900	AI059963	-	protein 2,	protein 2, vacuolar protein sorting 33B (yeast)
			General	RIKEN C	RIKEN cDNA 3110041018 gene, expressed sequence AI505894, lamin B receptor,
1031	23080	AA957423	Alternate	transmen	transmembrane 7 superfamily member 2
			E, I, J, K, X, Y,		
			TT, RRR,	RIKEN C	RIKEN cDNA 3200002106 gene, dynein, cytoplasmic, intermediate chain 2, dynein,
2862	1354	D38065	SSS, UUU	cytoplasn	cytoplasmic, intermediate polypeptide 2, hypothetical protein MGC20486
				RIKEN C	RIKEN cDNA 4833409F13 gene, expressed sequence Al303446, serine (or cysteine)
				proteinas	proteinase inhibitor, clade D (heparin cofactor), member 1, serine (or cysteine)
			General	proteinas	proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor),
4259	768	X74549	Alternate	member 2	CI
			K, M, N, X, BB,		
			CC, GG, TT, .		
			FFF, GGG,		
			UUU, General	RIKEN CL	RIKEN cDNA 4921511105 gene, RIKEN cDNA 4933404A18 gene, solute carrier family
3931	20707	NM 131906	Core Tox Markers	21 (organ transports	21 (organic anion transporter), member 3, solute carrier family 21 (organic anion transporter) member 5

Attorney Docket 4492/1-5088-0/W/V	Kuman Homologous Human Homologous Sequence Cluster IIIIe	RIKEN cDNA 4930533O14 gene, dipeptidylpeptidase III		RIKEN cDNA 4930579A11 gene, likely ortholog of rat vacuole membrane protein 1	RIKEN cDNA 5730408C10 gene, zinc finger protein 103, zinc finger protein 103	RIKEN cDNA 5730414C17 gene, hippocampus abundant gene transcript 1, hypothetical	protein DKFZp564L0864 similar to HIAT1, hypothetical protein FLJ14753	RIKEN cDNA 5730442K12 gene, emopamil binding protein (sterol isomerase),	emopamil binding related protein, delta8-delta7 sterol isomerase related protein,	RIKEN cDNA 6330407G11 gene, hypothetical protein FLJ10342	RIKEN cDNA 6720463E02 gene, dynein light chain 2	RIKEN cDNA C030022K24 gene, chromosome 12 open reading frame 8, endoplasmic	reticulum protein 29	RNA polymerase II transcriptional coactivator, activated RNA polymerase II transcription	Rous sarcoma oncogene, v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog	(avian)	S164 protein	SEC24 related gene family, member B (S. cerevisiae)		selenium binding protein 1, selenium binding protein 2	serine/threonine kinase recentor associated protein unr-interacting protein		
	Nocal Godo	OOO, General Alternate	B, WW, General	Alternate	8	MM, ZZ, AAA,	E	G, WW,	General	OO OO	99	-	ا, ب	L		٥	ww	2	K, GG, HH,	NN, OO	A P P P P P P P P P P P P P P P P P P P	D. BBB. CCC.	
	<u> </u>	D89340		NM_138839	NM 053438		AA891535		NIM 057137	AA874990	769080 MN	7000	NM_053961	KO2816	200	AA943307	AI639342	A1101465	1	NM 080892	A1009198		
ଜୁଲ	alec. Dino	1218		23166	5564		21951		8502	17303	17662	27.07	16553	23486		15319	14606	13261	3	52060	9150		
) Sed (D)	2879		3984	3765		476		2885	(1)	3904	1	3822	2038		841	2818	1778		3912	1306		-

TABLE S	ങ ബ്ര) Attornoy, Docket 44921-5038-010V0
	GLGG DNo.		eकाह्माः Ace or . RetSeq 10 Model Gode	Human Homologous Human Homologous Knowni Gener Rime Human Homologous Sequence (Suster Intie
1860	1440	AI104139	MM	SH2-B PH domain containing signaling mediator 1, SH2-B homolog, adaptor protein with pleckstrin homology and src, adaptor protein with pleckstrin homology and src homology 2 domains. src homology 2 domain-containing transforming protein C3
4146	1439	1157391	WW	SH2-B PH domain containing signaling mediator 1, SH2-B homolog, adaptor protein with pleckstrin homology and src, adaptor protein with pleckstrin homology and src homology 2 domains s
2129	7733	AI172086	. a.	SH3 domain binding glutamic acid-rich protein like 3, SH3 domain binding glutamic acid-rich protein-like 3
2768	13513	AI237091	. Cr	sialytransferase (N-acetyllacosaminide alpha 2,3-sialytransferase), sialytransferase 4C (beta-galactosidase alpha-2,3-sialytransferase), sialytransferase 6 (N-acetyllacosaminide alpha 2,3-sialytransferase)
1881	21522	AA944449	EEE, MMM	signal recognition particle 68kD
			FFF, GGG, PPP, General Core Tox	
2628	7888		Markers	similar to arginyl-tRNA synthetase
4050	6366	NM 153628	CC, LL, NN,	similar to signal peptidase complex (10kD)
2147	11623	AI172471	N, XX, YY, PPP, QQQ	small EDRK-rich factor 2
1121	2939	AA996885	BB, CC, UU, DDD	small inducible cytokine A19, small inducible cytokine subfamily A (Cys-Cys), member
732	22578	AA924105	≻ ×	small inducible cytokine A3, small inducible cytokine A6, small inducible cytokine A9, small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated, small inducible cytokine subfamily A, member 22

	(3) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	் <u>இ</u> <u>வேச்தியி</u> இக்கி		Islandolomoli memili	Altomey Docket 4/921-5038-01WO
	9	RefSeq ID	Model Gode	Known Gene Name	m Genet Nemes Humen Homelogous Sequence Oluster IIIIe : # - *,
			C, KK, FFF, GGG, HHH,		
			General	sms	small nuclear ribonucleoprotein B, small nuclear ribonucleoprotein polypeptides B and
3010	17123	M29295	Alternate	B4	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)
2357	12516	AI179651	nn (SM	SM I 3 suppressor of mit two 3 homolog 2 (yeast)
328	9299	AA851967	၁	solu	solute carrier family 16 (monocarboxylic acid transporters), member 6
				njos	solute carrier family 20 (phosphate transporter), member 1, solute carrier family 20
	(1	(bhc	(phosphate transporter), member 2, solute carrier family 20, member 1, solute carrier
1813	23538	AI102727	A, B, Q, R	fam	family 20, member 2
			E, I, J, KKK,		
573	17468	AA892545	NNN, 000	solu	solute carrier family 22 (organic cation transporter), member 1-like
				njos	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1, solute
				carr	carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2, solute carrier family
				s) 6	9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1, solute carrier family 9
3427	17340	NM_021594	E, BB, CC	os)	(sodium/hydrogen exchanger), isoform 3 regulatory factor 2
222	15117	AA819623	00	sort	sorting nexin 4
427	15115	AA874928	V, W, BB, CC	sort	sorting nexin 4
			NN, PP, QQ,		
427	15116	AA874928	ZZ, AAA	sort	sorting nexin 4
			H, Z, KK, FFF,		
			GGG, General		
			Core Tox		
2761	11404	AI237002	Markers	eds	spermidine synthase, spermine synthase
			H, FFF,		
			General Core		
3768	11403	NM_053464	Tox Markers	eds	spermidine synthase, spermine synthase
			I, J, III, JJJ, KKK General	, and a second	sterol regulators element binding transcription factor 1, sterol regulators element binding
1437	11191	AI013042	Alternate	tran	transcription factor 2

					Doeumant No. 1695823.1
(See	er.ec			Human Homologous	
<u>_</u>	(10 Me)	යිම්රින් (D	الالمظار وموه	Known Cene Neme	Humanillomologous Sequence Chuster Mile
1432	11197	AI012937	nn		stomatin (EPB72)-like 2
916	4207	AA945591	FF		stromal cell derived factor 2, stromal cell-derived factor 2-like 1
3475	2384	NM 022513	≻ ×		sulfotransferase family 18. member 1. sulfotransferase family, cytosolic, 18. member 1
815	11691	AA926193	M, X, Y		sulfotransferase family, cytosolic, 1C, member 1
<u> </u>			X, III, JJJ, General Core		
1991	11693	AI168953	Tox Markers		sulfotransferase family, cytosolic, 1C, member 1
2792	11692	AI638982	Σ		sulfotransferase family, cytosolic, 1C, member 1
					suppressor of potassium transport defect 3, torsin family 1, member B, torsin family 1,
1943	10754	AI137038	FF		member B (torsin B)
7	1607	AA799879	2		synaptogyrin 1, synaptogyrin 3, synaptogyrin 4
924	13751	AA945699	НН		synaptosomal-associated protein, 23kD
3206	20509	NM_022689	W		synaptosomal-associated protein, 23kD
2130	2509	AI172102	E, DD, EE		syntaxin 18
			. (
88	22457	AA944572	PPP, ada		TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31 kD
1967	11588	A1138121	V, AA		testis expressed sequence 27
3910	18902	NM_080887	A, B		thioredoxin-like (32kD), thioredoxin-like, 32kD
			SS, EEE, III,		tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1 (erythroid
2684	15004	AI235224	JJJ, MMM		potentiating activity, collagenase inhibitor)
			UU, EEE, III,		tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1 (erythroid
3834	15002	NM_053819	JJJ, MMM		potentiating activity, collagenase inhibitor)
285	16329	AA850542	JJ, KK, FFF		TNF receptor-associated factor 4, Tnf receptor associated factor 4
2468	17245	AI229630	Ţ		TRAM-like protein, translocating chain-associating membrane protein
3692	16039	NM_031811	J, FF		transaldolase 1
3480	7505	NM_022534	N		transcobalamin 2, transcobalamin II; macrocytic anemia
161	3709	AA818192	UÜ		transcriptional adaptor 3-like
2593	12463	AI232706	L, PP		translin-associated factor X

																								_				
Altomay Doctet (4.921-5033-91WC) - Altomay Document No. 1935323,	Humen Homologous) Known Gene Neme - Himman Homologous Saguenae Auster IIIIte		tubulin-specific chaperone e	tumor necrosis factor (ligand) superfamily, member 13	tumor necrosis factor (ligand) superfamily, member 13	tumor necrosis factor receptor superfamily, member 12, tumor necrosis factor receptor	superfamily, member 12 (translocating chain-association membrane protein), tumor	necrosis factor receptor superfamily, member 1A, tumor necrosis factor receptor	superfamily, member 1a, tumor necrosis factor receptor superfamily, member 22, tumor	necrosis factor receptor superfamily, member 23	U1 small nuclear ribonucleoprotein 1C, small nuclear ribonucleoprotein polypeptide C	U6 snRNA-associated Sm-like protein	U6 snRNA-associated SM-like protein 4, U6 snRNA-associated Sm-like protein	ubiquinol-cytochrome c reductase complex (7.2 kD)	ubiquitin fusion degradation 1 like, ubiquitin fusion degradation 1-like	UDP glycosyltransferase 1 family, polypeptide A8	UDP-glucose ceramide glucosyltransferase	UDP-glucose dehydrogenase	uncharacterized hematopoietic stem/progenitor cells protein MDS032	vanin 1	Vertebrate LIN7 homolog 1. Tax interaction protein 33, vertebrate homolog of C.	elegans Lin-7 type 3	vipirin, viral hemorrhagic septicemia virus(VHSV) induced gene 1	vipirin, viral hemorrhagic septicemia virus(VHSV) induced gene 1	voltage-dependent anion channel 1	WD repeat domain 1, coatomer protein complex, subunit alpha, coatomer protein	complex, subunit beta 2 (beta prime), expressed sequence Al256832	x 003 protein
10000000000000000000000000000000000000	Model Gode	G, Н	BB, CC	Z, AA	W			C, E, Q, R,	General	Alternate	UUU	00, PP, QQ	UUU	GG	Q, R	К, GG, НН	W	E, S, WW, DDD	aga	U, XX, BBB	PP, WW, DDD, General	Alternate	M	W	KK	000	X, Y, SS	В
A STATE OF THE STA	(content Ace or RefSee (D		AI171759		AA891690					5		AA956431	0			07	AI231479	5	3	AI179099					NM_031353		3	AI007881
න ක	GLGC D No.	17405	18994	9092	9091					1521	15286	23762	2588	9			13469		15576	2887		16125	4593		18539		ᅱ	3148
Tables -	8eq 10	1	8		487					_	\neg	7				\neg	2536	5	232	2325		3778			3632		\neg	1260
tine to	٠																											

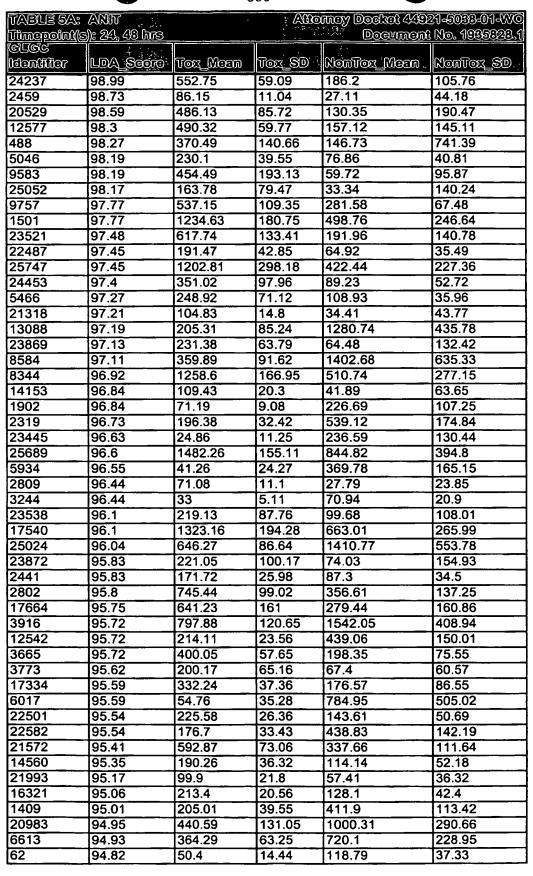
1723D	TABUE 8				Attorney Doctet 44.621-5038-011W0
් ලිලේ (ව	SE S	<u>ලෙකෑනෙ</u> /\se ග් Re(Seg ID	is to the first	Human Homologous Known Gene Neme	ran Homologous) Van Gene Neine Human Homologous Scquence Gluster Tittle
2712	3617	AI236021	۵۵		X-box binding protein 1
			A, B, General		
			Core Tox		X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound, membrane-bound
3888	12331	NM_057155 Markers	Markers		aminopeptidase P
			General Core		X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound, membrane-bound
3888	12332	NM_057155 Tox Markers	Tox Markers		aminopeptidase P
1259	4032	AI007875	Z, AA		X-ray repair complementing defective repair in Chinese hamster cells 1
1637	9069	AI059403	000		YY1 associated factor 2
2098	16102	AI171586	В, Н		zinc finger protein 259
1200	1201	AB000929	۵		zona pellucida glycoprotein 2, zona pellucida glycoprotein 2 (sperm receptor)
					ZW10 homolog (Drosophila), centromere/kinetochore protein, ZW10 homolog,
2492	14662	AI230413	Z, AA		centromere/kinetochore protein (Drosophila)
L.			G, H, X, Y,		
			GGG, HHH,		
			LLL, SSS,		
		- - .	UUU, General		
			Core Tox		
4033	4033 6824	NM_147138 Markers	Markers		ZW10 interactor

	-857-	
3		Afformay Dox
	-	
		100000000000000000000000000000000000000

TABLE 4: MODEL CODES		Wenney A	Docker 44921	<u> </u>
				lo. 1935328.1
Model	Model Type	Vilinepoint ((hrs))	Model Mode	
			Core Tox	
ANIT	Single Compound	24,48	Markers	Α
ANIT	Single Compound	24,48	Alternate	B
			Core Tox	
2-A35AAF	Single Compound	6	Markers	C
			Core Tox	_
ACYCLOVIR	Single Compound	24,168	Markers	D
	1		Core Tox	
ACYCLOVIR	Single Compound	6	Markers	E
			Core Tox	
2-AAF	Single Compound	24,48	Markers	F
			Core Tox	
APAP	Single Compound	24	Markers	G
APAP	Single Compound	24	Alternate	H
·			Core Tox	
APAP	Single Compound	3,6	Markers	<u>l</u>
APAP	Single Compound	3,6	Alternate	J _
			Core Tox	
AY-25329	Single Compound	24	Markers	K
			Core Tox	
AY-25329	Single Compound	6	Markers	L
			Core Tox	
BI-Liver Toxin	Single Compound	168,336	Markers	М
			Core Tox	
BICALUTAMIDE	Single Compound	6,24,168	Markers	N
			Core Tox	
CCL4	Single Compound	24,48	Markers	0
CCL4	Single Compound	24,48	Alternate	Р
			Core Tox	
CCL4	Single Compound	3,6	Markers	Q
CCL4	Single Compound	3,6	Alternate	R
			Core Tox	l
Chloroform	Single Compound	6,24	Markers	s
		 	Core Tox	
CI-1000	Single Compound	6	Markers	lτ
			Core Tox	<u> </u>
CLOFIBRATE	Single Compound	24,72	Markers	lu
			Core Tox	
Colchicine	Single Compound	24,48	Markers	V
			Core Tox	
Colchicine	Single Compound	6	Markers	lw
			Core Tox	
CPA	Single Compound	24,120	Markers	×
CPA	Single Compound	24,120	Alternate	Ŷ
	g.c Joinpould	,	Core Tox	
CPA	Single Compound	6	Markers	z
CPA	Single Compound	6	Alternate	ĀĀ
	- Ingio Compound		Core Tox	
DICLOFENAC	Single Compound	24	Markers	вв
DICLOFENAC	Single Compound	24	Alternate	CC

	-036-			
	· The . The house		Docket 44921 Document K	-5033-01-WO o. 1935323.1
Model	Model Typo	intogenitu]	Model Mode	Model Code
			Core Tox	
DICLOFENAC	Single Compound	3,6	Markers	DD
DICLOFENAC	Single Compound	3,6	Alternate	EE
			Core Tox	
DIFLUNISAL	Single Compound	24	Markers	FF
· · · · · · · · · · · · · · · · · · ·			Core Tox	
DIOXIN	Single Compound	168	Markers	lgg
			Core Tox	<u> </u>
DIOXIN	Single Compound	6,24	Markers	НН
			Core Tox	
DMN	Single Compound	6,24	Markers	ļu
			Core Tox	
ESTRADIOL	Single Compound	24,240	Markers	JJ
ESTRADIOL	Single Compound	24,240	Alternate	KK
		 	Core Tox	
Gemfibrozil	Single Compound	24,168	Markers	LL
			Core Tox	
HYDRAZINE	Single Compound	3,6,24	Markers	мм
			Core Tox	
INDOMETHACIN	Single Compound	48,72	Markers	NN
INDOMETHACIN	Single Compound	48,72	Alternate	00
		† · · · · · · · · · · · · · · · · · · ·	Core Tox	
INDOMETHACIN	Single Compound	6,24	Markers	PP
INDOMETHACIN	Single Compound	6,24	Alternate	QQ
		†	Core Tox	
Menadione	Single Compound	24	Markers	RR
-			Core Tox	
Menadione	Single Compound	3,6	Markers	ss
			Core Tox	
PHENOBARBITAL	Single Compound	24,48	Markers	TT
			Core Tox	
TACRINE	Single Compound	6	Markers	UU
			Core Tox	
Thioacetamide	Single Compound	24,48	Markers	 VV
			Core Tox	
Thioacetamide	Single Compound	6	Markers	ww
			Core Tox	
VALPROATE	Single Compound	24,96	Markers	XX
VALPROATE	Single Compound	24,96	Alternate	YY
			Core Tox	
VALPROATE	Single Compound	6	Markers	ZZ
VALPROATE	Single Compound	6	Alternate	AAA
	· ·		Core Tox	l
WY-14643	Single Compound	24,168	Markers	BBB
WY-14643	Single Compound	24,168	Alternate	CCC
			Core Tox	
ZILEUTON	Single Compound	24,336	Markers	DDD
			Core Tox	
LPS	Single Compound	24	Markers	EEE
		1. .	Core Tox	
Carcinogen - Genotoxic	Multiple Compound	Various	Markers	FFF

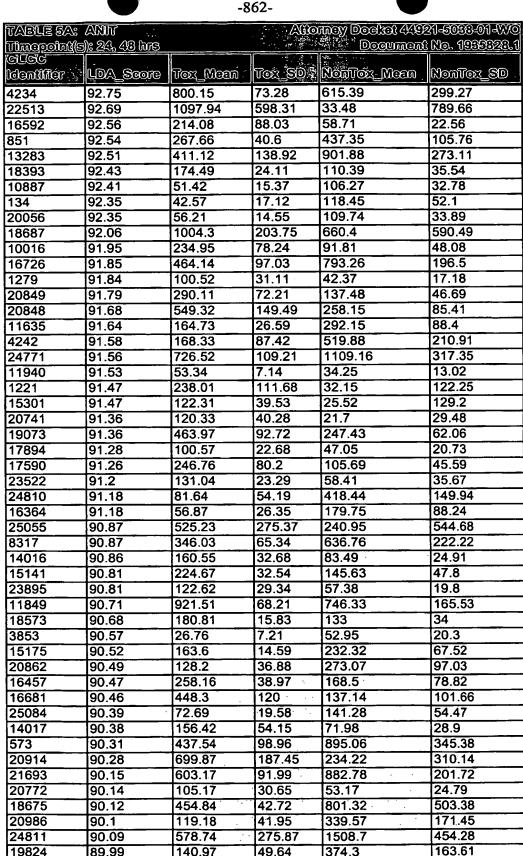
TABLE 4: MODEL CODES		AGOMEY	Dockel 44921 Document K	-5033-01-WO o. 1935323.1
Model :	Model Type	Mingeomit (End))	Model Mode	
Carcinogen - Non-Genotoxic	Multiple Compound	Various	Core Tox Markers	GGG
Cholestasis	Multiple Compound	Various	Core Tox Markers	ннн
Hepatitis	Multiple Compound	Various	Core Tox Markers	111
Hepatitis	Multiple Compound	Various	Alternate Core Tox	717
Human-specific	Multiple Compound	Various	Markers	ккк
Inducer and Liver Enlargement	Multiple Compound	Various	Core Tox Markers	LLL
Inflammation	Multiple Compound	Various	Core Tox Markers	ммм
Mixed Phenotype	Multiple Compound	Various	Core Tox Markers	NNN
Necrosis	Multiple Compound	Various	Core Tox Markers	000
Necrosis and Steatosis	Multiple Compound	Various	Core Tox Markers	PPP
Necrosis and Steatosis	Multiple Compound	Various	Alternate	QQQ
Peroxisome Proliferator	Multiple Compound	Various	Core Tox Markers	RRR
Rat-specific Carcinogen - Non- Genotoxic	Multiple Compound	Various	Core Tox Markers	SSS
Steatosis	Multiple Compound	Various	Core Tox Markers	ТТТ
Rat-specific	Multiple Compound	Various	Core Tox Markers	บบบ
			Core Tox	General Core Tox
Cross-species	General Hepatotoxicity	Various	Markers	Markers
Cross-species	General Hepatotoxicity	Various	Alternate	General Alternate





)): 24, 43 hrs		.3.	nney Docket 449 Document	
ldendifier 🔄	LDA_Score	Tox_Moen.		MEEM TEOLUGY	Roniox_S
12331	94.77	96.21	34.92	329.07	129.02
20891	94.77	222.12	39.38	105.73	53.58
2569	94.72	283.21	98.85	910.74	287.92
18902	94.69	348.23	36.04	207.64	68.65
10363	94.66	125.62	16.92	223.36	61.18
22413	94.64	1042.17	247.16	426.57	245.01
1246	94.64	21.33	9.13	78.41	30.25
8549	94.61	249.65	51.25	663.93	226.14
19712	94.56	58.27	14.39	140.93	49.49
6585	94.56	148.05	59.78	56.41	73.31
15372	94.53	298.67	45.21	182.61	54.97
25567	94.5	287.31	67.85	144.5	141.52
9150	94.48	765.05	74.86	542.38	139.66
6072	94.34	1123.87	157.59	1865.56	459.23
17507	94.34	653.29	69.84	426.71	114.42
9842	94.32	932.29	145.79	1605.99	413.18
19363	94.24	335.33	156.81	1903.78	901.87
3191	94.21	460.97	69.65	288.06	117.53
2799	94.21	124.02	33.41	493.85	224.72
20299	94.18	275.82	63.75	727.54	248.68
18315	94.08	111.16	28.31	46.38	38.06
			114.92	1508.71	396.35
6015	94.05	838.88	77.83	693.81	285.32
9191	94.03	199.23			
22005	94.03	166.87	42.15	71.94	46.17
11608	94	42.31	7.96	20.84	11.8
20502	93.97	1646.55	356.92	3230.99	912.05
7697	93.95	191.93	44.06	452.46	149.81
1562	93.89	472.76	94.52	883.41	225.53
9029	93.81	626.36	94.46	378.51	189.03
5899	93.76	640.44	154.51	1218.47	346.05
6403	93.76	112.12	25.49	59.08	28.84
16883	93.68	1388.39	131.94	2056.29	532.88
25479	93.6	870.55	66.41	1191.63	285.25
16993	93.57	548.16	138.45	1060.21	295.06
13294	93.55	547.53	69.75	347.35	106.73
1447	93.49	346.96	28.7	240.68	59.95
3755	93.47	261.07	39.71	146.88	162.03
15028	93.44	1069.77	84.48	1751.57	516.3
9016	93.31	1162.4	234.21	2638.32	991.62
22234	93.31	71.97	17.32	178.27	75.7
17688	93.31	96.81	18.02	55.85	29.66
15551	93.28	234.44	17.57	327.59	67.42
16625	93.28	498.4	50.08	345.84	83.51
16370	93.18	104.88	40.52	308.46	129.52
10310	93.18	406.77	47.19	264.53	84.75
15042	93.17	284.8	88.21	33.91	59.77
11164	93.17	222.25	38.73	500.62	201.04
the state of the s			59.13	481.7	150.93
4914	93.12	242.21			222.78
548	92.96	81.78	39.86	400.34	
20350	92.96	137.74	20.15	236.93	65.42
1475	92.88	193.91	103.16	83.12	266.04

59.85



214.28

18316

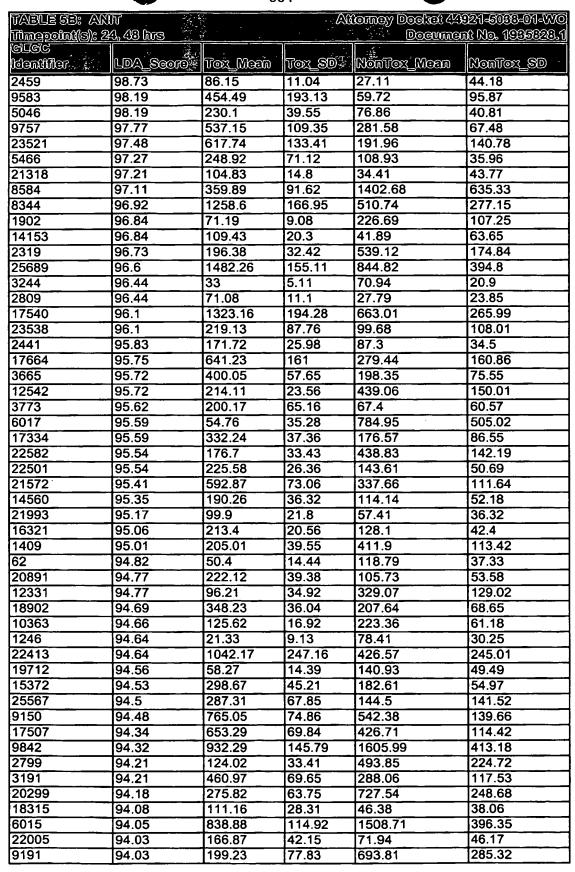
89.96

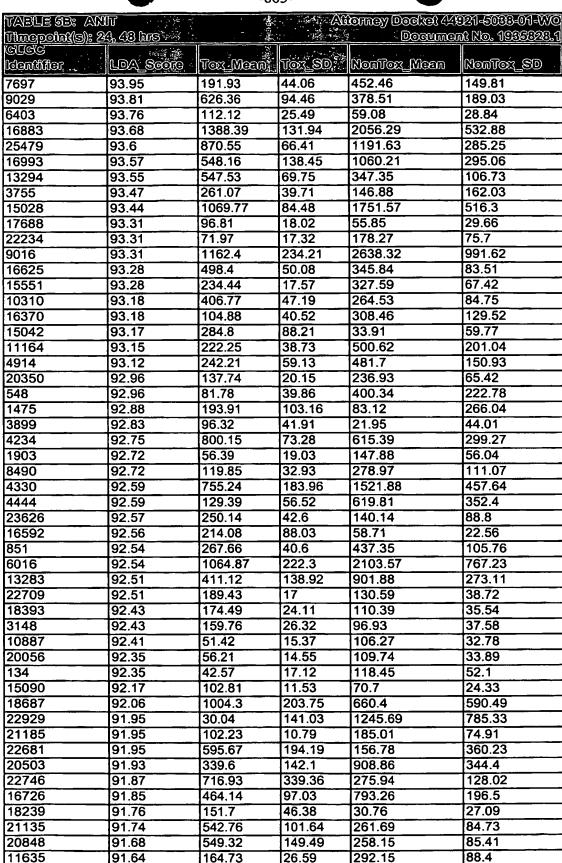
53.79

73.62



TABLE JA: Timopolnas			Affe	may Docket 449 Document	21-5033-01-W© No. 1935023.1
[G] [G] C	- 1,014	Tox_Meen	Tox_SD	Meeny_xolnom	NonTox_SD :
25467	89.94	111.59	66.67	368.48	173.35
3404	89.85	203.83	33.04	126.96	43.38
24767	89.85	250.13	58.48	113.77	45.71
18727	89.8	984.02	129.49	762.82	383.67
3424	89.8	54.38	8.67	34.22	15.48
4450	89.78	105.92	32.55	197.38	61.02
14959	89.78	701.59	85.62	537.61	175.22
23868	89.77	831.02	335.24	233.04	687.83





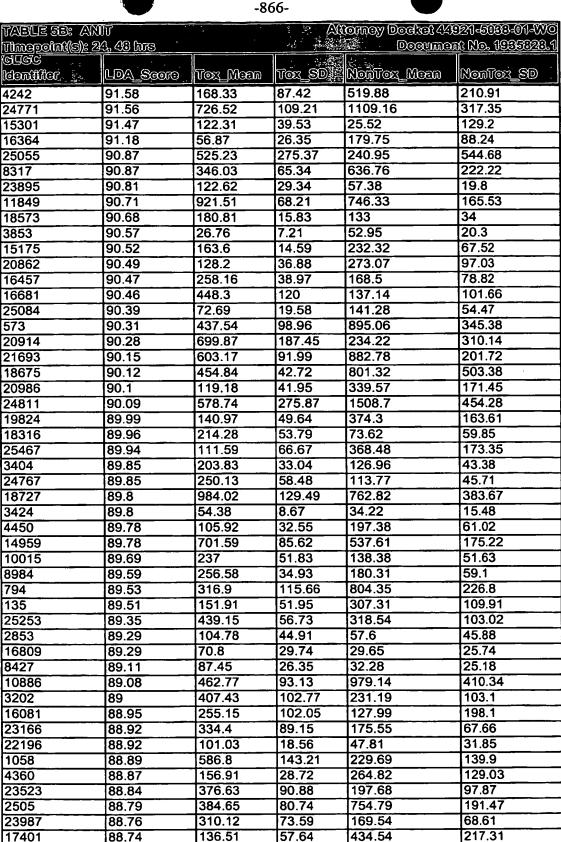
23417

15925

88.68

88.64





229.37

360.92

46.07

21.75

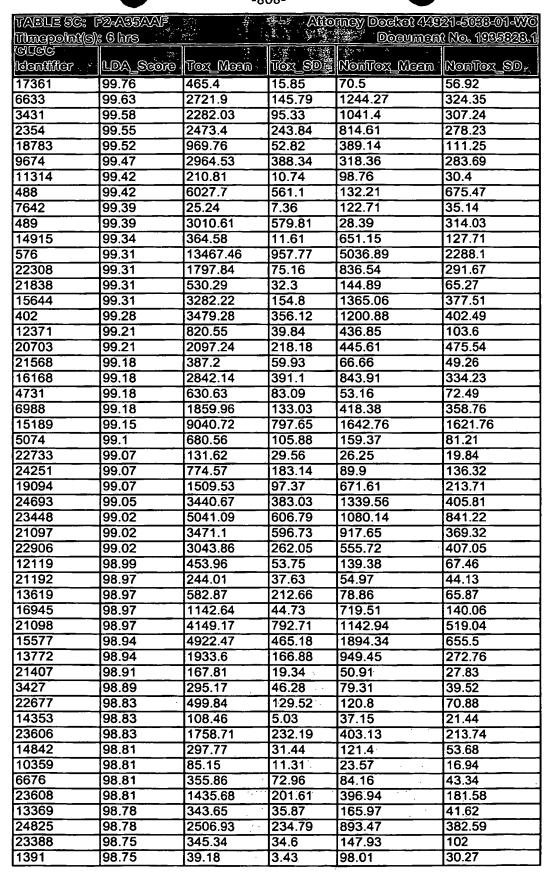
366.68

230.14

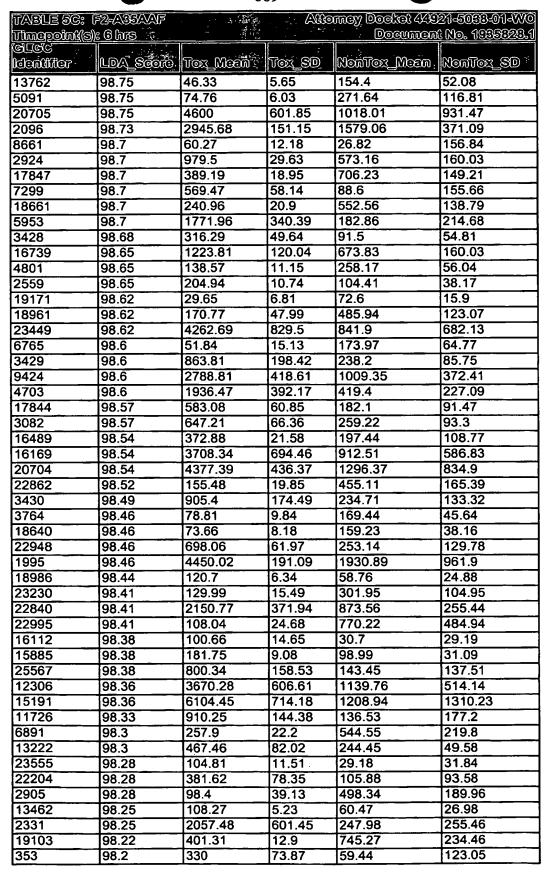
72.26

152.39

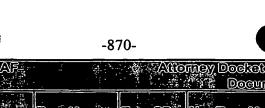
TABLESB: AXI Timopoin((s)): 2			. Au	enney Docket 449 Documen	921-5063-01-WO M No. 1935628.1
(e)[[e](c)	LDV Z	Tox_Meen			NonTox_SD :
820	88.5	1406.57	132.95	2101.86	665.57
13647	88.47	1553.38	170.97	1019.81	337.66
811	88.31	404.42	69.59	677.51	148.23
17613	88.23	489.47	69.01	306.16	126.07
18686	88.18	1174.3	178.47	705.85	614.14
21066	88.12	90.2	8.32	59.32	19.24
12087	88	689.77	141.68	1028.9	314.22
24219	88	519.04	78.12	380.22	189.11
19825	88	137.46	61.65	356.04	162.35
10509	87.99	24.56	33.79	139.01	53.7
9621	87.84	356.7	47.85	281.34	81.86
24597	87.83	433.97	80.84	254.9	98.22







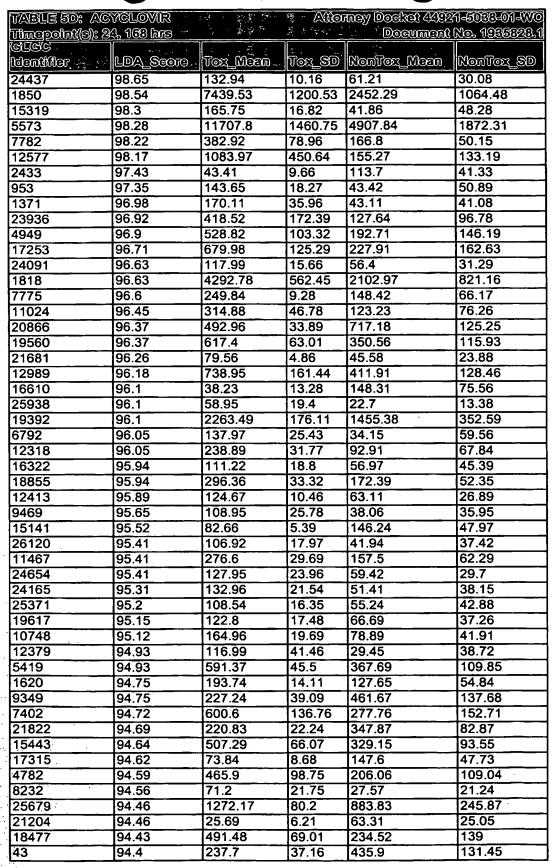




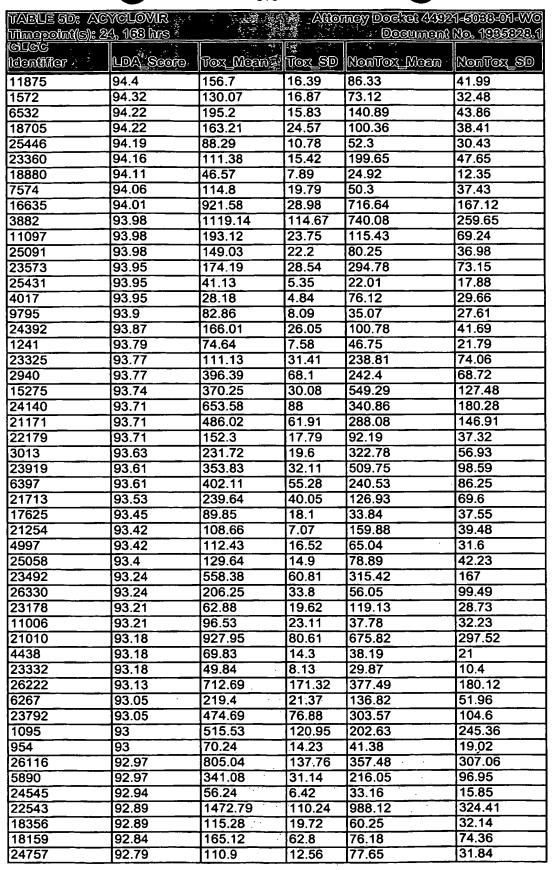
1/C11/C1/C	<u> </u>			Dogumen	21-5053-01-WO } No. 1935323,1
GEGG Man	LDA Score	Tox_Mean	Tox_SD:	Now Loss Wester	NonTox_SD
9254	98.07	76.91	12.28	183.99	48.15
355	98.04	191.66	29.67	64.68	37.89
8641	98.01	599.23	44.21	221.07	143.09
25284	97.88	106.74	33.48	36.04	36.55
15190	97.88	8422.33	1226.76	1823.47	1684.19
24204	97.75	147.09	19.64	71.88	19.82
354	97.59	377.35	126.64	81.44	151.82
15462	97.59	365.31	12.52	545.84	120.22
11611	97.54	85.4	3.78	151.89	45.52
1920	97.54	1321.53	174.27	439.98	267.69
21707	97.54	330.22	116.74	40.53	50.49
15642	97.48	789.63	109.72	375.46	159.27
351	97.46	123.9	50.73	21.95	52.72
21063	97.43	108.69	12.97	45.97	23.01
24284	97.43	89.1	22.22	30.54	16.02
16167	97.35	56.24	14.28	20.57	10.19
20826	97.35	95.36	11.37	220.81	69.9
15755	97.32	400.8	35.16	741.3	180.52
16450	97.32	127.65	5.05	249.03	92.1
14956	97.24	156.58	22.76	67.47	29.39
20744	97.22	1465.02	266.9	345.62	298.71
23321	97.11	154.57	8.99	238.22	65.16
2480	97.01	132.09	6.03	235.55	74.18
19085	96.98	199.82	21.43	86.52	46.2
1876	96.95	477.08	19.96	774.36	202.87
10544	96.93	303.76	19.68	179.51	71.34
1521	96.93	396.47	85.1	151.07	75.31
24161	96.93	256.17	14.6	460.56	124.42
17448	96.9	94.48	3.93	54.09	36.86
2727	96.79	34.54	4.68	89.98	57.66
64	96.66	54.97	9.05	134.71	44.08
17108	96.56	83.1	10.81	156.26	38.92
16362	96.56	29.38	5.67	68.14	21.64
1602	96.56	266.42	25.42	467.04	109.06
20750	96.53	104.81	5.33	165.33	49.28
17807	96.53	3744.42	281.96	2043.09	724.62
1607	96.53	21.01	6.24	57.63	21.56
18897	96.53	44.4 ,	11.48	122.52	46.47
19086	96.53	295.45	38.01	121.95	69.5
15996	96.5	154.51	10.49	108.43	137.77
	96.48	401.96	37.45	217.75	88.4
	96.37	20.27	9.78	73.45	28.57
	96.37	65.45	3.94	118.09	33.49
	96.32	897.02	68	581.9	129.53
	96.29	928.18	500.92	109.71	256.24
	96.24	113.09	7.92	61.18	28.86
	96.21	2006.24	1054.73	217.61	424.3
	96.21	2061.18	139.61	1253.28	378.26
	96.21	151.89	11.96	83.46	31.1
	96.18	57.15	3.78	30.41	15.51
	96.13	86.01	12.91	39	20.84

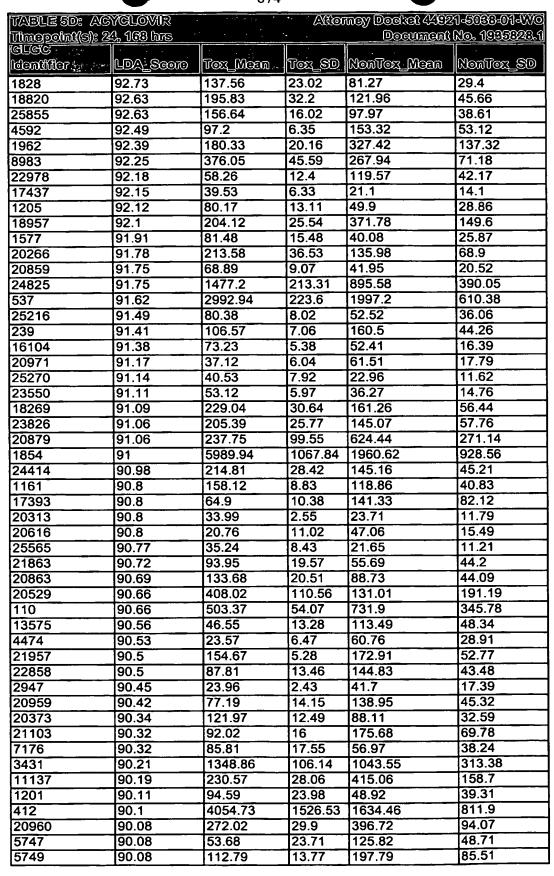
5000 E 600 00	valavie :	Torris Charles	5.55 - "N(X)	ncy Docket 4492	1.5000.01.100
TABLE 5D: AC Timogoin((s)): 2		10		Document	
		71 - 72 - 72	- 100 to	- Executive of the second of t	
ldendifier	LDA Seoto		JOX SD	NonTox_Mean	MonTox_SD
19900	90.08	136.38	14.08	98.21	28.18
25513	90.08	731.9	39.49	575.78	213.73
16165	90.05	45.74	6.02	29.35	11.29
10098	90.05	41.51	5.18	68.56	21.67
21051	90	84.29	10.88	169.02	87.64
20615	89.97	41.16	9.96	84.15	29.66
17535	89.95	92.08	9.61	151.64	51.7
25060	89.95	64.18	7.94	30.95	26
15791	89.92	158.14	27.64	101.53	78.26
7226	89.87	25.49	7.91	66.44	31.22
699	89.86	1045.91	208.34	610.13	156.14
12423	89.81	103.4	15.44	168.78	72.48
5666	89.73	55.55	15.61	97.65	30.58
25350	89.71	42.92	5.54	28.71	14.66
25930	89.71	34.55	5.77	22.05	10.16
1731	89.68	53.64	5.68	83.97	30.8

TABLE 60: F2-A35AAF Afformay Docket 44921-5063-01-WO					
Timegeint(s)			\$ 18 miles		<u> 2 (No. 1985923.1</u>
(G) CC(C			J. G. Š		
ldendifer	LDV Zecto	LOX [NOON]	Tox_SD :	MEEM_XOTAON	NonTex_SD
20902	96.08	54.98	6.13	108.3	36.68
18713	96.05	575.2	47.7	332.73	111.84
15558	96.03	533.62	64.05	309.56	116.77
12996	96	153.56	22.85	316.24	136.38
14957	95.84	237.18	39.21	126.07	46.49
357	95.84	153.81	26.35	74.2	34.31
19018	95.81	176.71	22.9	356.97	119.04
2435	95.81	242.07	6.34	189.05	46.62
20745	95.81	236.14	4.13	308.75	84.22
23949	95.76	57.07	2.28	40.34	13.2
17123	95.73	162.76	7.62	108.56	36.69
23491	95.73	48.95	12.12	140.25	66.72
12485	95.73	95.61	14.66	39.24	23.66
9952	95.6	302.46	19.52	194.72	53.2
20597	95.6	3322.9	273.36	1846.93	665.77
24577	95.57	1467.77	128.16	908.77	231.99









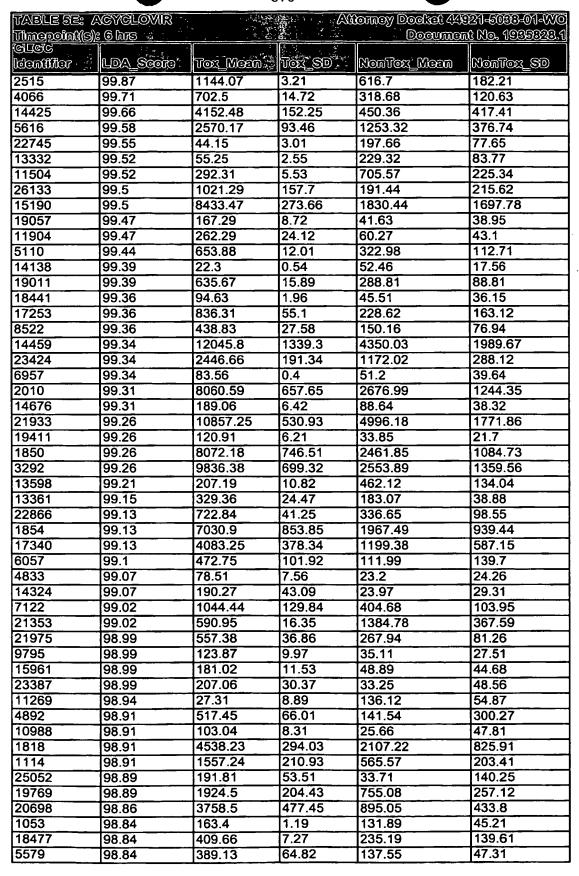






TABLE SE: A	CYCLOVIR	44	A	omey Docket 449	21-5033-01-WO
Three sources	EM 8	<u> </u>	6		(No. 1985323.1
CLCC (dondffer	LDA_Score	Tox_Meen	Tox_SD	NOOTOX_NOOTOON	NonToz_SD .
21740	98.84	2272.65	286.88	736.34	295.24
4904	98.81	1015.24	22.26	575.81	199.2
25290	98.81	224.01	20.84	50.46	74.59
21242	98.78	181.55	6.32	389.85	129.26
4274	98.76	571.79	62.71	267.12	80.09
13480	98.76	342.7	21.43	728.43	183.37
412	98.73	3290.22	187.08	1640.8	826.12
26368	98.73	115.98	0.54	160.52	113.24
402	98.73	2683.6	204.1	1204.56	415.08
9669	98.7	83.77	2.19	48.68	22.92
15094	98.7	224.06	23.05	88.9	37.46
9527	98.7	78.99	3.4	236.15	129.31
19064	98.7	284.38	16.82	159.62	44.27
3268	98.7	310.57	12.76	158.54	48.48
20524	98.68	224.04	58.85	23.35	47.45
10695	98.65	558.14	65.92	253	154.76
2304	98.65	404.56	15.67	221.82	85.74
24374	98.65	481.1	98.37	122.3	75.36
21310	98.62	293.66	20.94	118.39	79.64
15189	98.62	9903.79	1520.73	1649.22	1631.77
4199	98.6	1568.46	103.75	891.14	203.93
8053	98.6	127.84	0.53	173.34	101.01
17039	98.6	73.85	0.55	108.8	32.11
21564	98.57	161.83	1.88	241.1	44.62
20701	98.57	2765.01	300.14	880.19	387.19
18581	98.54	1060.08	64.13	583.75	157.39
17950	98.54	268.48	37.07	107.03	40.18
21446	98.54	85.24	0.44	103.22	34.05
6547	98.54	768.52	78.09	253.04	199.16
20354	98.54	437.67	64.63	51.75	57.48
20699	98.52	4872.96	438.32	2130.27	820.77
3467	98.52	42.97	3.79	126.09	53.01
12142	98.52	1579.83	43.54	910.2	278.22
4026	98.52	914.06	118.53	373.41	130.85
24200	98.52	1653.04	218.48	438.39	248.23
1159	98.49	87.49	16.35	275.08	107.4
13305	98.49	63.56	13.97	268.13	99.69
7451	98.49	2799.51	426.88	1138.17	304.14
21917	98.49	479.47	138.76	74.58	63.83
7318	98.49	27.05	0.27	26.03	44.21
3773	98.49	344.19	42.84	67.6	60.3
15191	98.46	7522.56	1192.86	1211.88	1309.42
19052	98.46	674.46	97.73	266.82	79.31
7736	98.44	30.14	4.35	99.18	38.67
18687	98.44	445.98	3.15	662.38	590.11
24211	98.41	122.68	5.08	277.05	108.57
169	98.41	237.82	32.93	84.07	35.94
10944	98.41	64.49	1.97	29.83	30.56
6056	98.41	51.55	0.98	22.01	53.36
15151	98.39	34	2.9	67.72	18.49
3131	98.33	323.3	4.01	436.11	155.15

TABLE SE: A		21- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1- 1		omey Docket 449	121-5033-01-WO 11 No. 1985323.1
	<u> </u>	<u> </u>		- Accelivitiv] [
	LDA_Score :	Tox:Moón	Tox_SD - ·	NonTox_Mean	NonTox_SD
5622	98.31	2803.59	276.46	1593.53	374.33
20313	98.28	43.64	1.34	23.71	11.76
22515	98.28	781.48	262.01	128.68	396.37
1809	98.28	310.57	124.78	135.11	741.7
9369	98.28	454.59	24.36	205.98	92.12
22513	98.25	2024.79	1015.66	35.39	788.1
18795	98.23	1052.33	44.11	541.08	204.55
25317	98.2	3169.06	371.09	1382.21	465.22
23368	98.2	20.29	2.72	76.21	35.32
20088	98.2	86.53	4.33	167.12	48.51
20090	98.2	325.25	97.77	109.24	41.45
1561	98.09	1597.16	175.74	871.83	221.15
15378	98.07	25.66	13.82	119.02	37.81
18597	97.99	452.82	3.45	605.52	200.99
1354	97.96	61.13	5.66	262.53	221.68
16564	97.96	512.39	78.58	215.32	84.22
14139	97.94	21.62	1.48	52.8	18.28
17589	97.94	154.28	25.6	33.41	33.9
23561	97.94	143.78	4.87	82.16	29.25
20529	97.88	636.99	164.61	131.24	190.69
1221	97.72	421.99	139.65	32.51	122.03
24860	97.72	291.72	3.23	390.7	272.94
1844	97.72	314.48	62.82	114.83	63.86
16562	97.7	502.07	109.41	205.9	72.48
16132	97.67	6910.51	137.1	3399.35	2221.37
21663	97.64	163.18	37.08	467.03	159.4
6477	97.64	4953.15	635.28	2260.24	859.45
20168	97.59	262.41	109.62	53.14	74.98
15134	97.54	398.07	26.44	736.12	183.35
19703	97.49	36.01	12.17	111.4	38.69
16080	97.49	218.9	76.7	71.37	143.14
25520	97.49	131.85	2.21	100.64	40.44
20700	97.46	7780.24	1061.32	2936.46	1587.23
13164	97.43	9474.57	689.84	3784.84	2461.92
9905	97.43	405.22	24.17	647.49	151.36
23491	97.41	48.52	7.81	140.16	66.75
1798	97.38	5998.85	389.31	2791.58	1330.94
17709	97.38	139.77	20.06	37.95	42.38
25797	97.38	61.12	6.48	28.61	21.9
15703	97.33	257.65	15.7	133.5	50.58
24228	97.3	1472.31	59.23	978.47	263.43
21980	97.27	1042.81	153.04	505.29	161.45
25567	97.17	173.36	4.43	145.14	141.7
699	97.17	1043.85	148.55	611.05	157.63
6478	97.14	8793.2	1557.95	3227.07	1789.85
730	97.11	25.99	0.68	46.47	36.75
4397	97.09	61.13	3.3	33.02	17.06
17468	97.06	380.46	12.17	562.15	116.39
18644	97.04	3730.28	140.75	2174.68	809.71
16305	96.93	549.44	65.09	1145.99	358.8
1521	96.9	396.76	84.68	151.33	75.74

TABLE SE: A	VCYCLOVIR		e Au	iomay Docket 449	21-5033-01-WO
Timepoint(s)			7.0		l No. 1995929.1
CLCC ldomilier	LDV Seore	Tox Moan #	Tox SD	NonTox_Mean	NonToz_SD:
5545	96.9	2504.37	135.61	1488.19	573.11
25747	96.9	721.3	98.79	425.68	233.76
17590	96.85	248.74	79.09	106.14	46.42
1583	96.77	52.3	5.92	28.62	14.14
17563	96.72	2590.83	193.84	1607.6	436.46
12848	96.69	86.03	9.48	194.04	65.28
9240	96.56	227.42	7.18	338.5	82.66
25041	96.53	45.23	1.14	101.87	66.17
20778	96.53	38.89	4.82	74.1	18.65
15613	96.53	482.03	28.45	1181.46	811.46
12312	96.53	350.33	106.28	973.18	267.1
17157	96.53	53.77	8.13	23.37	16.88
23949	96.53	75.43	9.76	40.33	13.15
21707	96.51	183.37	73.24	41.07	52.53
548	96.51	53.6	25.79	399.37	223.1
16081	96.51	318.63	127.02	128.29	197.9

TABLE SF: 2 Timepoin((s)):		en grad	Acco	mey Docket 449f Document	21-5033-01-WO No. 1935323.1
(GEGC	LDA Score	Tox Mean	Tox SD	NonTox Mean	NonTox SD
10611	99.47	363.63	98.16	23.36	34.41
17541	99.28	5057.19	615.94	1614.18	595.31
17097	98.73	213.97	24.02	66.58	45.79
7324	98.41	524.02	190.61	91.83	80.77
25705	98.41	1888.73	455.8	737.95	180.35
18445	98.38	612.92	368.87	186.97	63.66
21275	98.11	589.96	154.23	204.39	89.27
20755	98.04	376.4	218.11	54.36	58.29
20757	97.98	940.29	301.2	271.71	121.46
17474	97.85	501.14	128.44	197.27	54.31
8638	97.61	381.87	111.31	204.32	43.63
20915	97.5	1993.24	509.86	528.47	351.25
6344	97.42	105.03	33.93	39.25	21.1
17239	97	765.95	119.46	447.2	100.85
18726	97	152.74	19.37	363.54	114.88
11324	96.79	142.32	27.99	320.89	95.7
22677	96.76	271.76	111.37	121.08	72.74
18989	96.68	3106.24	554.98	1470.05	682.57
20867	96.52	552.43	66.7	327.43	75.39
21013	96.42	5732.48	728.09	2600.22	1200.14
12700	96.39	513.97	181.51	1374.12	410.69
23035	96.18	219.87	57.58	622.4	217.65
1562	96.18	364.5	89.44	883.93	224.47
15366	96.04	1224.68	131.98	845.37	146.49
8213	95.78	7294.78	1359.3	3424.5	1369.31
4268	95.65	873.06	83.51	482.67	185.97
10498	95.65	2112.71	211.88	1355.31	307.99
16123	95.54	21.98	4.22	82.89	68.35
18725	95.43	74.32	18.61	215.35	84.88
17100	95.35	1311.34	145.25	854.84	192.39
7524	95.3	899.76	122.53	574.07	163.52
18846	95.27	238.88	26.19	160.96	34.63
22051	95.27	295.3	36.19	154.8	65.27
11635	95.25	124.9	23.96	292.35	88.09
12306	95.14	353.02	127.81	1150.24	528.73
11954	94.77	2749.1	383.91	1701.87	479.59
5923	94.64	111.72	15.22	222.33	75.1
24359	94.61	177.24	32.92	98.57	37.57
4084	94.48	324.05	36.14	193.19	63.84
3496	94.4	175.6	15.41	103.45	39.7
7872	94.37	183.73	15.68	294.36	82.2
20807	94.26	1294.76	131.56	908.21	210.95
7208	94.13	448.27	25.87	653.67	153.76
26117	94.08	343.68	36.04	258.54	309.43
3167	94.08	436.32	30.55	276.79	105.19
2481	94.03	70.55	6.74	144.33	60.72
18430	93.95	35.25	6.58	76.24	27.02
12629	93.84	31.74	10.56	86.43	33.2
2725	93.81	215.82	22.77	79.66	98.99
7219	93.79	673.4	85.14	1084.53	245.06
3917	93.73	2451.68	254.31	1580.15	508.47

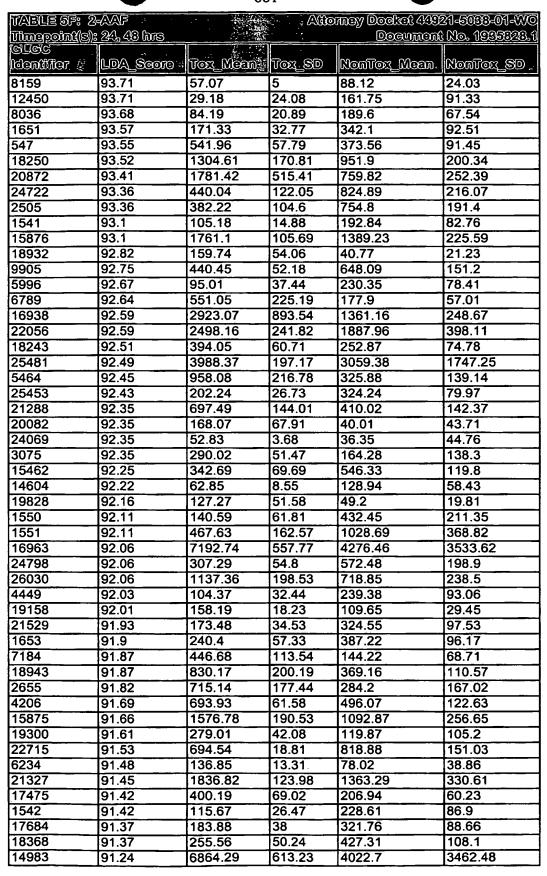


TABLE SF: 2			AGO	may Pocket 449	21-5033-01-WO
Timepoint(s):	24, 48 hrs		デジュー (1)	Document	: No. 1935323.1
ldomilier 🕌	LDA_Score	Tox_Meen	Tox_SD.		KonTox_SD
21011	91.2	5198.1	676.85	2347.81	1049.52
958	91.05	160.75	31.99	300.44	137.39
18724	90.95	215.7	48.15	425.56	146.34
16130	90.92	6035.7	494.5	3520.51	2335.7
764	90.92	46.13	13.87	100.61	38.26
17729	90.81	1338.1	141.59	920.81	211.35
17227	90.81	2318.08	216.99	1689.68	380.05
16320	90.71	50.4	11.67	99.79	32.5
1286	90.6	78.18	7.49	113.15	28.14
20832	90.55	562.04	80.75	356.5	128.9
11662	90.52	71.84	14.6	46.42	17.15
20994	90.49	182.15	33.76	97.27	31.41
21152	90.49	5511.74	443.57	3584.64	2477.89
8212	90.43	4309.1	1259.78	1969.91	710.55
24886	90.3	1725.7	158.64	1194.97	295.55
15492	90.28	167.02	14.68	297.14	115.18
1888	90.25	106.73	45.17	32.04	34.65
20839	90.25	1638.02	196.58	1132.82	215.17
255	90.25	304.25	47.35	462.3	125.07
2667	90.18	549.88	84.49	809.45	200.69
20865	90.1	24.25	13.73	90.1	95.26
6525	90.09	976.57	244.81	596.19	127.83
20429	90.04	230.98	93.85	626.27	260.17
1175	90.04	262.96	73.75	632.32	348.17
4198	89.96	787.82	72.47	1092.13	232.15
695	89.94	53.51	4.24	31.99	33.19
15626	89.93	1942.21	311.08	1328.22	250.13
21015	89.9	5258.26	551.43	2916.11	1039.43
575	89.88	490.74	134.07	907.33	309.68
20507	89.78 89.72	40.88	5.8 11.19	62.65	28.58
21305		99.49		160.04	64.71
4407 19952	89.7	78.85	10.44	144.37 127.66	57.75 51.76
24885	89.64	61.82	13.87		
	89.48	1395.22	230.59 153.23	891.7	189.42
1694 2696	89.43 89.43	1375.56 1018.77	164.73	1074.39 618.44	235.35 159.27
15850	89.4	1350.25	856.98	1238.02	294.94
17891	89.38	35.38	1.44	40.2	11.58
16918	89.37	1992.68	249.11	1268.47	366.85
24648	89.3	59.74	8.75	93.09	28.61
15468	89.27	1106.62	106.55	802.42	153.53
12365	89.25	617.12	46.17	800.73	149.11
18906	89.19	39.57	10.06	81.71	36.35
6109	89.09	5349.68	544.1	3580.97	2268.22
15201	89.03	2311.38	238.42	1589.31	329.09
4199	88.87	670.62	72.81	893.27	205.43
4242	88.87	113.57	73.69	520.14	210.47
4213	88.87	7593.34	881.96	4452.18	3874.69
15380	88.76	1643.87	301.54	810.83	357.11
20430	88.74	293.51	139.83	826.71	378.78
11955	88.71	1573.75	309.05	1034.07	261.95

-883-

TABLE 57: 2-AAF Thagoin((s)): 24, 43 hrs			Attorney Docket 44921-5033-01-440 Document No. 1935323.1		
[c]	LDA_Score	Tox_Meem	Tox_SD	Moniox Ween,	NonTox_SD
24577	88.71	1464.15	269.95	907.6	230.25
				1 • • • • • • • • • • • • • • • • • • •	
20057	88.69	74.6	19.11	140.47	55.04
20057 110	88.69 88.69	74.6 306.62		140.47 733.09	

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TABLE 5©: [:	VP(NP			omay Docket 449	81490505015060 81490505015060
vimepoint(S):				Dogumen	<u>((No. 1985328.1</u>
G C C C			G 669	Moniox Mean	HonTox_SD
dentifier -	LDA_Scoro	Tox_Meen	Tox_SD		
20818	99.44	681.68	396.76	58.76	50.48
21051	99.42	25.82	5.72	169.47	87.24
20817	99.42	1097.61	584.9	33.94	96.13
16958	99.26	163.73	20.5	46.79	20.77
14970	99.18	56.14	7.65	184.72	40.93
14960	99.12	3029.21	292.61	1295.98	395.82
14512	99.07	240.92	30.64	1059.86	373.66
8898	99.04	324.05	39.69	812.17	179.92
17090	99.04	205.95	36.94	58.19	25.45
8592	98.99	99.79	15.85	378.1	131.56
15462	98.86	241.96	32.59	546.98	118.67
25675	98.86	1595.4	148.8	737.99	198.87
12524	98.83	858.06	70.36	390.39	107.38
9134	98.8	977.58	104.07	470.65	100.91
17091	98.8	302.38	64.25	43.56	37.87
8899	98.78	325.26	73.6	909.22	196.27
2505	98.78	231.43	34.98	755.8	189.47
4650	98.65	268.49	45.07	63.08	57.13
3023	98.65	83.25	22.18	359.33	106.87
19254	98.62	532.26	122.72	161.17	64.73
11849	98.62	1250.42	49.16	744.49	161.92
7552	98.62	243	43.8	985.86	277.63
24234	98.62	713.75	261.49	144.01	113.63
5667	98.59	1314.23	121.68	814.6	304.56
9136	98.59	681.01	57.09	336.6	86.24
18610	98.57	409.16	46.24	787.48	153.52
21586	98.57	146.56	36.94	21.03	25.51
	98.54	125.56	15.95	39.51	33.97
6405	98.54	424.58	107.49	3943.76	2199.09
6189	98.51	1524.82	548.61	242.17	217.65
16311 11635	98.51	81.5	14.25	292.66	87.54
	98.49	173.45	21.77	387.65	95.53
1653	98.46	1360.15	244.77	515.57	179.76
19252	98.46	2198.28	189.16	1083.75	295.64
11850		1528	178.26	824.17	192.23
23109	98.46	693.77	71.61	1897.77	724.77
21053	98.43	1610.12	286	488.24	226.21
8872		258.2	51.4	110.12	43.9
6108	98.41	1558.1	470.33	454.77	201.18
5920	98.38	264.24	55.84	79.82	44.53
17092	98.35	309.22	85.55	91.76	53.88
6107	98.35	142.58	46.88	804.04	258.17
24321	98.35		134.54	443.75	150.3
23390	98.35	1120.41	12.42	233.12	43.91
11429	98.33	125.24	68.64	206.18	79.88
19253	98.33	511.68	10.52	145.7	33.05
6945	98.33	53.77		826.24	213.43
24722	98.33	225.62	65.8	658.82	134.04
25499	98.33	1244.43	134.74		74.9
15900	98.33	450.4	66.32	184.15	467.21
19732	98.33	157.23	27.45	990.44	141.24
22582	98.27	100.04	19.95	439.37	141.44



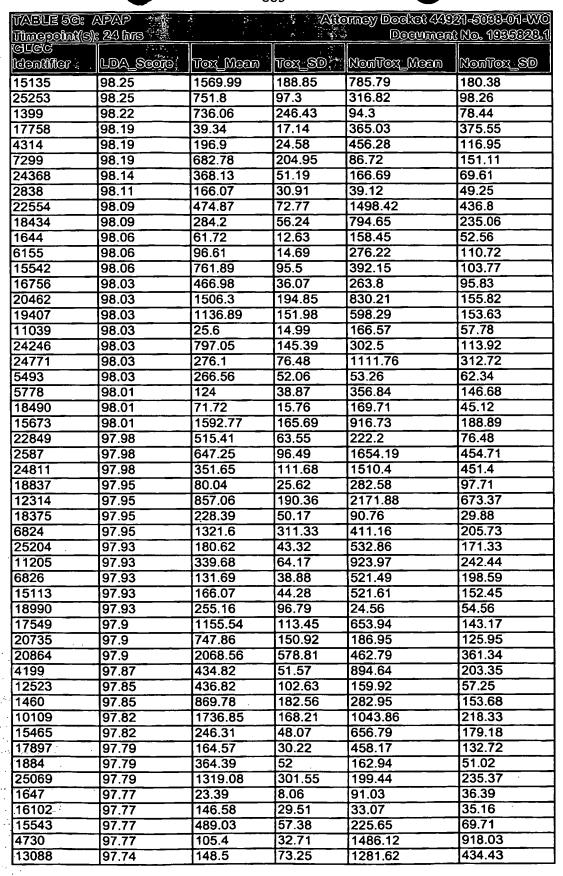
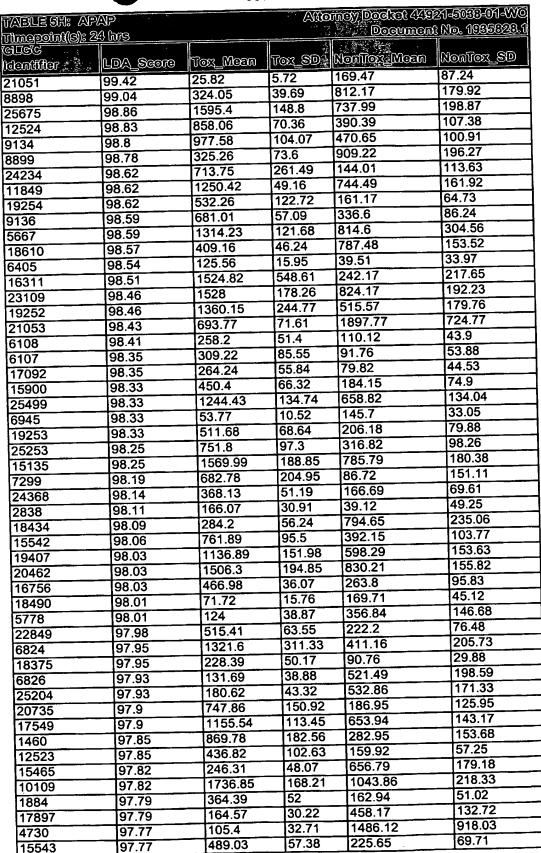
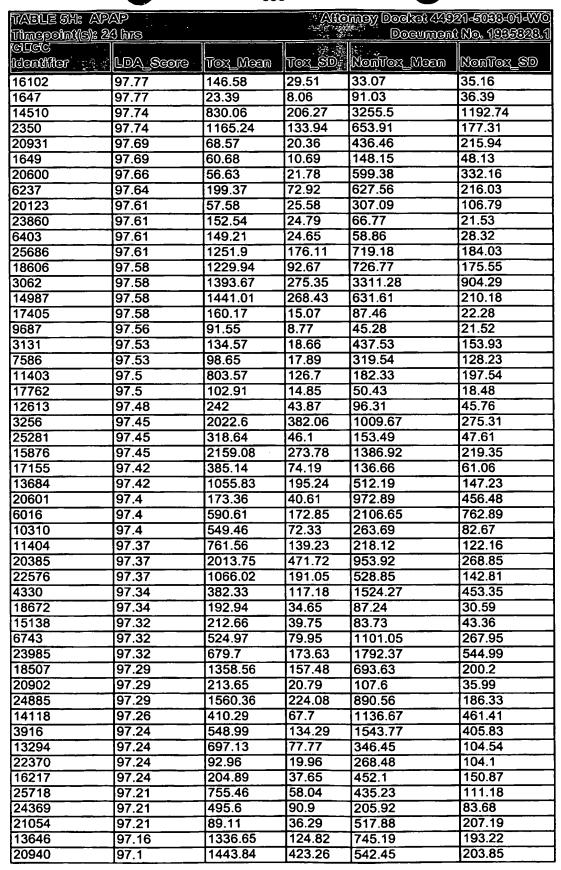
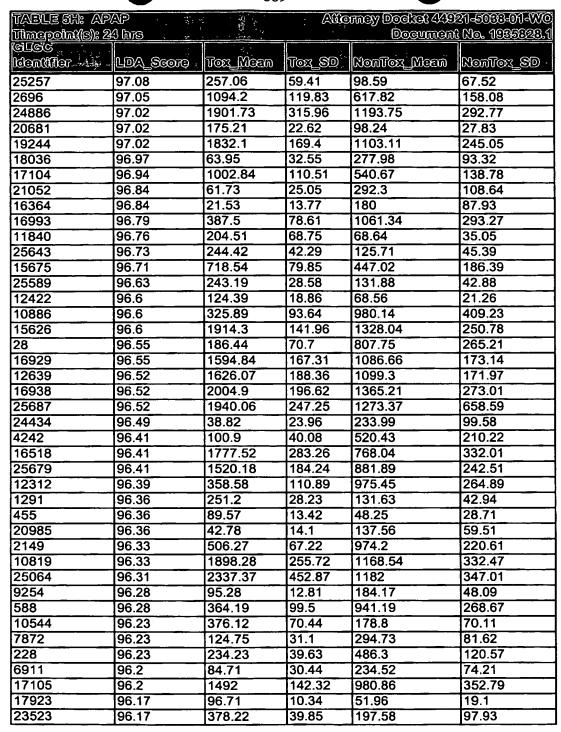


TABLE 56: (Timepoint(s)			ANG	omey Docket 4491 Document	21-5033-01-WO No. 19353 <u>28.1</u>
(dlec Identifier	LDA_Scoro	Tox_Mean	Tox_SD	NonTox_Neen	NonTox_SD
20931	97.69	68.57	20.36	436.46	215.94
20600	97.66	56.63	21.78	599.38	332.16
6403	97.61	149.21	24.65	58.86	28.32
25686	97.61	1251.9	176.11	719.18	184.03
14987	97.58	1441.01	268.43	631.61	210.18
17405	97.58	160.17	15.07	87.46	22.28
21950	97.58	310.54	60.16	694.88	151.27
18606	97.58	1229.94	92.67	726.77	175.55
9687	97.56	91.55	8.77	45.28	21.52
3131	97.53	134.57	18.66	437.53	153.93
5492	97.48	190.21	71.87	35.55	62.01
25281	97.45	318.64	46.1	153.49	47.61
15876	97.45	2159.08	273.78	1386.92	219.35
794	97.45	239.5	45.81	805.02	225.73
24810	97.42	75.11	33.12	418.65	149.72
25480	97.4	161.63	43.28	608.09	191.26
20601	97.4	173.36	40.61	972.89	456.48
22576	97.37	1066.02	191.05	528.85	142.81
20385	97.37	2013.75	471.72	953.92	268.85
15138	97.32	212.66	39.75	83.73	43.36
24885	97.29	1560.36	224.08	890.56	186.33
20902	97.29	213.65	20.79	107.6	35.99
17684	97.26	125.56	24.73	322.15	88.05
23854	97.26	969.78	127.99	449.89	145.83
16217	97.24	204.89	37.65	452.1	150.87
21054	97.21	89.11	36.29	517.88	207.19
25718	97.21	755.46	58.04	435.23	111.18
21977	97.18	207.43	59.84	710.09	218.42
11153	97.16	236.96	44.12	634.23	201.04
9905	97.16	292.18	56.38	648.99	149.67
13646	97.16	1336.65	124.82	745.19	193.22
20940	97.1	1443.84	423.26	542.45	203.85
25257	97.08	257.06	59.41	98.59	67.52
2696	97.05	1094.2	119.83	617.82	158.08
24886	97.02	1901.73	315.96	1193.75	292.77
20681	97.02	175.21	22.62	98.24	27.83
19244	97.02	1832.1	169.4	1103.11	245.05
1562	96.97	381.25	66.67	884.11	224.44
18036	96.97	63.95	32.55	277.98	93.32
17104	96.94	1002.84	110.51	540.67	138.78







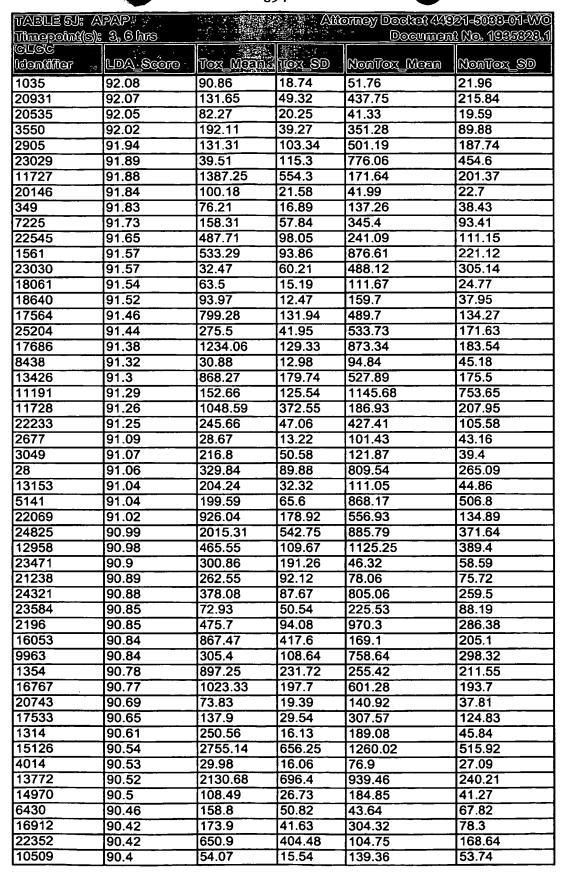
		-0>			
TABLES: A Threconush	PAP : 3, 6 hrs		AW	omey Docket 449 Documen	21-5039-01-WO t No. 1935328.1
GTGG [GTGG	LDV Scoid	Tox_Meen	Tox_SD	NonTox_Mean	NonTox_SD
4234	96.37	1562.41	228.3	606.16	282.97
9190	95.99	409.24	55.69	1023.78	355.45
21848	95.38	508.36	72.43	299.78	75.97
15070	95.33	59.8	20.57	366.97	192.1
4360	95.3	54.59	17.66	266.55	127.78
16215	95.27	425.16	58.89	782.02	174.56
2539	95.23	218.65	96.22	29.3	38.24
3131	95.19	144.5	37.62	439.05	152.9
15069	94.9	202.3	65.8	908.6	378.42
15997	94.88	813.65	351.32	122.49	170.98
1920	94.88	1504.99	398.7	430.96	246.08
8899	94.85	521.05	77.11	910.25	197.25
24249	94.85	180.01	39.13	1457.81	1262.86
18686	94.76	1999.23	361.77	694.29	601.03
64	94.63	59.26	14.42	135.3	43.74
9423	94.62	1693.26	379.24	806.14	285.06
1921	94.62	875.53	204.06	208.56	153.39
1501	94.46	164.01	82.59	505.88	250.23
20714	94.43	1591.59	292.98	557.8	697.68
20999	94.42	35.6	7.8	83.78	30.94
6861	94.35	72.59	30.82	171.58	37.22
16364	94.34	47.31	18.02	180.58	87.85
11726	94.27	1003.07	424.2	129.34	152.94
4291	94.26	73.8	39.53	311.61	138.1
1312	94.23	405.84	35.49	640.08	136.15
4003	94.2	65.49	22.78	179.63	79.96
23629	94.19	197.75	56.32	84.36	37.93
13933	94.11	201.22	38.22	103.76	35.78
17720	94.11	208.32	37.5	118.42	31.87
1431	94.02	95.78	34.77	435.85	187
23711	93.99	955.74	410.02	175.38	265.8
15996	93.97	531.17	191.59	104.03	129.76
15599	93.96	390.65	46.86	644.66	140.56
17334	93.95	456.16	134.26	174.33	81.45
1973	93.91	202.65	40.97	393.37	105.86
25705	93.91	480.04	58.52	746.23	197.9
7582	93.83	177.41	46.3	517.4	201.05
3548	93.79	21.78	11.09	80.61	29.95
23709	93.69	639.52	233.03	172.58	245.86
20779	93.68	2353.04	350.51	1361.2	334.8
10918	93.63	334.12	78.88	160.07	58.07
11079	93.62	31.23	8.61	92.7	35.85
16450	93.52	68.54	24.67	250.64	90.74
7837	93.51	96.9	18.89	204.81	65.61
2911	93.44	463.75	153.15	1194.47	357.16
17468	93.43	362.22	49.8	563.99	115.19
23044	93.42	387.95	117.87	150.64	50.01
19605	93.39	236.72	41.49	129.62	41.34
9776	93.25	1329.18	343.19	709.9	233.64
18727	93.25	1872.44	279.45	752.03	366.47
17506	93.13	399.01	349.67	28.06	50.99
		<u> </u>			

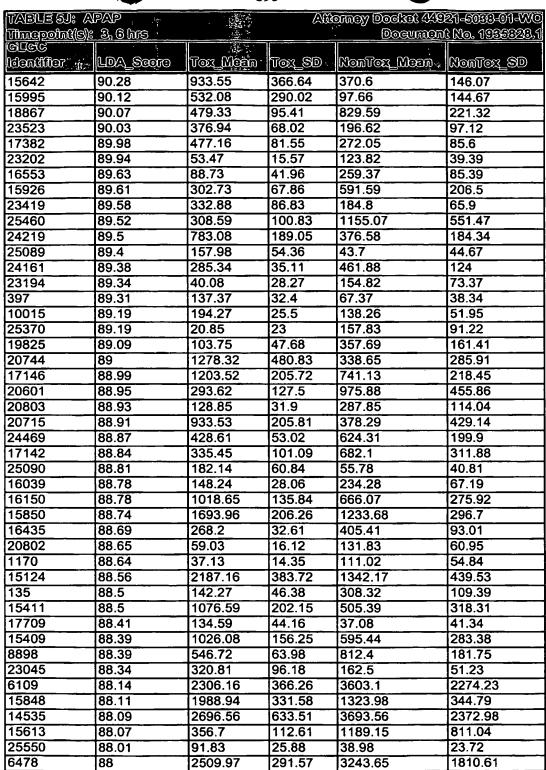


inatie at a	PAP		Ass	amay Docket 449	
Timepoint(s):	1			Documen	<u>t No. 1935t</u> I
ldendifer .	LDA_Score	FOR MOON	TOX_SD:	MoonTox_Mean	NonTox_8
16982	93.12	1641.85	437.99	322.65	457.76
15401	93.08	139.13	62.85	43.23	22.13
21842	93.04	83.37	32.47	568.46	292.58
8715	93.02	4368.81	1539.49	1535.24	565.09
18687	92.96	1938	349.18	648.4	576.75
5934	92.9	109.95	37.22	370.97	164.98
445	92.85	81.23	17.64	39.99	24.99
22378	92.8	21.7	19.29	100.06	39.37
5953	92.73	1310.4	496.07	175.05	193.14
7927	92.69	58.26	50.37	288.45	114.77
23606	92.65	1356.06	401.57	396.57	199.22
17183	92.52	220.92	28.69	347.74	76.33
6291	92.45	578.1	67.62	986.56	239.67
5952	92.44	481.14	170.63	103.14	98.67
9128	92.37	193.76	55.1	109.37	76.47
17897	92.26	206.99	46.02	459.28	132.2
15154	92.18	355.55	43.5	625.96	172.69
15127	92.1	1431.46	270.71	685.54	318.61
1035	92.08	90.86	18.74	51.76	21.96
3132	92.08	178.13	64.77	40.93	76.63
20931	92.07	131.65	49.32	437.75	215.84
20535	92.05	82.27	20.25	41.33	19.59
3550	92.02	192.11	39.27	351.28	89.88
1919	92.01	1065.82	400.77	236.46	159.88
2905	91.94	131.31	103.34	501.19	187.74
23029	91.89	39.51	115.3	776.06	454.6
11727	91.88	1387.25	554.3	171.64	201.37
21097	91.85	1927.2	412.81	913.68	378.2
20146	91.84	100.18	21.58	41.99	22.7
349	91.83	76.21	16.89	137.26	38.43
15170	91.78	83.81	34.97	197.37	55.8
7225	91.73	158.31	57.84	345.4	93.41
22545	91.65	487.71	98.05	241.09	111.15
8549	91.6	231.74	81.83	666.55	224.06
23030	91.57	32.47	60.21	488.12	305.14
1561	91.57	533.29	93.86	876.61	221.12
23710	91.54	208.44	92.17	40.21	129.93
18061	91.54	63.5	15.19	111.67	24.77
18640	91.52	93.97	12.47	159.7	37.95
17564	91.46	799.28	131.94	489.7	134.27
25204	91.44	275.5	41.95	533.73	171.63
17686	91.38	1234.06	129.33	873.34	183.54
22862	91.34	113.44	94.34	457.96	162.69
8438	91.32	30.88	12.98	94.84	45.18
13426	91.3	868.27	179.74	527.89	175.5
11191	91.29	152.66	125.54	1145.68	753.65
25814	91.27	42.6	15.87	139.24	72.71
	91.26	1048.59	372.55	186.93	207.95
11728	91.25	245.66 329.84	47.06	427.41	105.58
22233		1 4 / W X A	89.88	809.54	265.09 171.3
22233 28	91.06		74 20	1744 C4	
22233		454.39	71.38	741.61	171.3
22233 28	91.06		71.38	741.61	[171.3
22233 28	91.06		71.38	<u> 741.61</u>	[171.3
22233 28	91.06		71.38	 741.61	[171.3

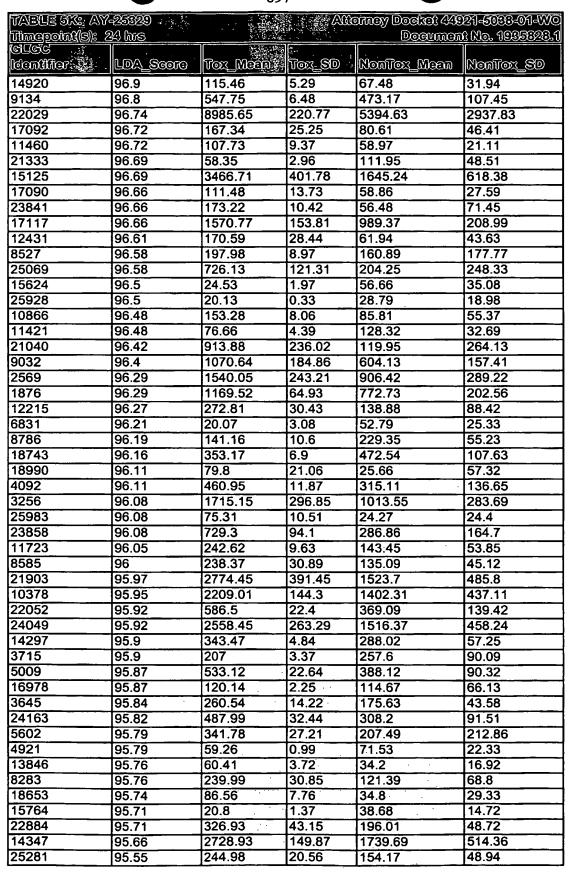
TABLES: A Timopoini(s):		, .			21=5033-01-WO t No. 1935328.1
idendifer Idendifer	LDA_Score	Tox_Meem	Tox_SD.	Nontox_Mean	NonTox_SD.
24825	90.99	2015.31	542.75	885.79	371.64
13568	90.96	21.64	6.81	47.5	16.27
21238	90.89	262.55	92.12	78.06	75.72
1354	90.78	897.25	231.72	255.42	211.55
16767	90.77	1023.33	197.7	601.28	193.7
20743	90.69	73.83	19.39	140.92	37.81
21980	90.66	283.16	46.28	508.52	161.96
17533	90.65	137.9	29.54	307.57	124.83
1314	90.61	250.56	16.13	189.08	45.84
15126	90.54	2755.14	656.25	1260.02	515.92
14970	90.5	108.49	26.73	184.85	41.27
18981	90.46	79.97	15.43	167.26	133.04
16912	90.42	173.9	41.63	304.32	78.3
22352	90.42	650.9	404.48	104.75	168.64
10509	90.4	54.07	15.54	139.36	53.74
15642	90.28	933.55	366.64	370.6	146.07
20799	90.22	263.93	35.28	487.22	132.92
15995	90.12	532.08	290.02	97.66	144.67
18867	90.07	479.33	95.41	829.59	221.32
23523	90.03	376.94	68.02	196.62	97.12
17382	89.98	477.16	81.55	272.05	85.6
23202	89.94	53.47	15.57	123.82	39.39
21909	89.81	74.84	16.14	155.4	58.67
15980	89.67	21.11	15.6	63.98	22.96
16553	89.63	88.73	41.96	259.37	85.39
15926	89.61	302.73	67.86	591.59	206.5
23419	89.58	332.88	86.83	184.8	65.9
25460	89.52	308.59	100.83	1155.07	551.47
24219	89.5	783.08	189.05	376.58	184.34
25089	89.4	157.98	54.36	43.7	44.67
24161	89.38	285.34	35.11	461.88	124
23194	89.34	40.08	28.27	154.82	73.37
397	89.31	137.37	32.4	67.37	38.34
10015	89.19	194.27	25.5	138.26	51.95
25370	89.19	20.85	23	157.83	91.22
19825	89.09	103.75	47.68	357.69	161.41
2727	89.03	37.93	10.97	90.39	57.7
20744	89	1278.32	480.83	338.65	285.91

			Acc	элюў Dodrot 440	
	3,6Me :		· · · · · · · · · · · · · · · · · · ·	nemused !	<u> </u>
Chec Chec	LDV Zeorie	Töx_Meen	ToxLSD	Noontion Live In the Noonting Contract of the	NonTox_SD
21848	95.38	508.36	72.43	299.78	75.97
4360	95.3	54.59	17.66	266.55	127.78
2539	95.23	218.65	96.22	29.3	38.24
3131	95.19	144.5	37.62	439.05	152.9
15069	94.9	202.3	65.8	908.6	378.42
15997	94.88	813.65	351.32	122.49	170.98
24249	94.85	180.01	39.13	1457.81	1262.86
8899	94.85	521.05	77.11	910.25	197.25
18686	94.76	1999.23	361.77	694.29	601.03
9423	94.62	1693.26	379.24	806.14	285.06
20714	94.43	1591.59	292.98	557.8	697.68
20999	94.42	35.6	7.8	83.78	30.94
11726	94.27	1003.07	424.2	129.34	152.94
1312	94.23	405.84	35.49	640.08	136.15
4003	94.2	65.49	22.78	179.63	79.96
23629	94.19	197.75	56.32	84.36	37.93
17720	94.11	208.32	37.5	118.42	31.87
13933	94.11	201.22	38.22	103.76	35.78
1431	94.02	95.78	34.77	435.85	187
15996	93.97	531.17	191.59	104.03	129.76
15599	93.96	390.65	46.86	644.66	140.56
17334	93.95	456.16	134.26	174.33	81.45
1973	93.91	202.65	40.97	393.37	105.86
7582	93.83	177.41	46.3	517.4	201.05
3548	93.79	21.78	11.09	80.61	29.95
20779	93.68	2353.04	350.51	1361.2	334.8
10918	93.63	334.12	78.88	160.07	58.07
11079	93.62	31.23	8.61	92.7	35.85
16450	93.52	68.54	24.67	250.64	90.74
7837	93.51	96.9	18.89	204.81	65.61
2911	93.44	463.75	153.15	1194.47	357.16
17468	93.43	362.22	49.8	563.99	115.19
19605	93.39	236.72	41.49	129.62	41.34
18727	93.25	1872.44	279.45	752.03	366.47
9776	93.25	1329.18	343.19	709.9	233.64
17506	93.13	399.01	349.67	28.06	50.99
16982	93.12	1641.85	437.99	322.65	457.76
15401	93.08	139.13	62.85	43.23	22.13
21842	93.04	83.37	32.47	568.46	292.58
8715	93.02	4368.81	1539.49	1535.24	565.09
18687	92.96	1938	349.18	648.4	576.75
5934	92.9	109.95	37.22	370.97	164.98
445	92.85	81.23	17.64	39.99	24.99
22378	92.8	21.7	19.29	100.06	39.37
17183	92.52	220.92	28.69	347.74	76.33
5952	92.44	481.14	170.63	103.14	98.67
9128	92.37	193.76	55.1	109.37	76.47
17897	92.26	206.99	46.02	459.28	132.2
15154	92.18	355.55	43.5	625.96	172.69
15127	92.1	1431.46	270.71	685.54	318.61
3132	92.08	178.13	64.77	40.93	76.63





Time soint(s):	24 hrs			Documen	nt No. 1936 1
ldendfjor :	LDA_Score	Tox_Moem		NonTox_Mean	KonTox
15127	99.42	2228.57	144.07	690.17	319.67
25284	99.31	228.35	29.98	35.82	35.65
5493	99.23	334.45	20.49	53.8	62.92
18989	99.23	3688.22	218.96	1473.15	684.27
5492	99.13	333.55	35.59	35.74	61.59
20705	99.13	6053.85	567.01	1016.82	920.69
18401	99.02	1192.86	19.51	790.14	166.79
20703	99.02	2972.37	407.67	444.63	468.56
15124	98.97	3499.62	356.01	1346.55	436.48
6236	98.97	2654.19	311	945.78	402.83
1793	98.83	4009.12	413.32	1154.04	604.09
20704	98.76	5184.07	583.26	1296.29	830.46
6143	98.68	1556.68	119.85	818.9	449.94
12589	98.68	54.45	0.24	45.08	47.36
1794	98.68	8293.54	1002.09	2160.55	1242.66
1795	98.62	1864.31	162.88	530.41	369.76
15126	98.6	3088.46	202.44	1271.98	533.53
6735	98.54	146.66	2.51	99.87	41.4
3816	98.46	575.25	19.66	377.74	104.46
1797	98.38	5433.84	613.82	1788.63	1017.3
		3106.16	814.21	626.16	657.08
12155	98.38			1	1
8661	98.36	94.12	31.74	26.77	156.77
20707	98.36	1648.89	164.54	603.99	295.97
25056	98.33	3664.54	860.18	928.86	704.24
12157	98.28	4167.9	1215.21	567.99	968.73
12156	98.2	3316.68	1192.33	495.67	848.47
1796	98.09	1014.79	217.2	236.88	176.87
6072	97.99	3160.03	286.02	1859.28	457.54
2424	97.91	1544.68	110.35	900.09	230.06
21957	97.88	127.91	1.18	172.94	52.7
17091	97.75	147.88	26.61	44.71	42.18
18027	97.72	104.69	21.33	48.98	32.44
7926	97.72	305.2	94.87	95.06	51.68
16703	97.7	1659.65	28.69	1168.22	385.13
22845	97.67	295.43	7.94	463.15	106.9
12447	97.64	134.56	6.18	63.62	36.34
1792	97.64	353.01	4.03	301.81	112.05
8872	97.51	1235.51	270.82	492.6	238.22
2615	97.43	119.21	3.95	203.42	60.45
2485	97.38	626.8	9.02	759.21	297.72
8864	97.22	127.38	6.48	51.24	84.26
25971	97.19	76.52	1.74	46.77	26.59
3438	97.17	33.8	0.49	39.49	24.65
15879	97.14	534.82	74.36	311.86	83.27
2158	97.14	228.23	4.29	156.69	90.9
2388	97.09	2352.96	69.04	1763.09	434.06
22595	97.09	822.73	9.6	1049.61	230.23
24860	97.09	1209.19	232.29	388.81	270.26
22953	97.03	625.19	120.94	213.93	156.52
53	96.95	22.21	9.24	73.81	42.08
1354	96.95	904.17	93.64	260.85	219.87



TABUZ 5K: AY-25329 Timopoinus): 24 hrs			Allomey Docket 44221-5088-01-WO			
GREC Hundfornder: 5		_ .	<u> </u>		<u>(((((((((((((((((((</u>	
ldentifer	LDV Z	Tox_Meen.	Tox_SD:	Kontok Mean	NonTox_SD	
23321	95.55	327.32	12.23	237.81	65.16	
25915	95.52	45.7	1.09	44.83	25.79	
16320	95.44	53.3	3.71	99.66	32.58	
1462	95.39	281.62	16.97	181.7	70.06	
21730	95.37	372.89	41.43	219.01	74.61	
25705	95.37	535.07	18.04	743.86	198.79	
228	95.29	359.03	13.58	485.24	121.65	
25400	95.26_	3529.97	320.24	1669.82	936.33	
20795	95.13	430.05	152.67	136.8	147.78	
7040	95.1	58.53	1.59	44.91	24.17	
4507	95.07	76.55	14.69	29.16	20.54	
4011	94.84	3393.88	485.3	1814.62	677.43	
21039	94.84	680.01	188.7	237.99	179.23	
17332	94.81	42.21	0.75	51.04	26.82	
21904	94.76	6107	612.37	2999.52	1590.33	
15623	94.7	43.16	3.57	71.32	24.27	
14925	94.7	304.2	4.07	323.51	105.18	
634	94.68	2339.09	155.16	1531.8	420.57	
18887	94.68	94.02	1.66	122.89	39.63	
15154	94.6	425.17	21.92	623.52	173.98	
21015	94.6	5326.56	750.73	2922.16	1044.87	
17374	94.57	92.28	4.99	155.79	47.59	
15848	94.52	2126.64	293.37	1329.33	349.48	
18293	94.52	1589.45	35.1	1370.84	446.65	
10097	94.49	63.75	2.56	98.75	30.52	
25064	94.44	2030.03	389.13	1186.32	355.39	
7635	94.39	100.8	2.18	127	27.75	
20809	94.36	213.36	13.63	323	81.99	
357	94.36	37.55	3.07	74.49	34.52	
1426	94.33	70.81	14.26	134.5	35.86	
24577	94.31	952.7	15.76	910.16	233.77	
17154	94.28	292.65	22.71	188.41	79.48	
20864	94.23	897.32	188.21	470.37	380.66	
14633	94.23	2097.19	131.15	1235.8	503.81	
20872	94.23	777.77	8.65	764.65	263.84	
25468	94.2	3173.3	126.12	2322.64	1103.63	
19942	94.15	95.56	6.27	145.09	54.11	
15134	94.15	399.35	71.1	736.3	183.22	
8984	94.12	137.4	2.65	180.76	59.27	
15384	94.12	42.75	1.45	33.76	18.34	
11153	94.01	361.07	30.29	632.71	202.42	
19433	94.01	313.24	91.01	107.04	118.97	
762	93.94	2847.63	424.59	1602.04	597.28	
17601	93.88	40.2	11.03	102.49	39.9	
20404	93.78	101.9	8.52	205.37	111.49	
4395	93.78	67.76	1.4	78.17	27.52	
17292	93.7	878.24	18.69	750.92	249.73	
25287	93.67	154.8	19.65	83.01	45.51	
15638	93.64	30.48	2.51	37.68	26.23	
20778	93.62	45.5	5.31	74.1	18.66	
70	93.62	281.42	35.86	472.99	143.44	

-899-

TABLE SK: AY Timegoin((s)):			ž Aûc	emey, Doctor 449 Documen	21-5033-01-VVO 11 No. 1935323.1
GLEC Identifier	LDA_Scoro ,	Meenl_xoI	Tox_SD	Meen Exolusin	NonTox_SD
1698	93.59	431.04	110.73	210.49	212.86
16604	93.56	40.05	7.29	85.4	33.96
15668	93.51	102.01	6.44	82.54	66.01
6127	93.49	23.69	1.27	40.44	19.63

		-900	_		
TABLEGL: AY- Timogodini(s): (100	Affic	may Docket 449 Document	21-5033-01-WQ Ko. 1935323.1
remailer Franklika	LDA_Score	RESMITE	Tox_SD	NonTox_Mean	NonTox_SD:
9128	99.47	354.27	42.02	109.61	75.79
20705	99.44	3201.5	243.39	1021.71	943.21
489	99.28	888.37	258.13	34.02	347.52
488	99.21	2923.89	441.22	140.43	726.58
6072	99.13	3706.97	408.43	1857.14	451.4
6071	99.07	530.75	42.79	251.17	84.27
20704	98.99	3555.4	254.22	1298.54	842
14737	98.94	3684.86	157.18	2006.22	547.49
14738	98.81	2448.85	138.8	1327.41	357.13
23449	98.68	4318.09	803.01	841.75	681.45
20703	98.65	1366.26	204.31	447.55	480.77
15644	98.62	1914.02	51.4	1368.69	389.22
1920	98.57	1514.84	112.1	439.47	265.88
7281	98.49	441.53	30.85	227.7	69.99
1794	98.46	6517.83	730.04	2162.01	1254.96
23448	98.41	4428.17	561.92	1081.77	848.31
9423	98.33	1313.51	45.22	814.2	299.43
13799	98.3	269.31	22.75	137.57	53.16
21913	98.17	211.98	28.07	105.73	26.92
1321	98.17	2755.45	228.85	899.36	612.89
356	98.07	272.75	15.73	145.76	65.24
1793	98.04	2716.62	269.59	1155.95	613.23
15190	98.01	5333.96	243.78	1831.66	1709.47
22586	98.01	126.81	110.11	4599.4	3587.54
12157	97.96	3316.91	1174.06	568.34	972.53
17091	97.93	99.36	8.07	44.78	42.37
16510	97.93	72.27	14.75	249.9	104
64	97.93	58.28	4.48	134.7	44.1
12155	97.75	2255.34	580.1	627.1	662.06
4133	97.72	221.29	5.17	375.25	112.42
1921	97.72	761.61	85.23	214.16	166.19
575	97.62	1703.39	109.13	903.24	308.03
23033	97.56	627.74	74.47	352.44	93.47
15189	97.56	4996.27	266.45	1653.47	1657.25
1919	97.54	697.95	65.39	244.03	183.41
20735	97.51	264.65	8.18	189.71	132.57
9079	97.51	205.9	4.58	313.27	94.32
2433	97.51	226.62	18.26	113.14	41.11
6236	97.46	2164.72	282.46	946.17	405.7
23243	97.3	4622.23	852.78	1788.3	771.99
21816	97.24	1775.09	46.91	1249.95	296.97
2354	97.22	1555.17	146.52	817.04	288.67
20088	97.22	104.24	3.39	167.16	48.53
22534	97.19	840.23	23.19	594.77	144.69
15879	97.11	504.41	53.68	311.82	83.36
15125	97.11	3095.98	168.95	1645.26	619.88
16035	97.09	32.98	3.75	90.85	50.8
8431	97.09	230.01	37.66	55.45	66.1
15126	97.06	2208.98	97.12	1273.35	538.07
11708	97.03	1694.02	180.11	978.63	234.58
15191	97.03	3612.61	253.19	1215.55	1328.85

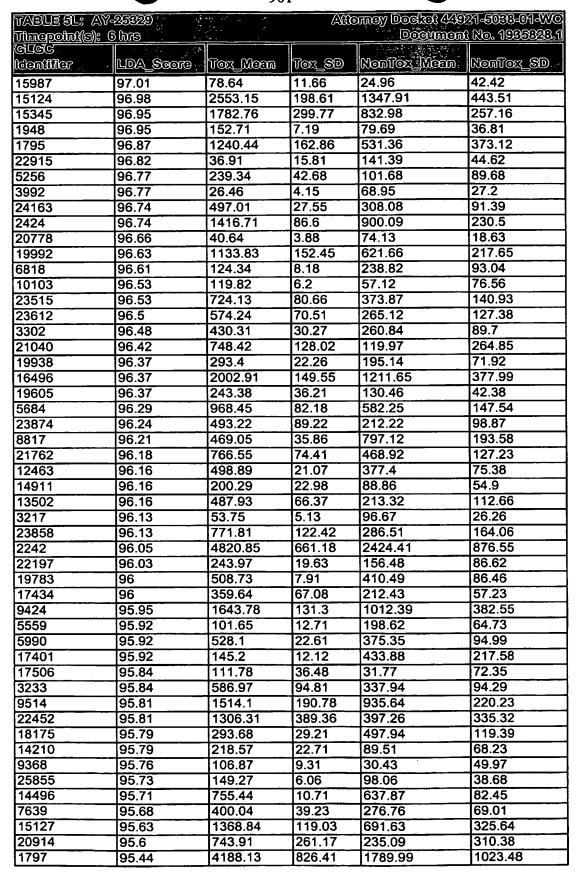
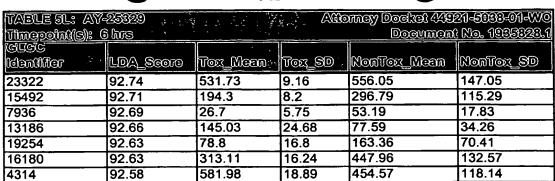
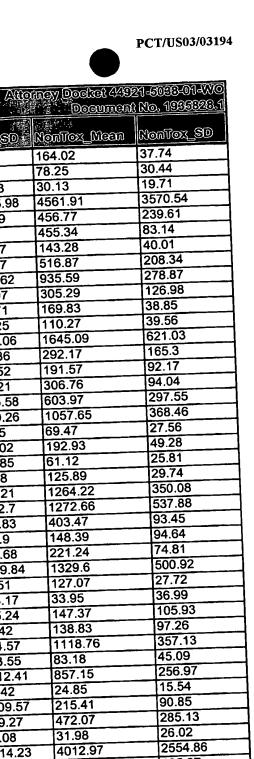


TABLE BL: AY		Attorney Docket 44921-5033-01-WO				
Mingeoinus): G	3 m			<u> </u>		
identifier Gues	LDA_Score	Toz_Meen	ToxESD	NonTox_Meen	NonTox_SD	
14621	95.28	107.41	1.84	142.85	46.25	
12060	95.26	47.87	5.63	91.21	25.83	
23045	95.15	255.48	37.5	163.93	54.17	
19949	95.12	86.53	7.05	146.55	42.94	
19222	95.02	768.75	33.94	1019.28	177.86	
5497	94.97	1000.21	88.11	641.4	187.79	
4234	94.83	956.41	63.22	615.37	298.73	
19096	94.73	57.63	0.95	64.45	22.13	
1796	94.54	443.71	62.76	237.98	180.37	
956	94.44	484.92	70.09	300.84	128.26	
17090	94.41	80.3	3.64	58.91	27.69	
18445	94.38	98.13	13.98	189.24	73.89	
6672	94.33	39.25	4.79	77.99	25.44	
1958	94.33	4985.87	190.85	3317.83	1944.19	
24352	94.3	27.75	0.9	33.04	14.34	
1159	94.28	162.39	10.62	275.08	107.56	
5033	94.2	265.2	27.03	515.49	286.9	
24670	94.09	360.02	26.89	541.68	137.35	
17740	94.04	3427.99	98.34	2194.96	956.73	
21980	93.99	274.05	41.72	506.75	162.58	
24458	93.91	449.26	21.59	632.05	154.86	
23044	93.77	227.6	25.98	152.95	56.53	
7148	93.64	92.3	2.5	130.59	42.98	
18727	93.61	1447.97	123.12	762.06	381.99	
2831	93.59	148.13	13.47	250.71	82.13	
1373	93.35	38.34	1.94	53.32	15.94	
17147	93.35	4539.57	228.13	3208.13	1955.57	
24767	93.32	42.13	12.79	114.61	46.62	
17324	93.3	227.18	24.03	378.67	117.83	
18327	93.27	70.58	4.34	44.61	27.29	
15274	93.27	53.53	2.94	83.66	27.09	
957	93.27	161	30.32	95.4	47.09	
108	93.22	2715.08	78.41	2174.3	1124.52	
16135	93.22	5731.84	306.06	3557.47	2538.5	
18452	93.16	687.01	47.14	1064.64	458.5	
15350	93.16	111.88	7.38	75.02	26.83	
173	93.16	245.25	41.89	111.96	81.02	
18453	93.08	279.46	51.57	643.35	266.26	
20700	93.08	4284.73	215.51	2940.59	1598.61	
19252	93.06	305.86	24.24	520.6	190.14	
20649	93.03	2181.55	127.02	1502.46	431.12	
21098	93	1700.79	105.75	1149.43	542.04	
18578	92.98	64.81	8.07	167.96	106.35	
24657	92.95	23.96	5.89	70.07	35.01	
11966	92.95	178.44	20.12	295.19	95.81	
15447	92.95	292.34	6.2	267.86	68.16	
18564	92.87	235.49	30.58	382	97.18	
811	92.85	517.78	35.52	676.64	149.1	
9905	92.85	465.99	40.53	647.58	151.46	
20919	92.79	250.19	34.31	498.34	222.82	
16730	92.79	44.05	4.89	24.97	25.22	
10730	132.11	177.00	7.03	24.31	120.22	

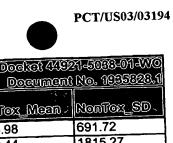




	50 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	-904	AW6	mov.Dooket 449	21-5033-01-WO	
ABLESM: E	LESM: BHLIMER TOMN Groin(S): 163, 336 ins		Dogument No. 1984:223.			
timepoint(S)): Higg	100, 200 1110		Tox_SD	Mean X	NonTox_SD .	
dendifer	LDA_Score	Tox Meen			342.76	
73	99.95	40.86	31.26	896.05	119.86	
6426	98.73	153.28	10.91	404.41	123.07	
83	98.65	732.58	101.14	160.15	406.15	
1866	98.44	58.74	24.69	413.23	94.77	
479	98.44	97	8.07	297	611.17	
1793	98.22	2741.37	246.03	1154.2	88.83	
17080	98.06	194.31	9.79	345.18	68.1	
12020	98.01	452.18	77.57	162.92	15.35	
12019	97.77	93.8	25.49	21.69	269.7	
24860	97.72	1100.32	127.02	387.9	149.23	
4312	97.69	416.83	132.18	62.43	118.96	
1478	97.69	163.67	14.87	424.08	481.85	
12682	97.67	79.05	63.79	1008.14	152.87	
15113	97.61	886.3	53.03	518.37	1255.94	
1794	97.56	5751.39	941.37	2160.23	81.87	
16427	97.37	62.04	13.17	223.4	110.92	
6155	97.24	105.36	15.91	275.91	37.43	
21595	97.19	169.42	60.29	32.1	72.38	
17506	97.11	105.56	21.71	31.71	126.03	
16781	97	565.92	57.82	328.2	374.13	
15571	96.95	20.98	7.92	136.96	191.57	
17281	96.87	330.14	29.37	629.22	47.67	
16448	96.82	47.05	13.47	130.14	63.34	
21968	96.82	292.73	48.83	154.3		
11692	96.79	168.31	21.93	65.64	96.66 279.42	
23711	96.66	388.27	76.76	182.86	48.73	
13157	96.55	165.11	70.49	40.42	761.82	
26150	96.42	59.8	68.6	955.38	35.45	
1955	96.37	183.79	59.05	62.73	81.49	
17703	96.34	199.28	17.25	346.38	114.96	
18726	96.31	145.27	29.51	363.35		
17079	96.29	549.49	52.57	871.34	166.2 179.21	
1796	96.21	614.82	119	237.13	55.96	
22824	95.86	115.71	17.87	214.57		
8789	95.84	288.79	19.27	182.49	76.4	
10529	95.84	22.39	8.22	110.84	49.73	
22717	95.54	53.38	5.07	101.61	46.15	
3661	95.52	396.98	37.77	200.82	83.43	
12192	95.36	112.15	9.74	192.87	52.01	
43	95.36	234.98	30.93	435.92	131.44	
21096	95.33	747.69	161.69		153.67	
15136	95.2	766.5	28.26	587.64	293.81	
11691	95.17	226.18	31.73	108.8	93.44	
23124	95.12	130.25	6.37	186.38	39.6	
13614	95.04	385.95	29.07	250.5	68.34	
20703	94.96	882.77	200.77		482.57	
14191	94.96	118.67	10.17	68.02	26.33	
23646	94.77	204.69	32.38	82.51	67.31	
5874	94.72	59.69	5.38	120.67	51.45	
6156	94.54	40.08	6.35	92.59	64.24	
19443	94.48	599.96	202.12	1369.67	434.97	



		-905		Aliomay Docker 44921-5053-01-440		
	BHUMER TOXIK	,	AWO	mey bocket 44.2 Documen	21-5153-11-00 1 Ma. 1985628.1	
Timepoint(S):	163, 336 hrs		1562	企業的	[]	
GUGC GUGC	röv See	Tox Meen	Tox_SD :	NOONTOX_MOON	MonTox_SD	
	94.46	121.26	4.76	164.02	37.74	
1827	94.43	47.88	3.7	78.25	30.44	
246	94.38	67.48	10.13	30.13	19.71	
9706 22586	94.35	11500	1785.98	4561.91	3570.54	
	94.32	298.53	14.59	456.77	239.61	
353	94.3	616.43	45	455.34	83.14	
15515 7554	94.24	82.53	10.47	143.28	40.01	
21054	94.16	177.38	38.97	516.87	208.34	
7362	94.14	1466.72	176.62	935.59	278.87	
16926	94.08	120.09	28.97	305.29	126.98	
16854	94.08	112.58	12.71	169.83	38.85	
24310	94.06	38.51	18.25	110.27	39.56	
15125	94.03	2727.66	290.06	1645.09	621.03	
15408	93.98	397.6	32.86	292.17	165.3	
8068	93.98	363.5	56.52	191.57	92.17	
13574	93.95	143.06	26.21	306.76	94.04 297.55	
20707	93.9	1207.87	255.58	603.97		
17566	93.85	1835.92	249.26	1057.65	368.46	
3775	93.71	39.87	3.85	69.47	27.56	
6968	93.69	266.85	15.02	192.93	49.28	
1870	93.69	106.51	12.85	61.12	25.81	
17880	93.63	83.82	5.38	125.89	29.74	
1869	93.61	1814.7	97.21	1264.22	350.08	
15126	93.58	2125.79	222.7	1272.66	537.88	
16435	93.55	535.9	24.83	403.47	93.45	
18301	93.55	30.49	13.9	148.39	94.64	
5923	93.55	372.72	61.68	221.24	74.81	
18719	93.53	2406.44	389.84	1329.6	500.92	
7635	93.45	92.29	4.51	127.07	27.72	
14878	93.45	71.05	13.17	33.95	36.99	
13930	93.42	228.98	25.24	147.37	105.93	
22931	93.42	28.54	5.42	138.83	97.26	
13634	93.4	1490.75	94.57	1118.76	357.13 45.09	
10573	93.4	140.75	13.55	83.18		
1868	93.4	1409.6	212.41	857.15	256.97	
20187	93.34	43.66	3.42	24.85	15.54 90.85	
23183	93.34	397.93	109.57	215.41	285.13	
20877	93.34	116.54	19.27	472.07		
7860	93.32	66.89	9.08	31.98	26.02 2554.86	
4254	93.29	4223.17	314.23		125.27	
18522	93.29	333.1	12.28	429.43	257.61	
11830	93.26	835.12	63.14	624.63	245.95	
15239	93.26	808.08	44.68	627.88		
6555	93.21	171.29	12.58	253.74	68.64 99.71	
5350	93.18	267.65	12.75	380.08	362.81	
17248	93.18	2233.53	133.45		564.18	
11115	93.18	1719.57	222.6	648.09	337.39	
21623	93.13	1132.98	45.92	1504.15	175.87	
17171	93.13	497.76	71.39		346.8	
20913	93.05	78.46	17.25		325.11	
15127	93.02	1302.98	314.6	9 691.16	1320.11	



rabledm: B	HUMER TÖXIK		Aftomey Docket 44921-5093- Document No. 199				
imegoin((s)): JUCC Jenii(ier	163, 333 hrs LDA Score	Tox_Meen	Tox_SD	. REEM_XOTROCK	KonTox_SD		
	92.94	1976.87	94.38	1475.98	691.72		
8989	92.92	2871.6	340.5	2973.44	1815.27		
4362	92.89	322.6	20.8	456.1	100.23		
17078	92.68	45.51	7.36	85.31	36.53		
1914	92.63	87.72	8.03	128.41	28.16		
12193	92.57	325.88	11.61	259.15	77.22		
22538	92.57	264.92	29.36	411.46	113.92		
1409		443.55	35.85	673.38	228.8		
20789	92.49	195.12	16.73	283.13	61.84		
25594	92.31	46.2	6.91	79.31	24.08		
8106		41.04	12.78	113.51	48.31		
13575	92.25	4420.78	385.43	3977.04	2711.34		
15017	92.23	1839.25	77.24	1367.43	415.42		
1508	92.2	122.42	12.52	86.69	46.54		
19085	92.07	4816.04	469.15	4272.22	3218.5		
17785	92.02	4273.88	388.33	4064.69	2676.34		
4212	91.99	373.56	42.75	609.46	205.83		
24535	91.96		61.95	802.79	228.92		
794	91.94	598.14	135.12	1571.58	485.76		
635	91.94	2286.92	21.8	89.57	95.24		
20865	91.86	149.14	23.56	297.56	83.27		
32	91.83	193.62	17.06	41.87	130.93		
23710	91.78	76.45	36.95	451.44	151.46		
16217	91.75	276.74	361.98	958.83	1094.24		
11116	91.72	2683.93	229.71	1632.97	751.8		
25469	91.72	542.02	545.38	4094.62	2902.22		
16274	91.7	4187.52		72.69	33.49		
25559	91.64	28.16	10.89 298	3931.89	2216.92		
109	91.54	4415.15		366.45	141.56		
19256	91.54	193.36	30.87	1142.91	358.01		
16305	91.54	1718.66	238.74	844.92	185.9		
24537	91.51	674.81	25.86	1970.86	958.83		
1854	91.41	3230.9	479.06	42.97	59.39		
17922	91.38	95.48	13.42	198.84	331.87		
26029	91.3	25.39	3.26	3589.09	2270.45		
6109	91.19	3670.01	391.99	4958.78	4395.68		
17109	91.11	5260.98	737.76	2465.64	1105.37		
1850	91.03	3844.53	525.52		250.67		
23709	91.03	266.31	39.91	177.19	27.99		
16221	90.9	33.13	3.91	63.17	28.55		
20182	90.8	77.53	3.31	60.98	120.55		

			07-	Dodros AA	991,5000.01AVA		
iable en: E	TCALUTAMIE	Œ	Attomey Docket 4/921-5038-01-WO Document No. 1935323.1				
itmepoint(S)	: G, 24, 168 ha	·S		<u> Dogamica</u>	1000 0000		
최다(전)	LDV Score		Tox_SD	Monitox Meen	KonTox_SD		
		7427.84	2543.95	2137.17	1182.95		
794	94.05	3555.66	1202.78	1143.5	578.82		
793	93.79	1877.82	801.13	523.93	352.85		
795	93.25	1223.64	178.94	815.66	248.41		
3121	92.34	423.59	48.33	311.56	83.55		
15879	91.94	1302.5	270.68	601.38	294.17		
20707	91.2	2568.8	273.68	1857.14	458.38		
6072	90.71	2528.93	425.29	1325.32	495.38		
18719	90.49	2184.68	296.87	1345.33	442.81		
15124	89.87	4631.18	764.51	2915.46	1042.21		
21015	89.57	5118.84	928.66	2842.92	1160.02		
12300	89.05	13466.57	1801.84	8082.94	4246.36		
22030	88.82		34	376.69	94.25		
5907	88.66	480.37 2661.26	403.65	1623.43	636.28		
17541	88.44	1071.22	69.29	821.81	218.52		
7892	88.12	68.19	10.19	99.31	24.37		
18728	88.11		22.33	24.85	42.46		
15987	87.82	60.44	3.22	39.49	15.06		
1623	87.73	24.55	1006.58	3915.34	2637.96		
15107	87.63	7407.83		935.03	347.66		
7881	87.51	1548.39	310.74	2973.05	1208.82		
24229	87.35	4789.35	635.23	166.08	65.8		
7891	87.27	261.97	35.47	8304.35	5705.98		
7460	87.17	15045.77	2149.01	1667.19	515.83		
17408	87.12	2263.76	190.08	766.67	545.96		
10893	87.03	1661.61	341.83	167.79	62.48		
3406	87	272.48	56.72		936.78		
25400	86.99	2864.27	395.4	1665.52	683.07		
18989	86.96	2768.68	658.79	1468.9	139.66		
15211	86.84	625.27	52.85	458.35	1082.47		
2970	86.84	4173.45	739.92	2286.92	318.5		
18717	86.83	1561.21	356.13	828.61	135.77		
22139	86.79	836.39	76.66	625.53	38.73		
8720	86.75	37.63	10.52	78.99	25.95		
202	86.7	56.51	7.34	84.25	758.53		
10625	86.63	3166.14	592.44		730.93		
8212	86.62	2734.92	303.96		300.25		
12299	86.52	1594.94	119.48		219.04		
15224	86.51	924.77	53.65	802.99			
11623	86.46	4860.16	399.89		1417.32		
6132	86.41	704.47	54.86	526.15	145.58		
20502	86.3	4281.17	395.39		915.05		
15125	86.27	2886.76	470.72		615.99		
19711	85.98	143.56	18.42	209.77	71.87		
8207	85.98	41.56	7.46	64.43	20.12		
2969	85.96	3867.38	685.26		1020.38		
25525	85.91	1894.47	314.56	3 1344.71	365.38		
	85.84	156.77	26.48	243.81	122.2		
15677	85.79	3773.15		2362.03	1110.56		
8211	85.75	128.57	25.59	230.41	78.61		
5996		3075.43			610.83		
20876	85.75 85.54	160.46	27.27		68.12		

10622

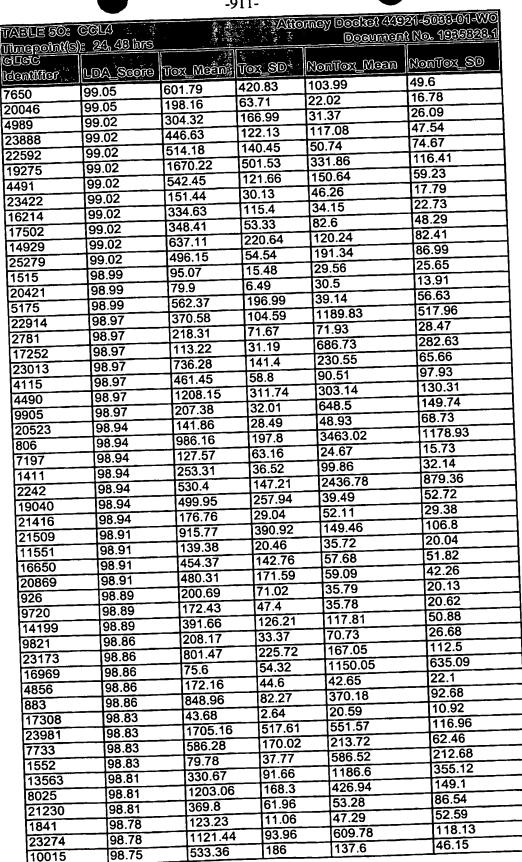
WO 03/0		-9	08-			
Ī	ABLE 5N:	EICALUTAMIE)[] -	Awo	May Docket 449	21-5033-01-WO k No. 1935323.1
Ū re	ime <u>poinus</u> Huge): 6, 24, 168 h	1			
	dondffer :	LDA_Score	TOX_MOED		NonTex_Mean	NonTox_SD
<u> - </u>	6947	85.43	1621.03		1149.72	321.34
1_	1904	85.35	5411.5		2989.45	1586.66
	20846	85.32	3770.81		2728.35	862.49
<u></u>	5050	85.31	73.92		141.83	61.38 475.21
L	20716	85.28	2021.87	149.83	1639.27	
L_	16203	85.27	116.04	19.61	78.78	34.59
E-	19425	85.13	14923.53	2865.23	9631.12	5918.03 5331.78
. L	14042	85.1	14415.82	2361.66	7961.54	328.47
	17560	84.89	440.74	90.35	736.93	148.03
L	14518	84.87	471.14	96.59	281.7	
L	8422	84.87	133.99	48.42	46.41	75.1
1	10626	84.86	3005.78	592.33	1670.17	646.71
ŀ	12363	84.86	220.65	34.33	291.82	61.88
	21156	84.61	8740.95	909.29	5062.58	2984.97
	2794	84.55	319.84	70.01	165.04	102.47
	8711	84.51	70.08	14.39	29.96	46.12
	24221	84.49	182.98	33.98	278.21	82.66
•	11151	84.46	319.39	68.02	509.45	187.63
	25768	84.43	90.39	13.5	129.43	42.46
	18299	84.41	78.66	11.12	105.73	25.03
	14232	84.39	1037.13	113.39	741.52	338.42
	5619	84.33	228.16	57.74	432.05	224.14
		84.32	642.65	246.6	291.81	246.83
	14887	84.29	185.45	14.52	236.81	65.71
	20350	84.21	2759.77	246.68	2106.24	520.92
	17672	84.19	120.93	10.11	161.79	56.6
	18269	84.09	119.14	8.62	138.98	45.63
	7505	83.98	2532.34	675.55	1362.87	597.43
	10624	83.93	258.17	44.43	347.18	83.93
	16625	83.91	1643.49	313.34	1018.88	554.33
	18178	83.91	222.84	36.37	140.6	60.97
	11888	83.89	5699.55	568.11	3668.94	1524.15
	17240	83.87	73.46	33.15	30.49	39.29
•	7345		4656.36	542	2888.16	1610.43
	18730	83.87	163.45	16.62	124.92	82.02
	746	83.86	4245.02	573.44	2603.84	1213.19
•	21013	83.86	709.56	55.38	567.34	114.22
	4445	83.86	2079.29	356.39		536.46
	15126	83.85	370.6	75.31	594.04	214
	19	83.79	2117.94	188.53		418.04
	4275	83.71	4405.66			1813.82
garan da Abrahaman (1991) (1991) (1991) (1991) Tanàna dia kaominina dia k	24362	83.69	575.67	203.3	236.19	178.15
	1796	83.67		1137.9		2936.67
	22029	83.62	8511.75	18.98	168.35	88.94
	4683	83.61	109.52			3313.7
	9307	83.57	10936.0	10.33	61.45	30.06
	20305	83.56	28.53	71.54	226.74	142.55
The state of the s	2387	83.55	387.6			1264.11
	1804	83.49	4039.69		1038.16	348.06
	21014	83.47	1662.37			364.31
	14346	83.43	1994.85			690.79
	10622	83.42	2853.67	1/20.00		



MONECEN	TRANSPAMI	EWK II) A	· · · · Amo	mey Dockot 4	1921:5033:01:WO hit No. 1985823:1
(VP) TE CIVE T	6 24 168 lh	rsace in		Dogum	mil No. 1985:223.1
PICC TE		San Marc	Tay Saff	മാലി തിരുപ്പ	Nontox SD
dentifier : -	FIDAY Segue		7.05	139.01	24.32
421	83.37	117.49	7.85	897.77	381.74
5069	83.35	1387.87	305.59	184.59	54.78
17433	83.34	138.7	13.95	218.67	86.27
23192	83.29	134.87	24.55	1006.16	481.15
17556	83.09	1606.64	280.26	1000.10	498.68
10623	82.97	2005.32	424.98	1776.86	559.41
20464	82.94	2338.81	290.91	3094.37	1638.93
17676	82.88	5304.82	859.63	641.02	251.92
18861	82.83	1041.37	175.77		32.92
21690	82.76	36.14	7.11	63.03	46
16043	82.65	95.36	12.38	131.18	160.74
15642	82.6	252.02	39.37	377.41	165.07
16257	82.57	758.92	115.75	492.54	20.26
3915	82.57	35.58	6.37	52.49	80.74
15371	82.54	201.09	28.22	278.09	488.06
21903	82.48	2069.84	261.63	1522.58	145.07
17561	82.46	130.52	39.79	261.8	58.5
15516	82.38	119.81	19.44	175.08	2242.88
8266	82.34	6200.92	1006.15	3536.09	65.71
2979	82.34	192.53	12.42	233.67	211.98
1550	82.34	246.3	48.26	432.34	
145	82.29	45.36	8.46	73.42	26.12
17083	82.28	49.53	8.95	73.48	28.69
18346	82.25	187.44	26.93	145.18	49.14
3439	82.21	43.01	7.52	78.15	40.33
18302	82.18	21.45	18.24	147.96	138.26
580	82.17	66.16	24.39	114.68	47.09
18357	82.16	278.1	27.48	355.74	87.59
9135	82.1	804.84	34.31	747.49	136.44
1481	82.04	40.66	7.52	58.58	29.87
24873	82.04	21.89	6.18	40.49	28.79
14981	82	6242.22	1306.4	3413.53	2306.41
18287	81.96	61.69	14.03	83.29	21.27
25430	81.94	420.24	84.04	621.61	179.45
	81.81	97.56	14.52	133.43	29.21
1133 19252	81.64	439.95	35.68	520.58	190.73
24798	81.64	410.66	52.61	572.33	199.49
	81.59	41.46	4.52	54.77	24.35
22860	81.55	1824.09	189.5	1387.45	423.02
19727	81.53	100	48.46	266.4	301.58
24345	81.52	2966.73	343.57	2259.65	866.25
6477	81.45	2269.56	339.72		379.17
17227	81.44	6691.79	944.48		2207.46
109	81.41	1140.81	82.04		163.38
15225	81.4	55.3	11.32		42.94
21287	81.39	1767.8	145.19		337.77

		-,	710-		5 2000 04 MMS
MILE 50: (CCL/3		AMO	TOOY DOCATOR CASE	21-50:3-91-400 ^ 00- 4005090 1
Timepoint(S)	8 24,45 ms			Dogumen	IL K KNOP JERROGARP II
ଖ 🗆 ଖ୍ୟୁ ଅନ୍ତ	1111		300 g	Monto <u>x</u> Mean	NonTox_SD
dendifier	The state of the s	ToxiMean		24.54	23.07
20589	99.76	285.48	30.99	167.97	77.14
6457	99.73	470.97	44.85	2756.96	666.96
7167	99.68	5178.1	150.52	66.44	19.21
3152	99.6	209.7	21.22	37.36	34.49
23631	99.58	162.76	37.05	30.27	19.34
13486	99.5	107.55	14.39	22.97	143.66
18800	99.47	220.37	68.88	59.45	96.47
15185	99.47	572.3	212.35	1107.03	351.19
19191	99.42	3081.98	281.59	42.2	33.29
4095	99.42	334.45	75.27	26.94	14.93
21802	99.42	99.74	8.27		195.85
16394	99.39	504.35	120.83	116.09	134.28
497	99.39	903.77	160.27	139.13	161.18
574	99.39	721.07	264.86	92.78	31.52
17158	99.39	347.11	70.42	52.67	47.37
23731	99.36	417.48	161.01	131.4	391.36
21097	99.36	285.19	53.54	926.43	
18002	99.36	403.4	125.9	2317.53	794.7 326.01
11161	99.36	117.22	13.58	602.61	
19456	99.36	1660.02	1205.05	20.54	95.38
4011	99.34	527.49	75.12	1822.06	678.03
4048	99.34	2846.7	1989.92	44.06	171.31
3909	99.31	174.34	42.84	28.67	20.5
2853	99.31	278.11	50.48	57.12	44.26
	99.31	1034.74	210.81	74.36	94.79
22321	99.26	623.69	96.26	1770.23	507.1
21091	99.26	263.24	88.27	36.49	20.82
4097	99.23	89.36	11.02	35.4	33.7
12035	99.23	124.37	37.27	40.1	28.33
24873	99.23	133.05	22.83	27.41	20.87
11376		260.19	96	37.57	20.85
2765	99.23	271.47	82.96	21.11	27.27
18385	99.23	138.05	18.67	42.94	19.7
17809	99.2	82.42	17.35	25.88	10.71
17255	99.2	37.47	8.02	233.51	77.8
12551	99.2		40.46	33.86	43.65
2042	99.18	211.79	128.76	286.5	83.26
2854	99.18	853.85	139.28	306.7	77.28
20745	99.15	892.06	97.66	120.88	42.78
19241	99.13	355.33	32.42	25.22	14.26
19177	99.1	137.75	230.25	245.42	387.38
20816	99.07	1019.58		1123.31	1303.12
12160	99.07	262.93	35.56	95.72	43.88
2107	99.07	249.59	34.94	32.62	11.9
4161	99.07	89.58	15.59		20.62
3895	99.07	223.53	60.87	26.67	35.16
14840	99.07	357.86	84.7	71.81	255.17
4049	99.07	1765.48	771.38	128.18	12.56
17156	99.05	92.63	21.28	38.99	45.5
4243	99.05	225.42	22.45	97.19	19.58
21836	99.05	71.79	5.88	28.13	17.94
17597	99.05	86.53	13.25	32.96	117.54







			112-		1000 00 WG
ABLE 50: (CL4		Affe	may Doglat 449	2145155914W9 No. 1955323.1
ilmepolin((S)	: 24, 49 hrs			noganingn	16 14 (A) 18 20 20 20 11
3 EGG		Tox_Mean	Tox_SD .	MOONTOX MOON	NonTox_SD
GC000000		537.67	102.07	98.03	63.7
5257	98.73	590.45	94.8	209.31	73.55
5296	98.73	90.46	14.25	28.7	18.76
8630	98.73	486.78	139.46	91.24	43.4
10016	98.7	90.18	15.72	28.02	18.46
1427	98.7	185	68.69	1028.7	367.63
1551	98.7 98.67	581.57	155.71	91.28	94.21
7063	98.67	63.04	7.65	20.62	13.07
12797		581.13	92.91	218.96	92.84
25252	98.65 98.65	351.6	64.71	92.09	54.37
6107	98.65	111.52	12.27	40.86	18.71
14423		258.45	173.76	1707.06	632.12
14881	98.62 98.62	321.77	139.65	41.26	31.89
20868		191.42	37.46	72.94	27.86
17083	98.62 98.62	983.99	159.57	420.92	108.26
20746	98.59	437.42	128.64	166.03	140.1
15888	98.59	802.14	181.07	2173.19	559.23
9841	98.57	234.05	49.82	87.56	27.43
17130	98.57	803.38	85.45	280.49	123.06
19768	98.54	84.2	7.61	46.06	13.16
15242		160.57	24.32	53.41	22.36
1514	98.54	86.24	21.43	21.87	10.87
8439	98.54	374.46	183.68	51.27	35.52
20783	98.54	757.87	159.09	217.11	97.55
14121	98.54	447.45	94.39	1017.11	250.9
20587	98.54	137.89	28.1	34.12	23.94
3831	98.54	50.04	25.96	432.28	211.08
1550	98.52	168.72	55.33	23.24	17.55
13973	98.49	336.2	97.41	122.7	48.5
16444	98.49	380.9	101.28	92.55	59.83
15884	98.49	122.16	18	57.58	32.58
4361	98.49	68.34	13.03	26.16	9.88
17727	98.49	61.54	32.04	534.73	374.12
1795	98.46	1302.3	114.63	634.55	170.6
11170	98.46	89.6	33.52	27.51	11.01
16118	98.46	438.37	58.6	180.59	68.47
21696	98.46	282.14	87.98	943.86	194.02
405	98.46	209.17	47.17	741.89	238.25
12606	98.44	49.88	7.39	21.58	10.52
18165	98.44	105.66	29.75	23.15	16.21
17157	98.44	153.13	49.66	43.48	27.52
21060	98.44	215.48	141.39	1303.65	412.9
14882	98.41	175.14	40.76	32.3	29.79
7427	98.41	174.49	27.28	50.56	36.82
13499	98.41	1201.76	365.51	226.06	115.51
13974	98.41		211.92	241.19	148.7
1435	98.41	977.21	61.88	940.43	268.63
588	98.41	216.49	114.28	200.54	80.15
3549	98.38	502.59	39.99	509.96	151.7
20298	98.38	182.9	141.46	99.06	44.13
1570	98.38	285.96 91.36	13.14	30.41	15.46



		-	13-	D = 0 = 0 00	0001 G000 001 000
ABLE 5P: C	CLA 1			omey Docket 44 Docume	nt No. 1985028.1
imopoint(s): Fles	24,48 hrs			PER CENTER OF THE PER CENTER O	
lentifier :	LDA Score	TOX_MEEM	Tox_SD 🐺	Novilox Meen	KienTox_SD
6457	99.73	470.97	44.85	167.97	77.14
7167	99.68	5178.1	150.52	2756.96	666.96
3631	99.58	162.76	37.05	37.36	34.49
3486	99.5	107.55	14.39	30.27	19.34
5185	99.47	572.3	212.35	59.45	96.47
8800	99.47	220.37	68.88	22.97	143.66
1802	99.42	99.74	8.27	26.94	14.93
1002	99.42	334.45	75.27	42.2	33.29
9191	99.42	3081.98	281.59	1107.03	351.19
7158	99.39	347.11	70.42	52.67	31.52
197	99.39	903.77	160.27	139.13	134.28
16394	99.39	504.35	120.83	116.09	195.85
19456	99.36	1660.02	1205.05	20.54	95.38
11161	99.36	117.22	13.58	602.61	326.01
18002	99.36	403.4	125.9	2317.53	794.7
21097	99.36	285.19	53.54	926.43	391.36
23731	99.36	417.48	161.01	131.4	47.37
23731 4011	99.34	527.49	75.12	1822.06	678.03
3909	99.31	174.34	42.84	28.67	20.5
21091	99.26	623.69	96.26	1770.23	507.1
18385	99.23	271.47	82.96	21.11	27.27
2765	99.23	260.19	96	37.57	20.85
11376	99.23	133.05	22.83	27.41	20.87
24873	99.23	124.37	37.27	40.1	28.33
12035	99.23	89.36	11.02	35.4	33.7
17255	99.2	82.42	17.35	25.88	10.71
17809	99.2	138.05	18.67	42.94	19.7
2042	99.18	211.79	40.46	33.86	43.65
20745	99.15	892.06	139.28	306.7	77.28
19177	99.1	137.75	32.42	25.22	14.26
14840	99.07	357.86	84.7	71.81	35.16
3895	99.07	223.53	60.87	26.67	20.62
4161	99.07	89.58	15.59	32.62	11.9
2107	99.07	249.59	34.94	95.72	43.88
12160	99.07	262.93	35.56	1123.31	1303.12
20816	99.07	1019.58	230.25	245.42	387.38
20046	99.05	198.16	63.71	22.02	16.78
7650	99.05	601.79	420.83	103.99	49.6
17597	99.05	86.53	13.25	32.96	17.94
21836	99.05	71.79	5.88	28.13	19.58
4243	99.05	225.42	22.45	97.19	45.5
17156	99.05	92.63	21.28	38.99	12.56
25279	99.02	496.15	54.54	191.34	86.99
	99.02	637.11	220.64	120.24	82.41
14929	99.02	348.41	53.33	82.6	48.29
17502	99.02	334.63	115.4	34.15	22.73
16214	99.02	151.44	30.13	46.26	17.79
23422	99.02	542.45	121.66	150.64	59.23
4491	99.02	1670.22	501.53	331.86	116.41
19275	99.02	514.18	140.45	50.74	74.67
22592 4989	99.02	304.32	166.99	31.37	26.09



WO 03/064624					101,000	
		-91				
	6814		AW	omey Docket 44	921-5033-01-WO	
TABLE 5P:	(6614) N: 24, 48 hrs			Documen	nt No. 1985323.1	
707C7070			- 00	Marsan Massa	NonTex_SD.	
ldentifier :	LDA Score	Tox Mean		NonTex_Mean		
5175	98.99	562.37	196.99	39.14	56.63 13.91	
20421	98.99	79.9	6.49	30.5	25.65	
1515	98.99	95.07	1,01,0	29.56 648.5	149.74	
9905	98.97	207.38	32.01	303.14	130.31	
4490	98.97	1208.15	311.74	90.51	97.93	
4115	98.97	461.45	58.8 31.19	686.73	282.63	
17252	98.97	113.22	104.59	1189.83	517.96	
22914	98.97	370.58	147.21	2436.78	879.36	
2242	98.94	530.4	36.52	99.86	32.14	
1411	98.94	253.31 127.57	63.16	24.67	15.73	
7197	98.94	986.16	197.8	3463.02	1178.93	
806	98.94	141.86	28.49	48.93	68.73	
20523	98.94	480.31	171.59	59.09	42.26	
20869	98.91	139.38	20.46	35.72	20.04	
11551	98.91 98.91	915.77	390.92	149.46	106.8	
21509	98.89	391.66	126.21	117.81	50.88	
14199	98.89	172.43	47.4	35.78	20.62	
9720 926	98.89	200.69	71.02	35.79	20.13	
883	98.86	848.96	82.27	370.18	92.68	
16969	98.86	75.6	54.32	1150.05	635.09	
9821	98.86	208.17	33.37	70.73	26.68	
1552	98.83	79.78	37.77	586.52	212.68	
7733	98.83	586.28	170.02	213.72	62.46	
23981	98.83	1705.16	517.61	551.57	116.96	
17308	98.83	43.68	2.64	20.59	10.92 86.54	
21230	98.81	369.8	61.96	53.28	149.1	
8025	98.81	1203.06	168.3	426.94	355.12	
13563	98.81	330.67	91.66	1186.6	118.13	
23274	98.78	1121.44	93.96	609.78 124.76	45.89	
22645	98.78	233.57	10.3	30.57	14.78	
14656	98.78	92.13	13.9	47.29	52.59	
1841	98.78	123.23		137.6	46.15	
10015	98.75	533.36	186 249.56	63.12	49.17	
23773	98.75	500.29	478.76	464.93	137.55	
15121	98.75	1228.37	278.22	117.37	82.5	
17489	98.75	659.58	14.25	28.7	18.76	
18630	98.73	90.46 590.45	94.8	209.31	73.55	
15296	98.73	185	68.69	1028.7	367.63	
1551	98.7	90.18	15.72	28.02	18.46	
1427	98.7	243.65	86.83	1135.66	461.2	
14118	98.7	376.52	22.67	195.26	56.33	
16267	98.67	581.57	155.71	91.28	94.21	
7063	98.67 98.67	63.04	7.65	20.62	13.07	
12797 24040	98.67	2606.92	1475.06	564.01	188.03	
867	98.67	845.8	252.31	299.25	82.39	
12401	98.67	617	333.35	118.67	54.89	
12401 12963	98.67	371.78	38.24	171.03	77.17	
112300	98.65	581.13	92.91	218.96	92.84	
25252 6107	98.65	351.6	64.71	92.09	54.37	
45 1 2 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1	100.00					
For the supplication of the analysis managed from the st						



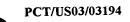
			Vitorney Doct 131 4/1921-5033-01-WO					
TABLE SP: (C Timepoint(S)	• 9/1 //2 hirs 🦠		\(\lambda\)	Dogument No. 1956:243.1				
COMMON CLOC	LDA_Score	Tox_Mean	TOX_SD	Konjoz Men	MonTox_SD			
14423	98.65	111.52	12.27	40.86	18.71			
	98.62	258.45	173.76	1707.06	632.12			
4881	98.62	321.77	139.65	41.26	31.89			
20868	98.62	191.42	37.46	72.94	27.86			
7083	98.62	983.99	159.57	420.92	108.26			
20746	98.59	437.42	128.64	166.03	140.1			
5888	98.59	802.14	181.07	2173.19	559.23			
841	98.57	234.05	49.82	87.56	27.43			
7130	98.54	84.2	7.61	46.06	13.16			
15242	98.54	160.57	24.32	53.41	22.36			
1514		86.24	21.43	21.87	10.87			
3439	98.54	374.46	183.68	51.27	35.52			
20783	98.54	757.87	159.09	217.11	97.55			
14121		447.45	94.39	1017.11	250.9			
20587	98.54	137.89	28.1	34.12	23.94			
3831	98.54	50.04	25.96	432.28	211.08			
1550	98.52	168.72	55.33	23.24	17.55			
13973	98.49	336.2	97.41	122.7	48.5			
16444	98.49		101.28	92.55	59.83			
15884	98.49	380.9 122.16	18	57.58	32.58			
4361	98.49		13.03	26.16	9.88			
17727	98.49	68.34	32.04	534.73	374.12			
1795	98.46	61.54	114.63	634.55	170.6			
11170	98.46	1302.3	33.52	27.51	11.01			
16118	98.46	89.6	58.6	180.59	68.47			
21696	98.46	438.37		943.86	194.02			
405	98.46	282.14	87.98	741.89	238.25			
12606	98.44	209.17	47.17	21.58	10.52			
18165	98.44	49.88	7.39	1303.65	412.9			
14882	98.41	215.48	141.39	32.3	29.79			
7427	98.41	175.14	40.76		36.82			
13499	98.41	174.49	27.28	50.56	115.51			
13974	98.41	1201.76	365.51	226.06 241.19	148.7			
1435	98.41	977.21	211.92		268.63			
588	98.41	216.49	61.88	940.43 509.96	151.7			
20298	98.38	182.9	39.99		44.13			
1570	98.38	285.96	141.46	99.06	49.41			
15662	98.36	91.92	14.56	36.5	43.88			
15347	98.36	346.75	87.39	117.28	15.46			
17854	98.36	91.36	13.14	30.41	49.21			
20767	98.33	280.71	144.4		35.41			
17321	98.33	221.21	22.9	97.97	53.44			
16456	98.33	358.94	48.34	147.37	67.26			
15175	98.33	106.35	12.21	232.4	19.29			
13731	98.33	67.28	8.03	25.13	57.57			
15295	98.3	440.81	58.59	193.54				
21538	98.28	112.07	31.82	33.42	15.07			
22903	98.28	223.21	29.54	114.26	35.65			
3404	98.22	285.46	52.41	126.82	42.71			
62	98.22	41.02	6.3	118.71	37.35			
18068	98.22	124.17	43.49	42.05	13.94			
15659	98.2	171.38	51.63	46.45	19.32			

		_			SA COOR ON WAR
	Y691 Z1		JA.	omey Decket 449	Standary Standary
TABLESP: C	10 100			Dogumen	it No. 1935323.1
Timepoin(S)	24, 45 ms		155.63		
				Monton Mona	NonTox_SD .
ldendffer 🧸	LDA Score	Tox_Woon .	lox an	MONTOX_MOON	
		331.72	46.32	177.27	47.72
22374	98.2			22.41	17.54
20514	98.2	86.21	16.85		84.72
20848	98.2	673.73	143.1	258.22	104.12

		-91		mey Docket 449	721-2682-641-67/0
ABLE 50: CC	ALA .	11		INGW LEXEDU KEWY WEWILDOO	k No. 1935322.1
imepoint(s):	3, 6 MS				
leviller Tece	LDA Scoro	TOX MOON	TOX_SD	MOONTOX_MOEM	NonTox_SD
4664	99.76	377.68	20.92	136.44	44.25
4004 2957	99.5	1374.12	163.04	258.41	141.69
923	99.47	792.04	81.55	255.07	88.84
2504	99.44	1075.8	276.85	143.28	79.8
	99.42	86.48	19.54	478.67	173.07
3055 2266	99.39	466.47	113.24	1709.02	349.89
2787	99.36	1345.7	116.52	547.14	157.98
24019	99.36	166.62	22.91	25.28	25.42
437	99.34	429.95	104.1	1419.15	416.74
11431	99.31	269.44	41.67	67.29	25.3
23595	99.31	152.68	18.51	36.24	28.72
17337	99.28	158.41	44.56	37.65	65.6
	99.28	115.8	13.78	40.16	18.76
22039	99.28	391.85	55.33	1062.9	303.62
4585	99.28	843.51	203.46	86.56	103.18
3710	99.26	199.08	13.67	323.31	50.68
8278	99.26	1045.83	179.14	251.37	107.33
23137	99.23	150.12	17.44	20.65	23.5
8795	99.23	469.56	157.25	29.61	43.11
25098		337.27	45.6	131.96	108.26
6678	99.2	51.73	8.72	192.66	73.89
6723	99.2	217.79	19.04	91.1	34.76
2685	99.2	145.29	21.13	38.44	16.93
25934	99.2	846.34	270.27	56.91	75.32
1183	99.2	320.8	69.98	1062.3	343.83
21592	99.18	520.6	59.06	184	66.08
15376	99.18	140.3	9.99	283.25	69.59
9757	99.18		343.4	113.68	53.9
4663	99.15	598.65 378.95	51.18	106.63	43.83
2501	99.15		728.7	22.74	133.08
8661	99.15	1338.84	114.29	376.26	99.16
3816	99.13	975.32	43.05	77.7	31.04
23157	99.07	247.88	724.98	248.1	258.83
15171	99.07	2247.86	27.1	253.6	73.58
21073	99.05	55.08		78.61	43.69
7380	99.05	333.92	139.31 31.25	52.52	28.51
7806	99.05	181.23		28.2	52.2
22443	99.05	414.09	134.18	70.61	110.14
17908	99.05	750.32	84.2	28.04	15.07
5200	99.02	142.98	57.87	155.42	39.37
22686	99.02	67.26	6.15	174.25	40.46
21974	99.02	446.28	79.04	202.67	63.14
11549	99.02	435.29	33.69		47.31
14560	99.02	473.1	197.32	113.37	37.36
3308	99.02	372.22	58.67	160.39	32.63
25907	99.02	239.1	54.52	34.6	55.13
22958	98.99	436.75	110.13	81.89	17.1
13911	98.99	99.9	12.46	30.54	25.84
16576	98.99	351.95	227.31	26.26	77.73
23407	98.99	850.19	261.07	152.52	39.79
12969	98.99	374.35	124.84	38.42	
19613	98.97	797.9	128.77	1866.41	483.03

		-918	-			
ABLE 50: CC	LA		OWA OWA	mey Docket 44021-5033-01-WO		
imopoln((s): E	. 6 ms			Dogumen	11. 3 1400° 11.8 1880 1400 1	
HLGC	LDA Segre	Tox_Meen	Tox_SD :	Moullo's Meau	NonTox_SD	
898	98.97	207.83	30.39	83.6	28.08	
3556	98.97	237.06	26.46	86.48	35.04	
9075	98.97	564.28	135.31	140.68	62.52	
4234	98.97	965.16	164.42	144.42	112.76	
925	98.94	217.47	61.66	818.72	302.08	
3202	98.94	595.06	88.74	240.17	79.72	
1115	98.94	515.24	89.29	90.34	97.17	
23463	98.91	144.81	17.94	48.66	27.11	
1047	98.91	610.16	209.12	91.93	64.22	
22625	98.91	1151.84	349.46	93.62	130.86	
15313	98.91	228.62	28.55	27.14	35.42	
2250	98.89	311.21	148.26	1885.66	742.62	
2049	98.89	730.9	175.18	134.47	65.43	
3587	98.89	1850.06	625.03	232.47	219.2	
	98.89	496.31	156.53	36.55	89.46	
1600	98.89	865.62	91.27	289.81	138.22	
6440	98.89	7011	2073.58	145.07	441.94	
8314	98.89	153.23	23.28	27.02	23.72	
15617	98.86	273.25	61	69.08	33.51	
8850	98.86	394.89	139.48	61.37	110.96	
1247		802.1	147.45	2209.27	578.15	
16840	98.86	118.41	35.11	27.46	24.66	
19205	98.86	344.09	59.51	112.71	39.33	
2433	98.86	146.6	69.04	28.76	14.66	
15303	98.86	466.93	51.64	202.4	58.69	
2615	98.86	601.55	169.12	86.98	95.83	
19184	98.86	1170.15	479.66	88.33	120.67	
16318	98.86	1802.74	352.74	87.21	265.6	
14424	98.86	204.76	30.06	72.78	32.14	
4942	98.83	122.44	35.96	431.95	110.19	
3963	98.83	295.15	73.84	101.59	36.59	
16965	98.83	1222.88	185.42	541.27	134.79	
9150	98.83		134.81	98.36	102.84	
23538	98.83	693.56	23.56	311.73	55.47	
10594	98.81	160.51	122.13	79.41	69.85	
13619	98.81	325.05 207.15	34.02	62.67	30.59	
10108	98.81	969.56	549.87	24.91	105.96	
19031	98.81	1598.37	236.63	559.86	206.83	
23505	98.81		55.24	905.82	265.7	
2752	98.78	257.48	24.19	189.91	52.97	
4894	98.78	358.13	17.65	82.35	36.41	
15469	98.78	231.5	15.11	21.8	29.6	
20741	98.78	139.6		53.12	85.83	
21230	98.78	419.61	95.31	149.09	130.12	
4952	98.78	864.71	114.38	25.44	16.35	
20303	98.75	93.9	13.06	65.22	43.1	
12965	98.75	309.33	64.95	194.78	53.96	
16267	98.75	525.9	87	404.54	146.49	
21654	98.75	976.32	105.17	42.14	180.33	
8664	98.75	1497.21	561.26		192.25	
17736	98.73	1365.61	587.99	46.77	54.81	





MILE 50: CO	ALA End B. E			mey Docket 449 Documen	21-5088-01-WO (No. 1935328.1
denijjer <i>*</i> 3792 1994		Tox Mean		NonTox_Mean	NonTox_SD
	98.7	1213.54	406.16	135.53	131.21
8259	98.67	469.43	62.34	180.49	68.07
21696	98.67	336.3	72.49	74.7	60.81
4004	98.67	594.76	151.11	24.69	75.49
1494	98.65	786.52	171.21	184.77	98.16
892	98.65	240.74	44.41	69.77	31.76
21380	98.65	70.82	12.55	20.79	11.54
11608	98.65	1730.84	626.04	92.49	280.74
17734	98.65	344.48	27.49	623.12	199.62
24469		83.05	10.58	24.94	14.94
347	98.65	382.31	62.02	125.53	43.81
25643	98.65	628	72.85	308.93	77.73
15266	98.62	1124.18	202.13	125.42	189.81
16081	98.62	613.84	177.95	105.97	80.62
15616	98.59	616.87	252.91	32.8	76.51
11483	98.57	572.08	113	187.41	76.45
17154	98.57		19.12	27.81	16.21
18584	98.57	101.66	823.9	78.44	245.8
1475	98.54	1719.67	90.16	44.66	45.13
18396	98.54	250.91	41.61	34.67	12.96
16964	98.52	112.52	57.81	60.38	16.42
21989	98.49	168.48	86.67	948.59	277.63
21123	98.49	288.69	35.13	90.83	43.02
1261	98.46	278.97		23.05	26.35
18043	98.46	207.91	88.03 17.81	403.07	139.25
17779	98.46	200.92		204.56	76.64
3203	98.46	523.66	63.95 150.75	155.32	99.91
14003	98.46	546.55		77	42.84
24596	98.46	261.04	57.85	50.33	35.51
13499	98.44	247.5	92.07	47.12	52.27
1841	98.44	174.45	18.33		85.77
20725	98.44	221.69	23.63	434.8	86.74
15839	98.41	159.71	15.04	334.99	10.55
16013	98.41	73.9	13.06	26.63 1123.17	248.1
17427	98.41	442.23	89.18		26.92
2686	98.38	140.88	14	61.31	45.22
651	98.38	235.13	90.07	39.8	39.41
2098	98.36	296.8	52.59	132.48	244.57
17735	98.36	1265.9	560.19	153.75	13.62
22865	98.33	84.22	16.52	33.01	46.71
20917	98.33	384.28	101.08	110.21	37.2
15291	98.33	263.22	103.05	69.99	124.03
20386	98.33	813.63	131.65	253.1	109.33
652	98.3	707.19	168.08	79.9	89.49
21653	98.3	614.7	96.08	263.68	133.04
3430	98.3	861.31	187.29	234.49	63.13
15292	98.28	464.17	85.1	161.74	41.75
3454	98.28	376.24	213.33	70.49	
16535	98.28	394.93	100.18	1180.15	435.02
11405	98.22	110.13	13.67	39.33	19.84
650	98.22	283.36	74.3	43.15	52.24
23343	98.17	72.52	17.26	24.66	13.59

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والمحافظة والمستورة والمواجع والمحار والمحار والمحار والمحار والمتارك

TABLE 50: GCL4 A1221-5033-01 Thagoint(s): 3, 6 hrs Document No. 1935					
(d) [c]C		Tox_Mean	Tox_SD .	NonTox_Mean	NonTox_SD
15487	98.17	235.67	74.15	64.8	29.61
1521	98.14	451.79	70.46	150.77	74.49
24235	98.14	1171	320.47	327.17	162.09
14822	98.14	422.28	113.63	140.33	50.8
15558	98.12	682.77	102.77	308.96	115.38
6891	98.12	1762.35	650.92	539.92	206.62
17599	98.09	148.14	48.1	43.77	27.85
25567	98.09	774.32	282.43	143.18	136.52
3831	98.09	117.78	39.92	34.18	24.15
20708	98.06	95.14	17.14	33.88	18.11
3455	98.06	696.64	186.22	234.44	123.5
15489	98.06	156.9	18.65	76.22	23.38
15265	98.04	519.21	104.55	235.65	75.36
22124	98.04	123	25.48	44.17	18.11
3202	98.04	694.27	103.9	230.56	100.47
23302	98.01	171.94	85.54	36.27	19.41
17226	98.01	597.37	62.52	1107.82	235.64
	97.99	215.07	54.25	75	26.83
9815	97.93	52.85	9.28	20.2	8.76
9745	97.93	365.92	76.84	141.95	57.6
15680	97.93	700.19	275.15	100.35	149.2
15995	Br. BJ	1700.10			

TABLE BR: C			/A@o		ney Docket 44921-5033-01-440 Document No. 1935328.1	
alge Hwegoing(s):				Noulox Weeu	NonTox_SD	
lentifler 🗼	LDA_Score	Tox_Mean		136.44	44.25	
4664	99.76	377.68	20.92	258.41	141.69	
2957	99.5	1374.12	163.04	255.07	88.84	
923	99.47	792.04	81.55	143.28	79.8	
2504	99.44	1075.8	276.85	478.67	173.07	
3055	99.42	86.48	19.54	1709.02	349.89	
2266	99.39	466.47	113.24		25.42	
24019	99.36	166.62	22.91	25.28 547.14	157.98	
787	99.36	1345.7	116.52		416.74	
1437	99.34	429.95	104.1	1419.15	28.72	
23595	99.31	152.68	18.51	36.24	25.3	
11431	99.31	269.44	41.67	67.29	103.18	
3710	99.28	843.51	203.46	86.56	303.62	
4585	99.28	391.85	55.33	1062.9	18.76	
22039	99.28	115.8	13.78	40.16		
23137	99.26	1045.83	179.14	251.37	107.33	
8278	99.26	199.08	13.67	323.31	50.68	
8795	99.23	150.12	17.44	20.65	23.5	
25934	99.2	145.29	21.13	38.44	16.93	
2685	99.2	217.79	19.04	91.1	34.76	
6723	99.2	51.73	8.72	192.66	73.89	
	99.2	337.27	45.6	131.96	108.26	
9757	99.18	140.3	9.99	283.25	69.59	
	99.18	520.6	59.06	184	66.08	
15376	99.18	320.8	69.98	1062.3	343.83	
21592		378.95	51.18	106.63	43.83	
2501	99.15	598.65	343.4	113.68	53.9	
4663	99.15	247.88	43.05	77.7	31.04	
23157	99.07	333.92	139.31	78.61	43.69	
7380	99.05	55.08	27.1	253.6	73.58	
21073	99.05	372.22	58.67	160.39	37.36	
3308	99.02	473.1	197.32	113.37	47.31	
14560	99.02	435.29	33.69	202.67	63.14	
11549	99.02	446.28	79.04	174.25	40.46	
21974	99.02		6.15	155.42	39.37	
22686	99.02	67.26	57.87	28.04	15.07	
5200	99.02	142.98	261.07	152.52	77.73	
23407	98.99	850.19	227.31	26.26	25.84	
16576	98.99	351.95	12.46	30.54	17.1	
13911	98.99	99.9	110.13	81.89	55.13	
22958	98.99	436.75		86.48	35.04	
23556	98.97	237.06	26.46	83.6	28.08	
4898	98.97	207.83	30.39	1866.41	483.03	
19613	98.97	797.9	128.77		97.17	
4115	98.94	515.24	89.29	90.34	79.72	
8202	98.94	595.06	88.74		302.08	
3925	98.94	217.47	61.66	818.72	64.22	
4047	98.91	610.16	209.12	91.93	27.11	
23463	98.91	144.81	17.94	48.66	138.22	
6440	98.89	865.62	91.27	289.81	89.46	
1600	98.89	496.31	156.53	36.55		
2250	98.89	311.21	148.26	1885.66	742.62	
15303	98.86	146.6	69.04	28.76	14.66	

		-92	.2-		
rablebr: C	CLA		- Acc	Magy Docket 449	31-5033-01-W0 No. 4005020 1
rimeredint(s):	3, 6 hrs	A. S		DOCUMEN	k No. 1935328.1
7.7070	LDA_Scoro	Commend north	Tox_SD	MEEM_XOTMON	KonTox_SD :
	98.86	344.09	59.51	112.71	39.33
433		118.41	35.11	27.46	24.66
9205	98.86	802.1	147.45	2209.27	578.15
6840	98.86	394.89	139.48	61.37	110.96
247	98.86	273.25	61	69.08	33.51
3850	98.86	693.56	134.81	98.36	102.84
23538	98.83	1222.88	185.42	541.27	134.79
9150		295,15	73.84	101.59	36.59
16965	98.83	122.44	35.96	431.95	110.19
3963	98.83	204.76	30.06	72.78	32.14
4942	98.83	1598.37	236.63	559.86	206.83
23505	98.81	969.56	549.87	24.91	105.96
19031	98.81	207.15	34.02	62.67	30.59
10108	98.81	325.05	122.13	79.41	69.85
13619	98.81	160.51	23.56	311.73	55.47
10594	98.81	419.61	95.31	53.12	85.83
21230	98.78		15.11	21.8	29.6
20741	98.78	139.6	17.65	82.35	36.41
15469	98.78	231.5	24.19	189.91	52.97
4894	98.78	358.13	55.24	905.82	265.7
2752	98.78	257.48		404.54	146.49
21654	98.75	976.32	105.17	194.78	53.96
16267	98.75	525.9	87	65.22	43.1
12965	98.75	309.33	64.95	25.44	16.35
20303	98.75	93.9	13.06	50.44	26.33
12343	98.75	164	25.68	46.77	192.25
17736	98.73	1365.61	587.99	96.51	46.31
19229	98.73	495.04	292.9	44.3	24.37
2897	98.73	167.15	29.71	180.91	85.03
7414	98.73	742.1	213.43		27.31
7161	98.73	217.02	58.52	48.34	54.81
4407	98.73	461.09	98.1	143.05	119.62
2226	98.73	133.54	26.66	440.38	196.11
14292	98.7	2440.9	1615.99	423.23	81.77
15557	98.7	274.54	20	470.85	39.41
13261	98.7	171.34	33.82	27.89	81.96
12794	98.7	698.16	263.66	266.05	
14004	98.67	336.3	72.49	74.7	60.81
21696	98.67	469.43	62.34	180.49	68.07
24146	98.67	321.22	15.49	179.9	56.48
17734	98.65	1730.84	626.04	92.49	280.74
25643	98.65	382.31	62.02	125.53	43.81
7524	98.65	1301.15	140.25	573.32	159.78
24388	98.65	696	353.6	146.01	82.84
11608	98.65	70.82	12.55	20.79	11.54
24469	98.65	344.48	27.49	623.12	199.62
15266	98.62	628	72.85	308.93	77.73
4171	98.62	355.59	52.61	155.68	61.97
18999	98.62	412.02	127.59	152.57	54.66
2099	98.62	860.94	104.52	451.67	98.49
11484	98.62	225.2	109.92	24.87	41.91
17154	98.57	572.08	113	187.41	76.45

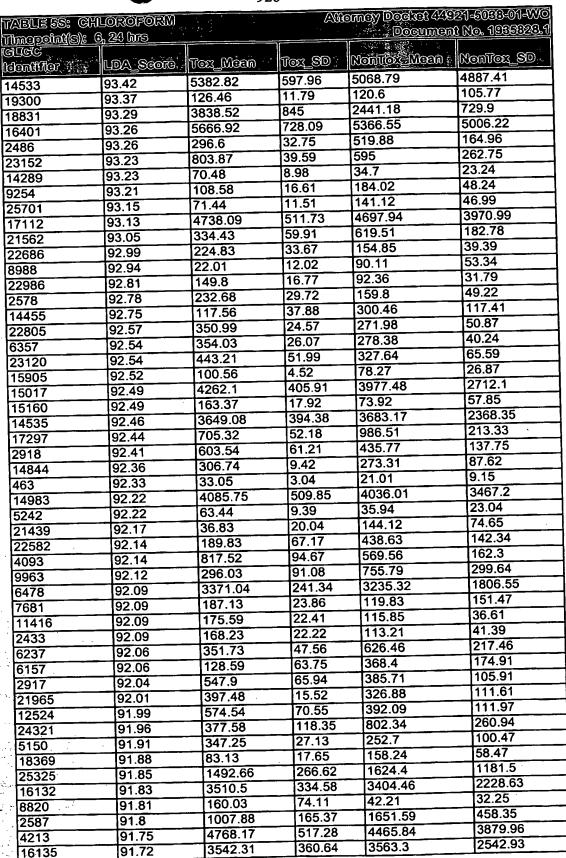


			23- 		24 5200 64 906
WBLE 57: C Imogoint(s):	CL4 3, 6 hrs	ONA.		may Docket 44921-5033-01-440 * Document No. 1935328.1	
FICE(C)	LDA_Score	Tex Mean	Tox_SD	NonTox Moem	NonTox_SD
		101.66	19.12	27.81	16.21
8584	98.57	250.91	90.16	44.66	45.13
8396	98.54	112.52	41.61	34.67	12.96
6964	98.52	168.48	57.81	60.38	16.42
1989	98.49	288.69	86.67	948.59	277.63
1123	98.49	278.97	35.13	90.83	43.02
261	98.46	200.92	17.81	403.07	139.25
7779	98.46	523.66	63.95	204.56	76.64
203	98.46	546.55	150.75	155.32	99.91
4003	98.46	261.04	57.85	77	42.84
24596	98.46	247.5	92.07	50.33	35.51
3499	98.44	174.45	18.33	47.12	52.27
1841	98.44	221.69	23.63	434.8	85.77
20725	98.44	159.71	15.04	334.99	86.74
15839	98.41	73.9	13.06	26.63	10.55
16013	98.41	442.23	89.18	1123.17	248.1
17427	98.41	140.88	14	61.31	26.92
2686	98.38		52.59	132.48	39.41
2098	98.36	296.8	16.52	33.01	13.62
22865	98.33	84.22	101.08	110.21	46.71
20917	98.33	384.28	131.65	253.1	124.03
20386	98.33	813.63	168.08	79.9	109.33
652	98.3	707.19		263.68	89.49
21653	98.3	614.7	96.08	70.49	41.75
3454	98.28	376.24	213.33	1180.15	435.02
16535	98.28	394.93	100.18	39.33	19.84
11405	98.22	110.13		24.66	13.59
23343	98.17	72.52	17.26	64.8	29.61
15487	98.17	235.67	74.15	150.77	74.49
1521	98.14	451.79	70.46	140.33	50.8
14822	98.14	422.28	113.63	539.92	206.62
6891	98.12	1762.35	650.92	43.77	27.85
17599	98.09	148.14	48.1		18.11
20708	98.06	95.14	17.14	33.88	123.5
3455	98.06	696.64	186.22	76.22	23.38
15489	98.06	156.9	18.65		75.36
15265	98.04	519.21	104.55	235.65	100.47
3202	98.04	694.27	103.9	230.56	19.41
23302	98.01	171.94	85.54	36.27	235.64
17226	98.01	597.37	62.52	1107.82	26.83
9815	97.99	215.07	54.25	75	30.44
17311	97.93	167.58	26.5	76.97	8.76
9745	97.93	52.85	9.28	20.2	57.6
15680	97.93	365.92	76.84	141.95	
15995	97.93	700.19	275.15	100.35	149.2 122.56
19768	97.91	783.1	280.56	280.55	
4282	97.91	495.44	106.03	1623.5	555.97
18731	97.85	243.22	32.46	131.34	31.87
15011	97.83	176.79	13.84	82.55	33.07
17530	97.83	71.94	8.5	256.97	108.02
2577	97.83	189.24	25.15	78	31.18
21670	97.8	83.35	21.31	25.73	15.06

TABLE SR: . C	G(4)			(Aliomey, Docket 44221-5133-01-WO Document No. 1935123.1		
Mingoin((S): ELEC Mingoin((S):	3,6 lits LDA Score	Tox Mean	Tox_SD	1000	KonTox_SD	
23950	97.8	100.27	16.13	40.96	15.41	
25618	97.8	542.4	51.08	281.65	140.72	
17379	97.77	337.8	34.18	117.76	70.29	
25496	97.75	191.87	40.42	88.96	39.35	
4327	97.72	159.36	24.83	51.28	33.42	
20755	97.72	242.86	61.02	55.3	62.98	
25203	97.69	96.94	38.36	24.73	16.47	
15083	97.69	80.76	19.1	27.27	14.34	
15324	97.69	67.26	11.56	29.55	10.35	
21122	97.69	666.25	69.55	1527.72	489.13	
4433	97.67	189.09	22.35	104.74	25.81	
15426	97.67	151.69	11.27	266.5	62.92	
1262	97.64	149.23	23.35	48.6	30.4	
16495	97.64	311.33	25.08	557.89	151.32	
20518	97.64	42.18	9.55	92.89	28.62	
4527	97.61	96.07	31.08	33.33	13.82	
21707	97.59	212.82	31.29	40.75	52.01	
24295	97.59	29.77	5.61	61.48	15.44	
15997	97.59	993.97	330.76	127.05	180.56	
20735	97.59	615.07	101.42	188.56	130.36	
25279	97.53	376.76	59.87	191.72	88.04	
3071	97.53	159.18	39.82	55.55	23.32	
18715	97.51	502.95	105.88	195.53	74.69	
1764	97.51	164.48	38.37	64.89	25.87	
15996	97.48	648.65	145.22	106.83	134.2	



TABLE 58: CH			Affic	OTTO DOCKE! 44E	21-5033-01-VVO 1 No. 1935323.1
Timgoin(S): (CCCC	5, 24:) MFS				
Identifier	LDA_Score .	Tox_Modin :	TOX_SD :	NonTox_Mean	Monton SD.
1698	98.51	1026.18	160.21	207.5	206.39
3650	97.58	91.37	23.19	35.71	20.82
11363	97.29	878.58	58.68	502.12	172.77
24048	97.19	914.74	77.01	526.63	176.68
17693	96.58	440.49	118.87	209.5	127.32
21052	96.52	75.18	22.88	292	108.97
17879	96.47	145.62	9.63	292.53	97.44
21054	96.36	154.08	23.04	517.15	208.09
23147	96.13	344.07	62.8	177.07	84.23
13574	96.07	145.4	12.84	306.84	94.01
16331	95.97	383.43	34.37	624.47	138.73
23835	95.94	129.05	12.22	67.5	32.77
19269	95.89	722.37	71.77	478.25	132.04
18642	95.86	380.48	76.72	828.49	218.16
18419	95.83	425.27	19.34	604.62	125.81
4187	95.75	81.61	10.56	25.38	28.98
229	95.73	411.49	47.15	681.58	159.02
5235	95.57	419.63	54.94	277.47	62.34
13164	95.38	4061.26	192.05	3792.73	2475.63
7887	95.3	241.94	25.5	144.43	79.78
16330	95.17	130.26	24.42	278.43	77.95
11321	95.14	319.83	57.09	196.51	49.03
1291	95.04	226.1	24.49	131.87	43.37
2339	94.85	859.71	128.51	534.59	128.92
12312	94.82	423.49	129.08	974.52	266.11
5696	94.75	112.23	29.12	298.61	106.77
23417	94.61	390.49	71.48	229.34	72.03
11291	94.53	45.99	5.76	84.42	26.18
14717	94.53	412	49.52	699.51	156.26
2874	94.51	104.89	10.71	44.65	39.9
6967	94.45	262.45	23.84	401.85	85.39
20386	94.43	406.83	37.75	254.24	127.82
1264	94.24	4746.55	317.98	4273.51	3342.66
16950	94.21	107.88	24.75	50.8	28.44
16922	94.21	446.17	63.09	835.72	195.15
16274	94.19	3918.47	367.71	4095.71	2903.05
1867	94.19	994.23	143.58	628.96	164
18095	94.19	1279.13	265.77	866.9	213.89
1959	94.16	2346.97	266.28	2985.07	1819.98
2632	94.08	197.56	14.25	140.56	30.34
12639	94.03	1480.19	215.18	1100.48	174.35
3167	94.03	490.05	61.74	276.65	104.77
22601	93.98	358.75	64.82	215.51	66.86
13294	93.9	520.88	49.01	347.57	107.05
24135	93.87	210.45	25.46	112.71	98.41
25479	93.87	657.86	120.96	1192.36	283.85
21120	93.68	177.75	26.51	107.33	34.74
17109	93.6	4837.18	479.82	4960.42	4396.98
6632	93.6	396.47	75.47	233.98	99.31
5703	93.5	120.47	15.8	209.61	64.01
1301	93.47	97.12	58.89	1382.83	961.51

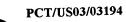




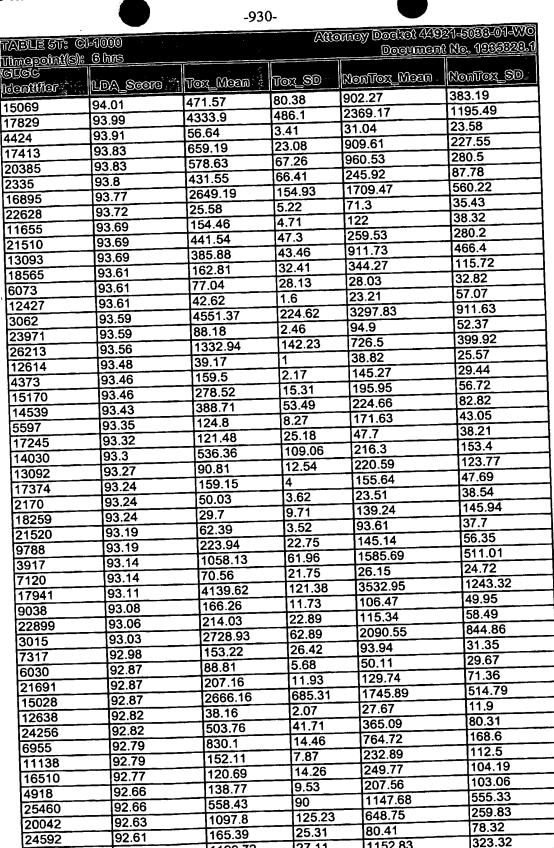


		-92					
TABLE 5S: CH Timepoin((S)::(C	3, 24 lws				21-5039-01-WC LNo. 1935323.1		
allec dentifier	LDA_Score	Tox_Meen:	Toz_SO	Klowlox Mean	KonTox_SD_		
0864	91.68	2218.86	659.9	463.85	361.94		
5439	91.51	2750.3	337.84	2576.24	1801.84		
403	91.51	101.08	23.11	59.16	28.95		
	91.43	1658.04	147.59	1186.11	356.78		
25064	91.43	1284.1	109.61	958.15	280.55		
20385	91.35	3458.19	424.55	3589.94	2271.01		
3109	91.27	369.94	126.96	1013.01	481.72		
17556	91.24	3278.13	238.08	2946.85	1758.3		
19421	91.22	4050.56	420.97	3591.86	2480.65		
21152	91.08	1100.03	176.98	691.7	326.55		
15127		75.59	41.77	233.63	99.98		
24434	91.08	78.16	11.75	47.96	27.24		
6601	91.06	1153.47	90.24	1597.32	376.89		
5622	91.03		638.84	4597.01	3861.97		
14534	90.95	5214.14	105.3	155.7	101.61		
14003	90.91	358.1	92.18	607.01	192.84		
25480	90.87	304.85	648.01	4311.5	3704.57		
17111	90.79	4713.84		61.88	112.43		
1247	90.78	191.1	72.3	4012.97	2555.4		
4254	90.71	4197.28	524.51		2377.51		
23670	90.71	3554.94	587.43	3553.81	1947.51		
1958	90.68	3307.6	376.65	3322.31	48.37		
13575	90.66	54.45	8.77	113.49	447.11		
15124	90.63	1806.5	204.59	1349.16	165.31		
22537	90.63	181.08	56.15	409.14			
18375	90.58	126.1	14.44	91.34	31.59		
17512	90.55	321.62	22.21	426.9	102.97		
16400	90.5	5044.8	654.29	4459.51	3326.87		
25051	90.47	2781.06	275.87	2693.41	1554.51		
16275	90.42	3576.01	401.31	3435.09	2264.21		
17740	90.31	2314.24	183.74	2197.72	959.51		
15535	90.31	709.04	67.82	519.81	136.99		
8899	90.31	638.2	71.63	907.27	199.96		
15462	90.23	364.1	69.92	546.13	120.02		
17092	90.17	165.26	74.28	80.44	46.1		
19679	90.15	176.94	67.51	391.26	140.79		
20700	90.1	3026.81	303.41	2943.79	1601.29		
2078	90.07	154.54	20.05	226.25	56.33		
17787	90.02	1425.8	223.77	1563.93	1005.39		
6017	89.94	176.77	72.97	784.04	505.84		
22025	89.94	2750.39	295.59	2698.62	1739.85		
15977	89.92	1258.29	69.49	1481.76	363.87		
1529	89.81	375.26	73.84	570.86	127.87		
15850	89.81	1621.86	170.59	1236.92	298.98		
	89.69	1033.3	244.85	603.46	198.84		
18597	89.6	165.1	38.21	292.09	88.42		
11635		44.76	4.27	32.69	16.24		
18023	89.57	770.56	96.78	1092.04	232.07		
4198	89.54	949.05	277.46	1506.63	457.27		
24811	89.23	1880.72	160.32	2112.05	832.53		
1818 10886	89.23 89.12	488.98	188.27	978.76	410.42		
				10.0	633.7		

10504	88.93	633.53	107.0		
	1	C22 E2	107.8	7 954.15	261.4
2010	88.99	2685.61	201.0	2685.53	
	HANT GRANG !	UCAL MACCINO			1264.49
Idoniifier Idoniifier	I IDO COMO	Tor Meson	Tions &	M_xoTook G	an KonTox_SD
vimeroini(s): (5, 24:) hits	1			
INVESTIRE SOS. COV	FOKOLORIU			Docu	<u>ment No. 1935028.1</u>
TABLE 58: CK	n ලපලපලපු		11	AMOTHRY DOCKE	44921-5033-01-WO
					MM 160 0000 10000 0



		-923		10/W-166-1969 1969-1969-1969-1969-1969-1969-		
variedi: G	0000 ESM 20			erney Docket 4/921-5053-01-WO Document No. 1955323.1		
impoin((S):	LDV Souis	Tox Mosa	1	Moullox Moou	NonTox_SD	
dendifier :			106.68	240.12	258.7	
348	98.49	1119.06	769.78	4841.79	2231.75	
689	98.44	11663.03	5.78	69.69	37.39	
3176	98.33	134.25 2816.27	190.75	947.13	757.25	
26150	98.22	1346.77	61.75	2450.01	734.56	
8831	98.09	4103.86	466.15	1622.37	743.26	
25469	97.93	84.74	0.74	69.03	32.02	
3695	97.46	5980.7	968.47	2559.55	1128.7	
17832	97.24		2.17	131.3	38.88	
17705	97.24	87.47	822.1	2315.04	1088.73	
25468	97.22	5871.4	413.05	1830.41	1706.66	
15190	97.19	5805.82	2.81	200.07	43.28	
2978	97.11	254.71	10	208.71	72.05	
10084	97.03	325.12	0.57	85.65	30.23	
900	97.01	72.3 166.28	42.24	65.9	44.07	
1831	96.9	221.4	10.34	129.59	47.69	
16448	96.87	5019.6	913.56	1963.38	912.68	
1687	96.85	30.93	1.62	59.35	24.22	
18702	96.77	204.05	60.82	72.17	44.75	
18907	96.66	2395.5	432.8	1028.14	440	
19358	96.63	408.27	6.44	330.36	81.06	
18973	96.53	1935.12	66.06	1302.84	849.41	
20704	96.5	321.92	36.91	774.58	339.34	
16518	96.45	4685.64	104.07	3331.65	1146.08	
20827	96.45	84.28	2	134.58	53.16	
8440	96.45	251.65	5.62	330.3	73.8	
16093	96.34	524.68	85.69	197.34	331.42	
26029	96.32	31.04	0.56	24.91	14.99	
4421	96.26	1149.56	10.22	1186.85	363.84	
2911	96.26	7293.26	1206.98	2884.54	1702	
1684	96.24	125.56	10.3	234.96	84.86	
1588	96.16	1531.89	110.26	2709.7	970.19	
18830	95.52	643.74	107.72	290.8	246.84	
15192	95.52	28.18	3.88	66.66	41.37	
11168	95.42	5549.7	1134.44	1652.01	1653.26	
15189	95.1	14035.38	1640.74	5499.6	4116.85	
1688	95.07	64.95	18.63	21.65	18.89	
1830	95.05	4136.71	785.92	1214.16	1325.62	
15191	94.99	195.25	6.77	136.73	50.51	
22358	94.86	168.9	6.08	115.42	48.42	
18779	94.75	31.12	0.59	37.35	9.79	
16106	94.7	61.5	2.62	86.95	44.13	
12513	94.62	79.23	2	69.15	48.04	
15152	94.52	968.4	164.48	398.16	337.68	
22452	94.46	49.78	1.54	42.9	28.15	
16799	94.41	517.69	30.83	848.73	396.58	
25689	94.36	168.93	9.54	250.4	79.22	
17516	94.17	55.19	0.68	64.32	15.7	
14934	94.14	557.56	20.35	740.89	141.7	
18277	94.12	38.08	7.5	89.66	55.5	
7248	94.09	344.6	12.95	462.37	110.4	



1568.73

699.94

27.11

316.14

1199.72

2804.78

92.55

92.47

16947



	-931-		THEY DOCKES 44921-5033-01-440			
ABLETT: CI	-1000		Affic	May Docker 44.6	21495941400 K No. 1935323.1	
imeroin(S):		3,75%				
dominor	LDA_Score	Tox Moan	Tox_SD ==	KonTox_Mean?	KonTox_SD	
		127.65	24.33	364.34	193.53	
5070	92.26	2040.62	192.33	1332.13	418.16	
3660	92.21	39.44	3.31	62.97	26.78	
3368	92.08	3932.88	355.54	2245.19	1050.2	
5883	91.94	93.73	3.33	106.04	32.97	
0887	91.94	1644.6	43.84	1449.04	289.09	
0821	91.89	2574.07	131.35	1888.13	621.48	
879	91.63	114.7	12.49	66.5	85.23	
4974	91.39	1380.58	285.09	904.09	309.56	
575	91.28		1.6	39.37	26.03	
15931	91.12	33.91 713.55	133.83	338.55	228.89	
10538	91.1		14.08	122.47	46.53	
18897	91.07	62.38 1416	36.06	1381.4	388.65	
18619	91.02	281.77	36.22	181.68	68.52	
5621	91.02		10.77	182.62	104.68	
20928	91.02	100.39	170.48	2825.69	936.69	
21153	90.91	3700.3	68.22	1246.06	337.2	
20998	90.89	1552.14	615.15	1967.12	1001.84	
25579	90.83	3697.94	18.41	808.22	201.34	
2667	90.81	806.53	1.26	21.97	13.43	
25073	90.81	24.52	48.53	824.6	380.17	
20430	90.78	664.84		99.58	68.46	
25257	90.57	40.41	10.14	3013.89	1815.85	
428	90.51	5291.38	342.33	629.33	347.89	
1175	90.36	1097.38	120.72	63.57	23.32	
15980	90.28	46.06	2.82	255.2	127.97	
20386	90.25	134.59	21.64	206.42	73.55	
16562	90.2	186.65	5.61	68.91	21.63	
12422	90.17	49.84	4.02	183.15	42.11	
24598	90.14	145.61	5.92	1978.57	730.81	
8212	90.09	2912.15	248.8	208.22	84.44	
2744	90.06	125.31	14.76		212.47	
20807	89.93	1034.09	39.88	909.72 156.67	91.78	
25370	89.88	47.15	17.84	154.44	38.67	
16178	89.83	119	5.56	40.87	24.45	
15803	89.69	55.6	3.15		23.7	
16871	89.64	38.44	2.92	57.14	22.17	
25233	89.61	32.66	2.3	42.98	49.47	
4244	89.61	105.22	8.16	153.57	82.64	
10260	89.59	130.8	10.92	201.6	261.28	
20429	89.53	483.9	39.45	624.76	128.25	
17693	89.53	134.8	9.36	210.68	1266.28	
1804	89.48	4358.97	669.93	2600.59	124.22	
18747	89.37	68.97	7.78	156.02	24.18	
7040	89.32	31.75	3.06	44.97	81.64	
13091	89.27	74.62	13.07	158.55	54.97	
13392	89.27	124.91	7.81	147.55	612.24	
1130	89.22	3021.37	272.48	2117.73		
15347	89.19	76.44	6.45	118.12	45.9	
24861	89.19	50.98	6.44	81.92	34.59	
4012	89.16	3659.54	300.47	2434.01	1159.92	
43	89.14	336.52	17.02	435.43	131.85	



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TABLEST: Q	1000 6 hrs		Alio	may Docket 4491 Document	21-5053-01-W© } No. 1985328.1
	I DV 2000: 0 M2	Tox Meen ?	Tox SD'		NonTox_SD
	89.11	95.1	3.6	100.23	35.19
5798 48605	89.11	60.44	12.13	116.06	47.35
18695	89.06	2010.3	92	1432.3	498.76
16942	89	108.63	13.82	185.27	68.68
15376	89	647.53	40.04	773.9	203.34
1876	89	30.98	4.98	75.64	62.63
14004		373.48	22.12	466.75	109.45
1602	89	44.95	7.72	43.45	36.04
90	88.98		31.2	738.5	215.53
21078	88.95	642.09	5.61	107.78	76.42
20126	88.95	47.69	617.73	3399.23	2224.03
16132	88.95	5548.49	017.73	3399.20	_1=

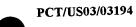
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imepoint(S):	24, 72 hrs	* 1		nogum.	and they described
	5.76	Tox_Meen	Tox SD	NonTox_Mean	MonTox_SD
		4343.21	266.24	350.65	300.88
7758	99.92	4832.38	271.82	1024.63	315.29
6148	99.92		187.28	708.32	486.48
0713	99.89	4038.49	109.05	130.53	184.3
20711	99.81	1748.68	358.1	409.89	405.06
20925	99.79	3531.08	404.2	694.99	568.56
8686	99.71	4822.54	201.74	336.43	174.09
20555	99.66	1569.01 4931.26	383.45	648.45	538.77
8687	99.66		314.97	1363.17	422.7
18293	99.52	3927.89	506.36	373.13	383.93
20715	99.52	3850.93	389.06	558.8	680.95
20714	99.52	3691.04	35.12	266.37	102.63
22370	99.5	639.52		345.13	326.42
23698	99.44	4628.68	846.64	633.78	254.45
23699	99.44	3687.73	615	662.49	244.25
16150	99.36	2966.93	455.8	753.37	196.56
16190	99.34	2283.8	349.19		97.78
9598	99.28	730.57	294.8	156.27	222.18
26109	99.26	2652.69	536.67	139.36	66.91
4272	99.23	643.72	136.8	32.17	222.62
6613	99.2	1727.55	232.16	715.2	115.6
18175	99.2	1053.29	94.78	495.63	361.51
10909	99.13	3621.5	389.28	1866.09	
320	99.13	4073.6	333.1	2163.76	430.02
18891	99.13	1311.32	273.41	298.09	158.9
11228	99.1	2002.17	324.97	752.04	242.27
18890	99.1	3058.12	535.31	742.82	331.65
4271	99.05	921.87	197.26	57.23	125.9
16703	98.99	2963.52	393.12	1163.55	371.89
16701	98.99	5433.88	638.56	2264.91	695.96
25070	98.99	1029.95	79.96	498.56	126.32
5887	98.99	946.58	182.54	66.01	129.21
9929	98.97	1402.26	95.75	669.81	178.07
22416	98.91	755.3	164.6	144.97	96.33
18742	98.91	1760.78	373.07	341.02	170.33
22603	98.86	824.94	95.95	259.6	106.55
15582	98.83	18064.61	3513.5	5681.19	2782.99
16768	98.81	1244.55	138.88	492.57	157.29
12094	98.78	13551.44	2053.03	4815.03	1760.05
	98.67	3584.95	392.45	1740.87	566.84
9889	98.67	1139.45	262.06	260.89	128.06
20554		1064.17	327.8	323.18	118.77
18958	98.67	2684.13	543.55	670.37	274
21010	98.59	509.16	79.42	120.78	84.99
22602	98.57	3217.77	515.96	1024.21	456.07
22604	98.54	185.22	28.32	62.89	37.76
26258	98.52	1007.51	198.15	249.94	147.3
2457	98.49		156.29	66.63	78.11
14595	98.49	543.46	895.71	1423.72	411.39
15085	98.44	3859.87	618.95	294.87	257.53
21355	98.41	2421.28	699.67	416.35	370.25
21354	98.41	3336.63	1033.07	[T 10.00	



				NA Codecilia in the control	921_G028_01_WO		
ABLESU: C	LOFIERATE		AV	Atterney/Docket 4/1921-5033-01-WO Document No. 1935323.1			
imepoint(S):	24, 72 hrs			VIII II DOMESTICAL III II I	III KISS IISSEESSSI		
inditor :	4.4	Tox_Meen	Tox_SD 🔹		NonTox_SD ~		
1488	98.38	919.49	146.95	502.88	102.68		
7554	98.38	3432.54	274.92	1567.61	599.69		
	98.36	1464.51	214.6	739.18	257.23		
882	98.33	783.36	128.64	248.59	110.26		
728	98.33	1354.82	126.05	603.35	194.09		
6767	98.22	1062.29	324.51	368.96	143.77		
8957	98.2	220.96	29.86	48.84	60.94		
944	98.2	1415.65	374.77	203.93	200.91		
602	98.14	216.97	70.09	67.64	37.91		
397	98.12	1959.77	170.24	1179.44	298.82		
0984	98.12	388.37	45.29	128.26	70.88		
7933		456.37	154.17	158.65	58.95		
268	98.09	326.92	39.31	202.01	75.56		
7907	98.06	22.99	7.77	102.61	39.77		
17601	98.06	1938.43	241.9	853.21	297.67		
21341	98.01	512.37	48.11	324.35	58.67		
6281	97.99	3349.54	340.65	1578.68	501.75		
3917	97.96	1081.59	238.46	392.5	156.93		
3860	97.96	917.62	239.04	313.02	109.95		
23427	97.93	1598.68	206.3	218.13	71.08		
21730	97.88		132.09	1611.12	445.42		
4940	97.83	683.55	56.87	282.13	68.97		
9757	97.8	494.26	680.98	1184.96	371.98		
14267	97.77	2984.22	170.93	366.19	168.41		
1977	97.72	1020.16	708.35	1616.91	652.35		
9192	97.69	4096.9	33.02	1030.04	949.07		
20705	97.67	221.95	122.04	489.63	135.64		
23884	97.64	925.8		1597.59	375.9		
5622	97.64	922.33	62.09	634	216.18		
14987	97.61	1228.83	106.11	636.69	183.04		
12071	97.61	265.94	25.71	41.86	20.29		
20859	97.59	101.49	17.4	76.78	53.53		
7274	97.56	196.38	35.41	998.96	358.46		
22598	97.53	497.2	54.98		84.79		
1588	97.53	112.74	10.64	235.05 849.99	310.11		
7420	97.53	1589.12	124.08	2667.52	735.19		
2888	97.51	5090.37	1013.68		963.8		
12095	97.51	4554.54	1260.62	1028.41	444.17		
15124	97.51	2386.45	98.41	1347.8	189.95		
3279	97.43	1355.2	310.06	696.96	106.45		
6439	97.43	552.98	103.15	250.84	221.91		
18867	97.43	342.54	49.74	827.42	39.17		
3439	97.4	236.56	73.58	77.41	246.95		
3121	97.38	1549.14	223.41	816.14			
14608	97.3	458.62	116.38	143.07	79.39 117.76		
2997	97.3	816.62	190.44	373.39			
19706	97.3	77.93	7.9	30.12	19.66		
15580	97.27	4145.83	506.31	2241.47	622.83		
9931	97.27	1120.73	160.22	613.76	152.17		
15391	97.24	1403.72	60.04	985.38	181.31		
16721	97.22	538.92	117.91	259.31 741.61	72.3 180.12		



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ARIBAU! (LOFIERATE	W.			921-5093-01-WO	
imapoini(S)	24,72 hrs				ont No. 1985823.1	
		Tox Mean		Monitox Mean	Moniox_SD	
lendifier			141.66	1026.35	174.25	
448	97.19	1513.44	63.54	1248.73	336.04	
0998	97.14	662.89	19.91	51.41	36.24	
0896	97.14	133.96	547.14	531.17	357.71	
0915	97.08	1874.74	242.15	784.31	188.66	
780	97.08	1478.51	75.63	190.97	85.98	
6546	96.95	483.39 1722.6	211.5	957.1	277.74	
20385	96.9	82.28	13.47	24.34	24.41	
23336	96.74	2472.12	192.84	1272.01	536.04	
15126	96.58	268.56	52.04	643.53	187.59	
5497	96.47	430.68	19.22	637.3	138.22	
9125	96.47	406.36	57	816.82	299.71	
9423	96.42	542.49	77.82	311.02	81.12	
15601	96.31	102.17	46.76	391.28	140.5	
19679	96.24	570.28	34.8	893.23	205.08	
4199	96.08	1695.04	435.99	596.51	278.51	
15409	95.94	3141.59	357.01	1644.35	618.57	
15125	95.92 95.86	641.65	99.05	403.2	92.68	
16435	95.86	301.49	35.02	673.71	228.21	
20789		420.47	70.14	176.47	91.01	
17934	95.84 95.76	106.23	30.01	320.84	127.13	
19391	95.68	198.58	22.06	376.74	127.18	
23344	95.63	816.14	113.28	423.56	180.45	
18361	95.6	696.37	52.9	1091.93	231.88	
4198	95.55	198.29	57.48	493.64	155.04	
5496	95.52	882.69	232.18	290.68	161.55	
15408	95.52	3710.41	370.55	2042.29	723.87	
17807	95.52	104.01	32.08	33.88	44.51	
23778	95.52	268.23	28.95	117.26	70.6	
420	95.49	1184.2	42.45	909.18	212.05	
20807	95.41	354.67	24.95	231.61	67.27	
15175	95.33	55.1	5.13	109.2	38.26	
19831	95.23	2237.41	263.73	1174.29	432.96	
16535 17752	95.2	246.91	27.29	472.26	141.98	
	95.15	778.62	49.59	1082.87	201.61	
2368	94.99	118.82	5.95	186.38	57.29	
11982 4407	94.99	65.96	8.89	144.31	57.72	
24722	94.91	460.51	72.03	824.22	216.67	
4473	94.91	26.49	3.24	55.54	22.35	
15872	94.83	207.44	49.53	499.69	169.76	
32	94.75	424.08	20.75	296.77	83.18	
7927	94.75	76.06	38.92	286.68	116.24	
17886	94.75	714.79	133.15	1253.26	424.96	
2149	94.67	593.63	63.58	972.93	221.98	
3844	94.67	125.56	21.18	66.73	28.7	
15127	94.67	1402.98	197.11	691.16	325.01	
21849	94.62	243.88	13.57	156.96	60.6	
20703	94.57	62.56	49.61	451.21	482.8	
16847	94.57	964.06	60.35	716.81	171.47	
24535	94.54	261.56	52.28	609.69	205.34	
23660	94.41	501.98	224.21	1336.65	417.15	



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able 5v: C	ରୀ ଭ୍ୟାଣାଧାଞ	57.70	A	tomey Docket 4	<u> </u>	
imgpoing(2); Artes on: G	24. 43 hrs	September 1		Dogument No. 1933:223.		
17676	LDV Scolo	Lox Weav	Tox_SD	NonTox Moon	KonTox_SD	
2852	99.02	930.09	103.59	404.94	141.26	
4184	98.81	613.16	114.48	195.53	106.93	
4185	98.7	1105.25	252.52	313.86	179.44	
0529	98.14	795.85	286.58	129.22	186.3	
0783	98.09	165.38	29.95	51.81	40.33	
0869	98.04	173.46	44.44	59.95	48.66	
743	98.01	218.51	24.38	111.11	54.34	
2897	98.01	136.82	41.12	42.67	24.36	
20698	97.96	2770.67	743.06	891.64	430.09	
3438	97.88	139.37	41.23	39.05	23.66	
20701	97.88	2652.49	668.34	875.67	375.55	
14927	97.8	119	27.02	46.5	19.88	
12577	97.8	719.04	218.56	156.33	141.68	
22721	97.66	34.18	8.2	82.29	21.3	
19315	97.51	290.65	38.36	107.83	59.7	
4969	97.51	1091.37	441.09	260.97	253.83	
22898	97.45	359.56	66.18	134.14	71.92	
4267	97.43	933.47	240.99	350.09	150.71	
3895	97.37	76.83	14.81	27.09	23.39	
3695 14766	97.27	975.69	251.84	499.81	119.99	
14926	97.27	196.66	37.87	85.9	30.44	
1520	97.11	69.78	11.41	27.44	14.49	
20042	97.08	1364.3	159.08	646.91	256.74	
24654	97	154.31	32.81	59.27	29.32	
	96.97	366.7	89.43	150.41	57.38	
6986	96.97	134.96	13.59	60.91	29.76	
20305	96.92	123.07	7.89	51.4	38.22	
24165	96.87	1067.13	252.66	626.68	244.11	
15239	96.87	1374.11	381	401.62	265.64	
1437	96.87	91.8	10.55	39.1	24.08	
1050	96.82	103.64	45.53	249.18	62.96	
22522	96.79	1886.68	290.38	783.37	364.98	
17161	96.76	114.07	30.63	28.28	31.26	
25303	96.71	266.95	43.79	612.19	161.23	
6554	96.68	121.92	30.1	47.21	52.54	
1841	96.68	239.38	18.39	355.73	59.41	
17901	96.63	57.54	46.24	306.83	107.02	
20123	96.58	157.41	20.98	80.72	45.18	
14777	96.58	239.36	49.97	140.67	43.43	
6532		1831.26	405.3	1095.62	258.1	
16205	96.52	2015.45	253.29	1355.67	239.94	
23276	96.5	150.96	44.19	65.53	27.13	
13569	96.5	152.08	157.25	1578.02	697.32	
1173	96.5	123.08	21.01	55.44	24.23	
18236	96.47	627.7	72.81	360.25	115.78	
10940	96.42	280.2	46.68	136.28	49.69	
22358	96.42	131.24	26.57	65.71	25.55	
4286	96.42	75.44	29.39	22.27	17.5	
10155	96.39	136.78	30.94	59.92	31.83	
14187	96.36	290.52	56.52	161.43	45.47	
16725	96.31	52.07	6.32	26.41	13.57	



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rable 5V: C	OLCHICINE · · ·			Attorney Docket 4/1921-5033-01-W0			
imagoinus):	24, 43 hrs			Control of the second of the s	NU NOS TERROLISAS.		
यासद	1	For Moss	OS XOT		NonTox_SD		
	LDA Score	1404.73	260.81	951.28	198.32		
8250	96.26	1494.73	126.56	422.95	179.57		
8361	96.23	861.64	515.34	1188.51	342.23		
828	96.2	2125.02	10.45	84.56	30.09		
3220	96.2	142.44	43.46	167.49	63.88		
4278	96.18	322.46	23.55	101.45	46.48		
8794	96.15	201.16	66.22	611.89	139.05		
5606	96.07	318.81	8.11	37.13	21.12		
3116	96.05	75.96	89.03	702.78	167.92		
658	96.02	323.68	15.53	43.43	22.87		
9150	96.02	98.77		633.13	346.79		
175	96.02	26.68	53.03	151.38	63.04		
1491	95.99	270.2	34.05	200.03	80.9		
3400	95.97	88.54	17.75	8643.43	7670.41		
22027	95.94	4655.49	554.23	261.35	69.5		
23578	95.94	432.39	66.61		127.5		
2649	95.91	291.82	59.57	47.4	181.72		
15128	95.89	641.44	181.52	332.73	28.5		
11991	95.86	151.29	10.76	90.47	270.06		
20879	95.86	98.02	96.4	625.24			
22121	95.83	53.25	8.34	21.37	16.77		
20055	95.83	211.75	55.29	67.85	74.1		
22961	95.81	189.36	48.95	87.7	38.66		
2078	95.81	112.19	21.19	226.43	56.03		
4449	95.78	76.38	27.23	239.43	92.91		
21866	95.78	320.77	48.03	177.88	78.44		
4450	95.75	89.71	18.25	197.4	60.95		
	95.73	336.75	311.78	1422.01	540.85		
16367	95.65	325.5	69.75	675.31	194.49		
16577	95.62	29.96	22.6	148.09	63.97		
1524		127.98	15.48	43.22	41.48		
1371	95.59	62.9	59.18	619.83	352.07		
4444	95.54	453.23	46.32	279.3	72.41		
15130	95.54	37.7	22.25	223.31	129.67		
18988	95.51	290.02	55.7	140.73	60.71		
6050	95.51		8.99	109.66	48.1		
12587	95.51	25.2	15.81	976.29	189.31		
15524	95.36	779.76	63.9	174.69	82.83		
2732	95.3	368.18	109.42	74.15	82.69		
7001	95.3	259.45	54.07	1090.18	261.1		
11213	95.28	664.44	117.3	883.62	224.76		
1562	95.28	371.61		71.95	28.77		
17577	95.14	126.3	11.61	80.79	29.72		
12372	95.14	151.49	24.17		347.1		
2536	95.14	121.28	32.12	599.69	49.73		
17323	95.12	156.38	30.55	47.9	18.9		
14159	95.09	76.07	14.93	34.46	30.87		
9984	95.04	36.18	9.59	83.2	41.07		
14056	95.04	147.43	46.32	64.43			
11588	94.98	31.62	11.38	91.34	35.27		
16178	94.96	230.36	20.52	154.03	38.4		
11024	94.96	286.35	45.67	123.25	76.43		
15202	94.82	1360.13	309.95	652.72	553.54		



Timepoint(S):	OLCHICINE 24, 43 hrs		\$P\$人称:	Corney Docket 4 Docum	13
(dentifier (dentifier	LDV Zeoio	Tox_Moon:	Lox 80	MEEM_XOTROU	NonTox_6
23670	94.82	3160.82	338.65	3555.49	2377.55
1069	94.8	2504.18	433.23	1607.59	389.6 129.02
556	94.77	483.7	42.63	669.24	243.95
25777	94.51	318.97	85.7	686.72	32.75
21690	94.35	117.13	14.99	62.61 121.52	47.23
17086	94.32	63.38	8	564.78	141.56
15598	94.29	294.91	49.72	376.22	127.27
20170	94.29	230.07	21.39 128.05	534.39	128.49
21575	94.27	833.24	87.14	651.06	143.58
1548	94.27	366.2	13.02	145.03	41.04
20798	94.24	77.23	8.65	28.04	13.3
19870	94.21	314.74	97.02	1013.24	481.42
17556	94.19		8.75	29.59	16.79
24662	94.06	59.66	5.35	26.9	17.61
19381	94.06	52.89 465.66	20.9	612.87	105.01
20938	94.03	177.05	33.05	96.6	68.57
24280	94.03	4019.15	282.51	3933.32	2217.69
109	94	22.52	30.34	138.95	53.74
10509	94	56.69	3.87	35.25	14.04
23107	93.84	87.58	21.75	39.77	49.97
16382	93.6	30	9.05	71.35	24.33
12069	93.52	67.84	9.93	38.19	21.02
4438	93.5	4403.33	474.85	4273.69	3219.49
17785	93.39	2114.65	109.27	2329.39	893.94
7459	93.39	89.17	10.32	148.08	39.59
21646	93.31	239.24	99.77	477.76	113.28
19469	93.31 93.29	356.65	146.81	648.34	150.42
9905	93.29	53.93	18.21	141.33	54.37
25084	93.18	44.89	9.04	20.38	23.93
19108	93.13	312.03	41.91	524.74	145.93
23130 25678	92.99	84.27	15.23	37.42	123.26
960	92.94	110.27	25.79	215.94	65.71
10247	92.89	60.51	7.38	33.74	22.82
22781	92.86	147.35	12.71	94.08	54.86
18820	92.81	186.68	17.72	121.96	45.73
1572	92.81	127.62	22.72	73.1	32.46
17934	92.7	346.45	78.42	176.52	91.37
7897	92.7	3762.04	261.66	3454.37	2130.8
23543	92.6	867.78	78.37	585.69	160.55
16269	92.54	96.43	12	58.05	21.96
1481	92.49	112.99	21.45	58.22	29.63
1205	92.49	74.93	7.42	49.91	28.89 47.19
1.000	92.46	143.78	16.61	82.05	4887.3
14533	92.44	5361.59	747.63	5068.88	21.79
13488 4228 4185	92.44	43.02	6	74.03	68.63
4228	92.44	110.28	15.82	199.05	2986.
4185	92.41	3631.55	542.24	4098.24	176.1
4185 17171 634	92.41	136.2	29.48	286.4	416.2
634	92.4	434.92	266.41	1538.17	723.3
1809	92.34	2513.01	1078.75	125.3	720.0
and the second s					



TABLE 5V: C	FOLCHICINE *	The state of the s	: U	Ytomay Docket 44 Docume	1921-5083-01-WO mi No. 1935323.1
kgavijiai kgarijiai	LDA Score	Toz Meen	Tox_SD	New Text	NonTox_SD :
	92.22	38.62	11.73	86.71	30.18
2846		23.72	37.72	203.01	224.06
1299	92.14		249.85	1352.55	362.92
25525	92.13	391.78		107.48	28.89
18333	92.12	67.56	8.25		230.28
24247	92.06	24.23	11.88	208.45	
5622	92.05	3055.75	524.7	1589.25	364.4

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940-		

TABLESW: COLCHCINE Threpoin(s): 6 hrs		Attorney Docket 44921-5033-01-WO Document No. 1935328.1			
Mimepoini(S):	3 6 m/s 1		3 534		
ldeniliter -	LDA_Score	TOX_MEEM	TOX_SD:	Mognifox Mosu	NonTox_SD
3431	99.92	3003.78	137.68	1039.49	297.06
12309	99.87	103.17	6.79	394.9	128.08
1322	99.81	152.11	57.45	4147.31	2078.8
8817	99.79	1652.09	73.44	793.99	189.21
14380	99.76	104.76	24.58	686.81	268.39
18657	99.76	1070.31	92.78	283.11	78.12
3365	99.76	141.98	8.14	805.22	237.27
9805	99.76	102.1	16.87	392.85	100.3
3924	99.74	61.79	13.53	327.39	114.57
8815	99.74	1667.42	133.87	537.52	121.88
18999	99.68	672.86	62.96	152.02	50.17
15300	99.68	3063.12	397.15	224.88	176.58
15147	99.66	1984.86	272.98	434.67	269.97
5466	99.66	311.72	16.39	109.06	36
	99.66	701.23	73.28	152.16	68.4
23194	99.63	1929.61	166.63	624.27	214.67
8639 7176	99.6	473.27	90.16	55.97	31.41
	99.58	969.49	161.91	220.76	103.89
15146	99.58	60.89	5.14	397.24	127.85
7003	99.55	209.43	14.77	29.37	24.23
16809		2201.06	140.82	497.76	236.01
1501	99.55	327.38	10.42	105.78	45.45
17590	99.52	370.95	91.31	1587.52	507.88
3917	99.5	107.12	12.8	336.5	104.7
8065	99.5	628.63	89.56	178.93	69.93
1455	99.5	209.57	9.38	489.28	117.19
4843	99.5	37.55	4.37	260.43	96.17
11021	99.5	337.07	55.28	52.04	34.64
17477	99.5	71.08	3.9	24.09	13.68
659	99.47	659.77	23.86	322.94	96.45
21529	99.44	1516.47	193.51	22.03	103.56
15301	99.44	144.42	12.71	45.05	46.53
18396	99.42		261.46	2439.35	721.08
18831	99.39	5369.55	103.83	70.09	100.96
9541	99.39	910.79	16.63	42.19	162.72
4593	99.36	124.94	263.05	78.72	248.28
5059	99.36	582.33	50.19	51.29	21.07
13981	99.36	220.09	91.5	120.32	67.79
22677	99.36	679.46		328.05	447.29
16982	99.34	3559.85	425.59	69.18	33.89
8850	99.34	275.16	43.63	21.52	12.04
3014	99.34	124.98	27.93	28.79	15.23
13469	99.34	92.95	8.22		258.46
4594	99.31	179.56	52.13	51.1	47.56
22242	99.31	205.26	26.42	47.27	36.92
4607	99.31	239.07	21.78	92.71	70.59
23944	99.31	763.5	65.73	359.91	149.74
24431	99.31	497.97	36.23	62.76	396.93
22515	99.28	525.18	166.82	128.66	109.9
21579	99.28	456.96	47.95	201.32	265.55
21574	99.28	2212.4	196.93	979.84	46.22
12751	99.28	502.26	102.49	139.18	140.22



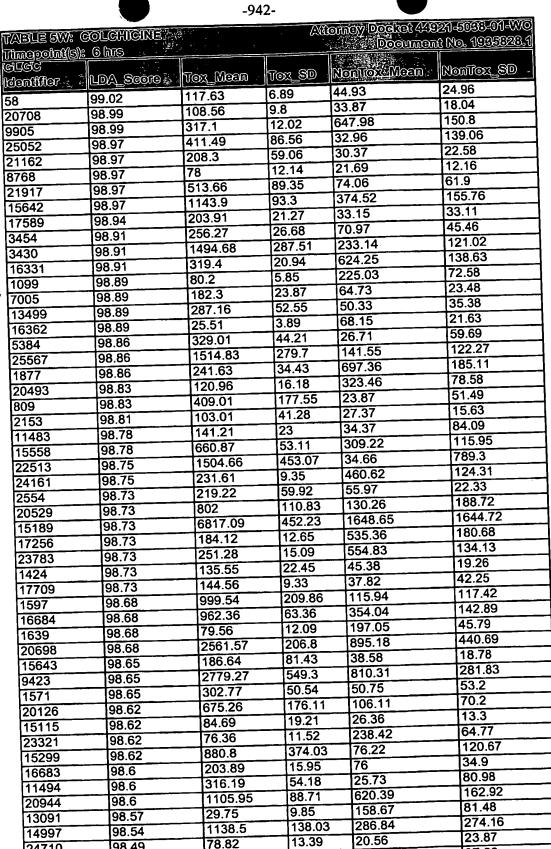
					200 E000 04 W		
rable 5w: (OLGHIGINE:		. : de 26 200 (* : * : *	omey Docket 444 Docume	omey Docket 44921-5093-01-Wo : Document No. 1985328.1		
HMGDOMM(S)):	OMS A		The state of the s	MOONTOX_MOON			
e e filline	LDV Segio	Lox Meau					
5644	99.28	3580.73	254.81	1364.27	373.04		
8529	99.28	316.71	27.18	70.52	38.9		
297	99.26	123.7	11.89	32.51	32.47		
7499	99.26	283.23	105.3	25.57	88.72		
15934	99.26	21.46	6.55	128.62	55.85		
3206	99.26	3401.55	303.15	1045.12	515.69		
3837	99.26	62.75	7.7	217.89	57.87		
20448	99.26	569.14	151.04	41.49	68.65		
21654	99.26	1204.09	81.08	404.24	144.25		
1809	99.23	1532.27	217.07	131.69	738.56		
13446	99.23	294.87	45.69	33.66	33.96		
13633	99.23	1384.8	96.79	496.93	213.99		
21414	99.23	729.49	177.7	118.2	172.81		
6431	99.21	558.21	120.21	185.97	237.27		
20920	99.21	2028.46	278.16	787.34	254.71		
11852	99.21	69.06	12.64	206.91	59.32		
13549	99.21	804.95	145.11	195.07	123.29		
15645	99.21	2319.1	172.44	896.55	376.2		
22681	99.21	2994.7	468.23	151.35	329.73		
17908	99.21	510.9	42.69	71.6	114.43		
8477	99.21	835.72	41.61	300.88	115.6		
2555	99.21	1057.83	181.9	124.95	74.9		
7380	99.18	229.62	32.08	79.02	45.87		
	99.18	284.79	27.62	57.13	38.91		
23583	99.18	1098.04	281.78	141.17	171.13		
14504	99.15	198.8	40.87	40.65	30.8		
7006	99.15	269.06	21.19	774.91	201.78		
1876	99.15	2065.98	202.96	365.35	266		
2161	99.15	958.14	123.29	319.92	103.52		
1802	99.15	420.66	33.32	198.94	64.82		
3817	99.15	1593.8	259.08	506.57	117.73		
12928	99.15	395.82	51.09	73.02	49.29		
21130	99.15	277.53	21.42	66.12	45.47		
4822	99.13	172.8	60.11	26.22	182.1		
8092	99.13	630.45	41.76	1186.15	265.28		
2516	99.13	368.13	53.74	137.06	55.51		
2492		6793.8	359.02	2695.75	948.83		
18830	99.13	786.03	179.41	38.81	96.78		
20449	99.13	517.14	63.34	53.46	74.66		
4731	99.13	134.91	17.76	31.8	53.72		
2629	99.1	501.65	99.54	120.56	47.2		
8849	99.1	41.73	3.35	134.74	44.02		
64	99.1	706.13	34.54	276.91	131.44		
22746	99.1	951.19	208.78	86.33	89.57		
19184	99.1	536.91	153.9	165.87	596.39		
8314	99.07		117.41	637.1	123.23		
22140	99.07	1120.9	24.59	79.62	37.6		
9668	99.07	234.87	69.49	20.06	48.59		
21445	99.07	261.65	153.45	43.24	32.31		
14250	99.05	448.93		48.23	66.12		
20523	99.05	424.46	47.64	30.57	14.08		
20421	99.02	63.91	3.34	130.57			

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65.21

48.43

244.99



98.49

98.49

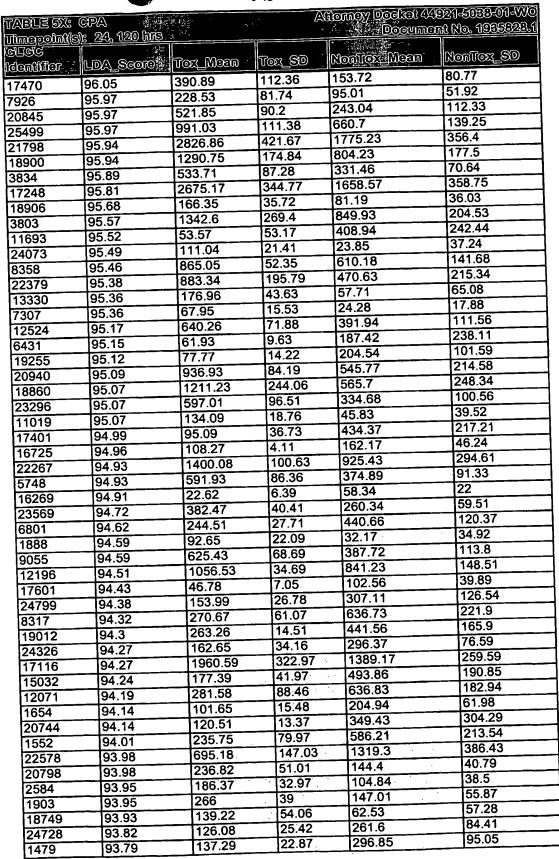
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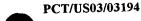


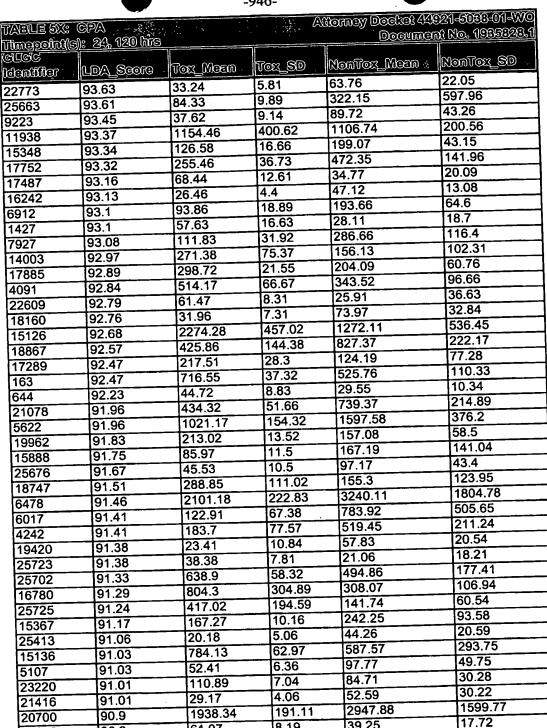
TABLE 5W:	TABLE 5XX: COLCHICINE Timepoin((s): 6 ins		Afformay Docket 44221-5133-91-WC Document No. 1985223.			
Gentifor: Gentifor:		Tox_Mean	Tox_SD &	Nowwest Meen	NonTox_SD	
17494	98.49	21.86	2.23	50.18	38.03	
20701	98.49	2378.94	191.39	879.22	387.02	
	98.46	93.05	4.91	178.23	48.36	
22567	98.46	34.22	12.21	220.74	123.58	
13092		183.83	20.42	493.52	155.09	
5496	98.44	3539.42	970.19	1007.36	358.45	
9424	98.44		12.73	74.41	23.42	
20819	98.41	166.5	553.35	1209.98	1314.12	
15191	98.41	5712.2		214.96	83.52	
16564	98.41	530.29	61.97	254.51	97.78	
23300	98.41	90.83	11.7		27.34	
20589	98.41	55.68	6.96	25.28	104.3	
13930	98.38	507.15	82.87	146.72		
6071	98.38	48.48	15.1	252.45	84.87	
23871	98.38	129.96	26.44	34.63	68.3	

	PCT/US03/03194
y boatat 449	21-5083-01-WO
Documen	1 No. 1935323.1
OX_MEEM_xo	NonTox_SD,
	29.89
	110.59
06	217.92
91	319.14
.19	290.22
38	664.86
)9	33.54
09	855.32
15	324.29
78	543.35
34	543.19
5	42.93
6	144.67
	40.04
	1466 74

15987 99.84 515.74 75.37 23.28 29.89 20803 99.55 789.49 72.91 284.3 110.59 286.23 39.55 789.49 72.91 284.3 110.59 286.75 39.23 2165.94 258.75 467.96 217.92 215127 98.81 1907.99 118 688.91 319.14 177.88 98.67 2455.63 377 1067.19 290.22 20.25 22.35 24.93 24.93 24.93 23.54 24.95 24.53 24.9 22.31 24.53 24.9 24.53 24	(G) [] G C	m((s): 24, 120 hrs	Tow Moon	Tox_SD	NonTox_Mean	NonTox
15987 99.84 315.74 72.91 284.3 110.59 20803 99.55 789.49 72.91 284.3 110.59 28672 99.23 2165.94 258.75 487.96 217.92 115127 98.81 1907.99 118 688.91 319.14 11788 98.67 2456.63 377 1067.19 290.22 12155 98.62 1713.86 190.39 627.38 664.86 3381 98.57 244.53 24.9 113.09 33.54 12156 98.54 1995.76 290.54 496.09 655.32 16278 98.54 1995.76 220.23 647.15 324.29 113.09 33.54 12156 98.54 1995.76 220.54 496.09 655.32 16278 98.54 971.01 195.58 239.78 543.35 25055 98.46 921.01 195.58 239.78 543.35 12158 98.44 363.27 103.63 79.75 42.93 17092 98.44 363.27 103.63 79.75 42.93 17092 98.44 731.8 248.9 61.26 144.67 17091 98.44 267.29 74.19 44.1 40.04 1766 98.44 1349.34 239.43 234.4 166.74 17696 98.44 1349.34 239.43 234.4 166.74 17696 98.44 1349.34 239.43 234.4 177.9 25056 98.22 2327.46 332.28 929.48 711.47 17090 98.2 180.69 44.89 58.52 26.59 26.5			Tox_Meen			
28083 99.23 2165.94 258.75 487.96 217.92 18127 98.81 1907.99 118 688.91 319.14 15728 98.82 1713.86 190.39 627.38 664.86 3381 98.62 1713.86 190.39 627.38 664.86 3381 98.54 1995.76 290.54 496.09 35.54 12156 98.54 1995.76 290.54 496.09 35.54 12678 98.54 1784.96 202.31 647.15 324.29 25055 98.46 921.01 195.58 239.78 543.35 12158 98.44 312.04 196.88 230.34 543.19 17092 98.44 731.8 248.9 61.26 144.67 17091 98.44 1349.34 298.9 12.6 144.67 17091 98.44 1349.34 299.43 234.4 166.74 17575 98.41 245 56.74 742.24						110.59
15127 99.81 1907.99 118 688.91 319.14 17788 99.67 2456.63 377 1067.19 290.22 17155 98.62 1713.86 190.39 627.38 664.86 13381 98.67 244.53 24.9 113.09 33.54 12156 98.54 1995.76 290.54 496.09 855.32 12156 98.54 1995.76 290.54 496.09 855.32 122565 98.46 921.01 195.58 239.78 543.35 12158 98.44 912.04 196.88 230.34 543.19 17092 98.44 363.27 103.63 79.75 42.93 17092 98.44 371.8 248.9 61.26 144.67 17091 98.44 1349.34 299.43 234.4 166.74 17096 98.44 1349.34 299.43 234.4 166.74 17096 98.44 1349.34 299.43 234.4 166.74 17096 98.22 2327.46 332.28 929.48 711.47 25066 98.22 2327.46 332.28 929.48 711.47 25066 98.22 2327.46 332.28 929.48 711.47 17090 98.12 1467.53 237.6 386.54 264.88 24860 98.12 1467.53 237.6 386.54 264.88 24860 98.12 1467.53 237.6 386.54 264.88 24860 98.12 1467.53 237.6 384.91 150.72 2084 97.88 1046.26 104.59 534.91 150.72 2084 97.88 1046.26 104.59 534.91 150.72 20707 97.75 1684.19 229.15 602.2 292.56 20707 97.75 1684.19 229.15 602.2 292.56 20707 97.75 1684.19 229.15 602.2 292.56 6824 97.19 1676.23 383.3 466.8 373.76 18401 97.67 1407.45 183.53 788.7 163.35 1850 97.99 1676.23 383.3 466.8 373.76 1966 97.29 66.24 15.74 32.06 15.58 1966 97.29 66.24 15.74 32.06 15.58 1971 97.45 366.81 109.9 204.59 89.6 10315 97.03 890.69 109.82 334.68 343.45 212.15 10315 97.03 890.69 109.82 337.6 389.87 10316 97.70 1676.23 383.3 466.8 373.76 18473 96.66 591.31 72.52 377.48 88.39 9940 97.14 536.15 109.9 204.59 345.66 10316 97.70 198.68 198.69 198.82 343.23 211.25 10315 97.66 181.42 77.60 36.62 183.47 35.22						
15127 98.51 1507.19 1507.19 1290.22 17188 98.67 24456.63 377 1067.19 290.22 12155 98.62 1713.86 190.39 627.38 664.86 648.86 38.57 244.53 24.9 113.09 33.54 12156 98.54 1995.76 290.54 496.09 855.32 16278 98.54 1784.96 202.31 647.15 324.29 205.55 98.46 921.01 195.58 239.78 543.35 25055 98.46 921.01 195.58 239.78 543.35 12158 98.44 912.04 196.88 230.34 543.19 17092 98.44 363.27 103.63 79.75 42.93 17092 98.44 731.8 248.9 61.26 144.67 17091 98.44 1349.34 299.43 234.4 166.74 17091 98.44 1349.34 299.43 234.4 166.74 1755 98.41 245 56.74 742.24 178.9 15755 98.41 245 56.74 742.24 178.9 225056 98.22 2327.46 332.28 299.48 711.47 17090 98.2 180.69 44.89 58.52 26.59 24860 98.12 1467.53 237.6 386.54 264.88 126.49 97.98 298.43 72.1 87.77 56.08 226.49 97.98 298.43 72.1 87.77 56.08 22084 97.88 1046.26 104.59 534.91 1507.2 2084 97.88 1046.26 104.59 534.91 1507.2 2084 97.88 1046.26 104.59 534.91 1507.2 2084 97.75 1684.19 229.15 602.2 292.56 180.69 47.98 298.43 72.1 87.77 56.08 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 1551 97.64 393.37 56.95 1028.38 368.77 1551 97.64 393.37 56.95 1028.38 368.77 1551 97.64 393.37 56.95 1028.38 368.77 1551 97.64 393.37 366.81 90.21 110.09 113.61 1036 96.76 318.65 30.66 318.44 32.06 32.59 345.65 32.59 345.65 32.59 345.65 32.59 345.65 32.59 345.65 32.59 345.65 32.5						319.14
17/88 98.62 17/13.86 190.39 627.38 664.86 3381 98.57 244.53 24.9 113.09 33.54 12156 98.54 1995.76 220.54 496.09 855.32 16278 98.54 1784.96 202.31 647.15 324.29 25055 98.46 921.01 195.58 239.78 53.54 12158 98.44 912.04 196.88 230.34 543.19 17092 98.44 363.27 103.63 79.75 42.93 4312 98.44 731.8 248.9 61.26 144.67 17091 98.44 1349.34 299.43 23.4 166.74 17096 98.44 1349.34 299.43 23.4 166.74 17096 98.44 1349.34 299.43 23.4 166.74 15755 98.41 245 56.74 742.24 178.9 2804 98.25 2575.88 572.75 888.23 388.15 25056 98.22 2327.46 332.28 929.48 711.47 17090 98.2 180.69 44.89 58.52 24860 98.12 1467.53 237.6 386.54 264.88 12160 98.06 2523.88 553.06 1115.37 1301.16 5824 97.98 298.43 72.1 87.77 56.08 5824 97.98 298.43 72.1 87.77 56.08 20707 97.75 1684.19 229.15 602.2 292.56 18401 97.64 393.37 58.95 1028.38 165.74 18401 97.67 1407.45 183.53 788.7 163.35 18401 97.67 1407.45 183.53 788.7 163.35 20864 97.29 66.24 15.74 20864 97.19 1676.23 383.3 468.8 373.76 20864 97.29 66.24 15.74 20864 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 234.56 1849 96.66 581.31 72.52 337.48 88.39 1940 97.14 536.15 109.9 204.59 89.6 1945 96.67 137.45 536.45 148.54 555.57 2266 96.71 589.47 29.66 24 15.74 32.06 15.58 1851 96.69 137.77 60.49 82.59 344.56 23279 96.69 523.77 60.49 82.59 344.56 24860 96.71 589.47 230.63 1701.8 382.64 24860 96.71 589.47 230.63 1701.8 382.64 24860 96.66 581.31 72.52 337.48 88.39 19536 96.61 11.12 10 3.66 63.36 43.92 2387 96.62 1488.62 304.6 734.58 355.58 1864 96.66 1583.43 160.49 259.25 35						290.22
12153 98.57 244.53 24.9 113.09 33.54 12156 98.54 1995.76 290.54 496.09 855.53 12156 98.54 1798.496 290.51 647.15 324.29 16278 98.54 1784.96 290.31 647.15 324.29 25055 98.46 921.01 195.58 239.78 543.35 12158 98.44 3912.04 196.88 230.34 543.19 17092 98.44 363.27 103.63 79.75 42.93 17092 98.44 731.8 248.9 61.26 144.67 17091 98.44 267.29 74.19 44.1 40.04 17096 98.44 1349.34 299.43 234.4 166.74 17096 98.44 1349.34 299.43 234.4 178.9 15755 98.41 245 56.74 742.24 178.9 280804 98.25 2575.88 572.75 888.23 388.15 25056 98.22 2327.46 332.28 929.48 711.47 17090 98.2 180.69 44.89 58.52 26.59 24860 98.12 1467.53 237.6 386.54 264.88 12160 98.06 2523.88 553.06 1115.37 1301.18 5824 97.98 298.43 72.1 87.77 56.08 2004 97.88 1046.26 104.59 534.91 150.72 20707 97.75 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 1795 97.72 1816.8 319.33 346.8 343.3 21391 97.45 366.81 90.21 110.09 113.61 18401 97.67 1407.45 183.53 789.7 163.35 20864 97.19 1676.23 383.3 466.8 373.76 20864 97.19 1676.23 383.3 466.8 373.76 20864 97.19 1676.23 383.3 466.8 373.76 20864 97.19 1676.23 383.3 468.8 367.7 1550 96.6 591.31 72.52 337.48 83.39 1946 96.76 347.82 74.55 148.54 365.57 10396 96.76 347.82 74.55 148.54 365.57 10396 96.76 347.82 74.55						664.86
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8624 97.88 1046.26 104.59 534.91 150.72 20707 97.75 1684.19 229.15 602.2 292.56 1795 97.72 1816.6 318.44 528.46 366.46 18401 97.67 1407.45 183.53 788.7 163.35 1551 97.64 393.37 58.95 1028.38 368.77 21391 97.45 366.81 90.21 110.09 113.61 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 432.3 211.25 10315 97 70.49 7.36 183.61						56.08
2084 97.86 1040.29 229.15 602.2 292.56 20707 97.75 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 18401 97.67 1407.45 183.53 788.7 163.35 1551 97.64 393.37 58.95 1028.38 368.77 21391 97.45 366.81 90.21 110.09 113.61 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 6824 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1850 97 99.1 32.68 432.3 211.25 1550 97 70.49 7.36 183.61 88.5						150.72
20707 97.75 1816.6 318.44 528.46 366.46 1795 97.72 1816.6 318.44 528.46 366.46 18401 97.67 1407.45 183.53 788.7 163.35 1551 97.64 393.37 58.95 1028.38 368.77 21391 97.45 366.81 90.21 110.09 1113.61 113.61 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 3940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 10315 97 70.49 7.36 183.61 88.52 12587 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.63 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 10396 96.76 317.82 74.55 148.54 56.57 1258 96.63 112.16 3.6 63.86 43.99 17553 96.63 112.16 3.6 63.86 43.99 13.36 13.54						292.56
1795 97.67 1407.45 183.53 788.7 163.35 1551 97.64 393.37 58.95 1028.38 368.77 21391 97.45 366.81 90.21 110.09 113.61 906 97.29 66.24 15.74 32.06 15.58 6824 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 210.01 1850 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.63 12613 96.76 181.42 17.69 96.77						366.46
18401 97.67 130.7 155 1028.38 368.77 1551 97.64 393.37 58.95 1028.38 368.77 21391 97.45 366.81 90.21 110.09 113.61 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 317.82 74.55 148.54 56.57 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td>163.35</td>						163.35
1551 97.64 353.37 110.09 113.61 21391 97.45 366.81 90.21 110.09 15.58 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 38.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.63 18718 96.84 1880.88 305.12 827.92 345.63 12266 96.76 317.82 74.55 148.54 56.57 <tr< td=""><td></td><td></td><td></td><td></td><td></td><td>368.77</td></tr<>						368.77
21391 97.43 30.06 15.58 906 97.29 66.24 15.74 32.06 15.58 6824 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 18718 96.84 1880.88 305.12 827.92 345.65 18013 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.66 9136 <td></td> <td></td> <td></td> <td></td> <td>110.09</td> <td>113.61</td>					110.09	113.61
906 97.27 1094.63 340.68 413.45 212.15 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 18718 96.84 1880.88 305.12 827.92 345.65 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.66 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.						15.58
6824 97.27 1676.23 383.3 466.8 373.76 20864 97.19 1676.23 383.3 466.8 373.76 9940 97.14 536.15 109.9 204.59 89.6 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.6 22266 96.71 2589.47 230.63 1701.8 88.39 17553 96.63 112.16 3.6 63.86 43.92<						212.15
20864 97.19 150.55 109.9 204.59 89.6 9940 97.14 536.15 109.9 204.59 210.01 18473 97.03 890.69 109.82 434.29 210.01 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.66 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.6 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 <td></td> <td></td> <td></td> <td></td> <td></td> <td>373.76</td>						373.76
9940 97.14 360.69 109.82 434.29 210.01 18473 97.03 890.69 109.82 434.29 211.25 1550 97 99.1 32.68 432.3 211.25 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.66 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 125281 96.53 298.97 51.27 153.82 48						89.6
18473 97.05 09.03 32.68 432.3 211.25 1550 97 70.49 7.36 183.61 88.52 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.65 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 125281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34						210.01
1550 97 70.49 7.36 183.61 88.52 10315 97 70.49 7.36 183.61 88.52 25287 96.95 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.60 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 125281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 2384 96.26 1488.62 304.6 734.58 233.3 <td></td> <td></td> <td></td> <td></td> <td></td> <td>211.25</td>						211.25
10315 97 237.77 60.49 82.59 44.56 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.65 22266 96.71 2589.47 230.63 1701.8 352.65 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 12157 96.6 1823.08 515.18 570.97 981.3 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 <t< td=""><td></td><td></td><td></td><td></td><td></td><td>88.52</td></t<>						88.52
25287 96.95 251.11 827.92 345.65 18718 96.84 1880.88 305.12 827.92 345.65 12613 96.76 181.42 17.69 96.77 46.74 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.65 22266 96.71 2589.47 230.63 1701.8 352.65 9136 96.66 591.31 72.52 337.48 88.39 9136 96.63 112.16 3.6 63.86 43.92 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87						44.56
18718 96.84 1506.35 17.69 96.77 46.74 12613 96.76 317.82 74.55 148.54 56.57 10396 96.71 2589.47 230.63 1701.8 352.65 22266 96.71 2589.47 230.63 1701.8 352.65 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53						345.65
12613 96.76 181.42 17.95 30.41 56.57 10396 96.76 317.82 74.55 148.54 56.57 22266 96.71 2589.47 230.63 1701.8 352.65 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21						46.74
10396 96.76 317.62 74.03 1701.8 352.63 22266 96.71 2589.47 230.63 1701.8 38.39 9136 96.66 591.31 72.52 337.48 88.39 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 2384 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 <td< td=""><td></td><td></td><td></td><td></td><td></td><td>56.57</td></td<>						56.57
22266 96.71 2589.47 230.03 77.52 337.48 88.39 9136 96.66 591.31 72.52 337.48 43.92 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 2384 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07						352.62
9136 96.66 591.31 72.32 651.16 17553 96.63 112.16 3.6 63.86 43.92 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07						88.39
17553 96.63 112.16 3.0 55.50 981.3 12157 96.6 1823.08 515.18 570.97 981.3 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07						43.92
12157 96.0 1625.65 48.28 25281 96.53 298.97 51.27 153.82 48.28 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07		<u> </u>				981.3
25281 96.53 298.97 31.27 160.52 163.47 52.34 1884 96.47 307.9 56.62 163.47 52.34 23272 96.42 190.64 22.58 357.83 89.87 2384 96.26 1488.62 304.6 734.58 233.3 1354 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07		·				48.28
1884 96.47 307.9 30.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 156.02 157.83	2528	1 96.53				52.34
23272 96.42 130.6 734.58 233.3 2384 96.26 1058.43 260.49 259.25 216.1 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07	1884	96.47				89.87
2384 96.26 1486.62 304.3 159.25 216.1 1354 96.26 1058.43 260.49 259.25 141.4 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07	2327	2 90.42				233.3
1354 96.26 1056.43 200.45 250.45 19256 96.13 172.27 21.81 366.53 141.4 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07	2384	96.26				216.1
19256 96.13 172.21 377.21 122.5 24262 96.07 579.48 43.59 377.21 122.5 20842 96.07 529.22 43.55 355.58 71.07		96.26				141.4
20842 96.07 529.22 43.55 355.58 [71.07	11925	6 196.13				122.5
20842 96.07 529.22 45.55 656.65	1272					71.07
	2084	96.07	529.22	43.55	[333.00	
	the section of					
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109.55

93.58

8.19

16.2

61.07

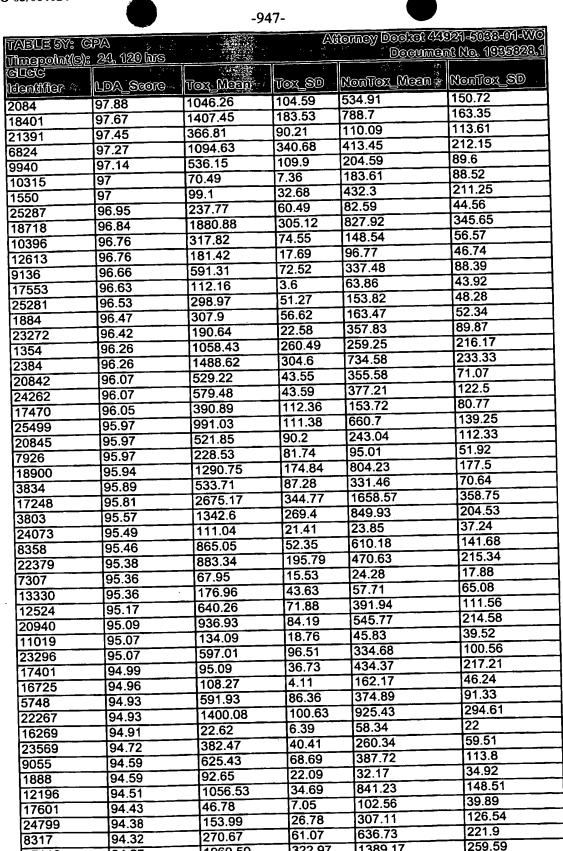
23.9

90.9

90.9

17052





162.65

94.27

94.27

17116

24326

1389.17

296.37

76.59

322.97

34.16

		-94				
TABLE 5Y: C	PA 24, 120 livs		Atterney Doctot 44921-5083-01-WC Document No. 1995323.1			
(G) E(G) C	LDA_Score	Tox_Mean	Iox_SD:	Moodox Meed	NonTox_SD	
15032	94.24	177.39	41.97	493.86	190.85	
12071	94.19	281.58	88.46	636.83	182.94	
1654	94.14	101.65	15.48	204.94	61.98	
1552	94.01	235.75	79.97	586.21	213.54	
20798	93.98	236.82	51.01	144.4	40.79	
22578	93.98	695.18	147.03	1319.3	386.43	
1903	93.95	266	39	147.01	55.87	
2584	93.95	186.37	32.97	104.84	38.5	
18749	93.93	139.22	54.06	62.53	57.28	
21382	93.9	97.87	11.74	181.33	63.63	
18141	93.85	519.6	86.6	329.77	177.47	
24728	93.82	126.08	25.42	261.6	84.41	
7691	93.79	136.99	10.3	92.88	79.96	
22151	93.63	318.16	38.95	167.57	107.58	
22773	93.63	33.24	5.81	63.76	22.05	
25663	93.61	84.33	9.89	322.15	597.96	
19452	93.5	233.52	29.35	136.21	119.58	
9223	93.45	37.62	9.14	89.72	43.26	
11324	93.4	186.39	23.41	320.54	96.1	
11938	93.37	1154.46	400.62	1106.74	200.56	
18325	93.37	479.38	32.88	349.34	84.22	
15348	93.34	126.58	16.66	199.07	43.15	
17752	93.32	255.46	36.73	472.35	141.96	
4073	93.24	479.14	69.74	249.74	143.79	
17487	93.16	68.44	12.61	34.77	20.09	
22477	93.16	163.46	16.79	90.74	43.66	
16242	93.13	26.46	4.4	47.12	13.08	
1427	93.1	57.63	16.63	28.11	18.7	
24049	93.1	2308.97	299.37	1515.64	458.38	
6912	93.1	93.86	18.89	193.66	64.6	
3993	93.1	141.68	12.68	217.35	57.14	
7927	93.08	111.83	31.92	286.66	116.4	
26147	93.05	2363.23	231.98	1652.18	369.56	
19363	93	377.23	202.42	1901.96	903.09	
14003	92.97	271.38	75.37	156.13	102.31	
5241	92.97	227.52	24.55	347.52	86.28	
17885	92.89	298.72	21.55	204.09	60.76	
7870	92.86	60.29	9.12	117.22	46.33	
4091	92.84	514.17	66.67	343.52	96.66	
7316	92.81	43.05	8.75	85.7	38.62	
22609	92.79	61.47	8.31	25.91	36.63	
21694	92.76	347.26	62.65	196.44	83.9	
18160	92.76	31.96	7.31	73.97	32.84	
15126	92.68	2274.28	457.02	1272.11	536.45	
17865	92.65	289.95	12.58	375.54	68.28	
18867	92.57	425.86	144.38	827.37	222.17	
23597	92.52	1130.39	155.89	779.7	193.25	
23768	92.49	305.94	59.08	194.01	80.27	
17289	92.47	217.51	28.3	124.19	77.28	
163	92.47	716.55	37.32	525.76	110.33	
644	92.23	44.72	8.83	29.55	10.34	





TABLE 5Y: GPA Timogooing(s): 24, 120 hrs			Allomay Docket 44921-5083-01-WO Document No. 1985328.1			
glec Mucpoliti(S)		<u></u>	3			
dendifier	LDV/Zeolo	Tox_Mean	Tox_80	MOON TOO MOON	KonTox_SD	
5622	91.96	1021.17	154.32	1597.58	376.2	
19962	91.83	213.02	13.52	157.08	58.5	
25676	91.67	45.53	10.5	97.17	43.4	
18747	91.51	288.85	111.02	155.3	123.95	
6478	91.46	2101.18	222.83	3240.11	1804.78	
6017	91.41	122.91	67.38	783.92	505.65	
1242	91.41	183.7	77.57	519.45	211.24	
19420	91.38	23.41	10.84	57.83	20.54	
25723	91.38	38.38	7.81	21.06	18.21	
25702	91.33	638.9	58.32	494.86	177.41	
15367	91.17	167.27	10.16	242.25	93.58	
25413	91.06	20.18	5.06	44.26	20.59	
15136	91.03	784.13	62.97	587.57	293.75	
5107	91.03	52.41	6.36	97.77	49.75	
23220	91.01	110.89	7.04	84.71	30.28	
21416	91.01	29.17	4.06	52.59	30.22	
20700	90.9	1938.34	191.11	2947.88	1599.77	
17052	90.9	61.07	8.19	39.25	17.72	
11691	90.9	23.9	16.2	109.55	93.58	
20703	90.85	127.49	46.01	451.17	483.02	
20511	90.82	36.97	4.35	67.72	28.83	
15623	90.8	42.73	7.25	71.36	24.25	
348	90.8	118.07	13.49	76.64	27.12	
17226	90.77	1383.07	60.33	1105.17	236.84	
4234	90.74	289.19	42.96	617.48	298.74	
24763	90.69	59.82	6.57	94.14	40.29	
20299	90.53	349.05	95.57	726.79	249.41	
656	90.42	80.81	4.24	102.91	33.62	
727	90.4	279.18	41.4	203.61	51.79	
17972	90.34	37.81	3.51	24.09	15.8	
22396	90.24	59.2	12	99.3	28.76	
5545	90.08	1203.76	78.41	1490.87	574.88	
1159	90.05	119.01	58.08	275.36	107.3	
1973	90.03	306.32	17.08	391.67	107.24	
23481	90	36.24	11.6	69.21	23.13	
25069	89.97	1231.6	563.43	201.55	239.64	
20802	89.91	329.77	64.64	130.33	59.89	
25964	89.89	57.21	7.22	92.15	30.97	
7163	89.87	41.35	7.14	84.31	36.76	
8977	89.81	43.82	4.74	30.37	10.16	
11981	89.81	57.97	4.93	83.71	22.13	
20865	89.79	38.26	8.04	89.98	95.27	
6108	89.76	143.11	13.88	110.78	45.26	
15579	89.73	1458.15	137.46	1679.56	675.17	
17936	89.73	1113.54	83.94	832.34	227.17	
3788	89.71	26.18	1.98	35.84	12.76	
4749	89.68	1019.89	203.98	1655.2	434.34	
24419	89.66	160.97	22.33	99.16	63.61	
1798	89.58	2071.22	211.5	2799.36	1337.75	
819	89.55	2302.42	356.69	2548.98	1185.9	
9527	89.5	89.49	25.07	236.44	129.28	

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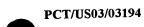


	Tox_Moen :		83.99	43.8
LDA_Scoro#:				
	DIONALIA MANAGAMA	けいいかく みつりしり デジ		000000000000000000000000000000000000000
15 St. Golden T. Co.		152~~ GM 3		しいべいりかいしく ぐっぱつ マー・・・・・
				NonTox SD
24, 120 hrs			Construction of the Constr	T
04 490 BOS		1.5	LOCUME!	WRIEF DEBEGRACE
2/4\		يب.		nt No. 1935023.1
11557101		N/Y	ന്നുത്യ മാരിത്രി 🚧	921-5033-01-00
ì	《数数数》 。	24, 120 hrs	24, 120 his	PA 24, 120 hrs

ABLEFAL G			THE WAS A	omay Docket 449 Documen	21-5068-01-WO K No. 1985328.1
<u>:(e))niogoni</u> Self	6 MS		A CONTRACTOR OF THE PARTY OF TH		4
lentifier.	LDA Score	LOX MOSU	TOLEO	Kouno i Meeu	
1968	99.66	336.13	5.88	154.33	63.23
900	99.58	919	67.9	332.92	144.12
050	99.42	100.04	5.64	28.38	21.7
128	99.39	482.11	106.87	109.27	74.26
3231	99.21	382.85	49.17	122.87	53.82
7506	99.1	212.71	17.76	31.5	71.88
3799	98.97	375.73	72.34	137.29	52.07
754	98.89	387.64	90.19	88.96	55.53
9605	98.89	318.04	35.9	130.26	41.67
7434	98.86	815.52	40.4	394.11	132.33
9467	98.83	963.65	78.28	439.31	162.93
15847	98.73	117.99	17.88	22.43	32.95
18337	98.6	315.9	43.13	156.61	101.32
6272	98.41	397.42	83.96	149.81	45.88
12203	98.36	306.83	80.61	45.36	78.73
20063	98.36	648.97	93.85	267.86	98.57
16053	98.33	292.73	14.22	176.18	220.38
18235	98.3	267.49	51.1	140.41	28.19
9514	98.25	1625.14	124.57	935.34	219.48
18484	98.25	127.21	44.53	44.76	16.71
19069	98.25	180.08	21.52	739.35	315.83
2866	98.17	783.55	140.13	118.19	180.78
13746	98.09	58.47	5.72	162.03	69.53
4937	98.01	631.7	70.25	361.28	90.51
9775	97.96	517.09	98.93	129.4	107.22
15345	97.93	1898.16	268.14	832.68	256.03
14740	97.91	251.1	42.02	92.06	56.78
16043	97.85	65.23	5.34	131.11	45.88
7618	97.75	366.94	73	146.38	58.39
4032	97.72	225.35	46.24	93.86	33.44
7639	97.69	482.34	97.28	276.54	68.37
8305	97.64	281.02	23.78	132.68	83.1
11463	97.59	61.05	6.38	130.46	52.77
6821	97.54	661.11	100.08	231.1	132.5
15551	97.51	212.76	8.45	327.45	67.4
26379	97.48	32.66	3.64	79.32	39.73
15251	97.4	100.59	11.43	43.06	22.57
15387	97.38	330.99	11.81	521.41	121.08
15959	97.35	372.85	69.25	170.23	55.63
	97.35	128.68	14.4	57.53	30.83
14463	97.27	62.42	7.34	125.37	37.49
16087	97.24	195.7	21.08	103.42	33.5
22092	97.24	834.02	110.46	397.43	186.02
19993	97.22	281.74	34.36	125.15	84.24
6582	97.19	89.8	6.76	40.58	25.26
22239	97.19	1007.83	135.25	470.74	215.11
22379	97.16	1219.93	141.04	560.56	425.46
22906		195.88	40.57	70.08	47.32
16509	97.11	1288.15	215.83	530.38	220.05
22548	97.09	510.86	87.31	247.82	74.29
12956	97.06 97.03	100.36	12.46	234.31	80.47

ABLE 5Z: C	PA		AG	Omey Docket 449 Docket	omey Docket 449211-5033-01-WC Document No. 1935328.		
	<u>වැග් වි</u>			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
	LDY Zeco	Tox Mean	TOX_SD	NonTox_Mean	NonTox_SD		
	97.01	564.74	28.69	377.08	92.2		
2235	96.98	356.8	31.13	220.75	53.99		
1514	96.95	85.49	23.62	28.9	16.14		
282	96.95	65.04	8.21	23.62	16.34		
1813	96.93	210.37	37.9	108.38	36.17		
372	96.87	952.01	106.22	524.25	162.71		
647	96.77	29.11	3.32	62.1	23.9		
4419 0369	96.74	302.69	27.14	175.06	59.32		
4844	96.69	105.77	26.25	273.9	87.14		
19992	96.66	1058.37	103.5	621.86	218.14		
	96.58	1547.41	149.55	933.02	715.67		
25056 10637	96.56	100.18	9.48	198.87	66.32		
	96.53	95.36	9.99	176.13	49.95		
14662	96.42	423.3	9.9	601.29	149.1		
9391	96.34	69.88	8.09	28.65	19.93		
10805	96.32	83.46	9.27	31.51	22.46		
11125 10200	96.29	71.26	11.83	24.75	24.84		
	96.29	141.4	10.43	66.67	42.65		
3912	96.29	162.12	31.26	79	28.17		
24051	96.29	370.75	48.03	195.08	67.46		
22981	96.24	212.48	55.64	74.57	47.43		
16199	96.24	1418.52	135.45	817.4	289.52		
2354	96.21	27.93	0.74	42.68	23.4		
15713	96.18	95.25	13.13	24.59	118.53		
4725	96.18	503.31	122.16	238.04	92.28		
4449	96.18	182.57	7.24	307.66	102.75		
16609	96.18	527.26	117	267.03	108.03		
22380	96.13	590.95	73.32	347.49	100.8		
21454	96.13	116.46	23.06	26.8	44.19		
10641	96.08	309.46	45.16	95.94	83.94		
2860	96.05	279.76	35.52	164.4	44.88		
22436	96.05	1149.91	100.8	714.57	206.69		
16910 22929	96.03	609.02	48.31	1241.57	788.34		
	96.03	103.92	25.99	40.82	25.78		
2594	96.03	868.99	125.61	408.26	165.84		
5038	96	20.76	10.18	111.16	53.99		
18925 5624	95.97	144.44	43.05	461.94	196.46		
	95.97	259.18	20.49	174	37.86		
5246 11782	95.92	38.48	8.47	89.15	31.4		
21150	95.89	199.42	28.46	43.82	130.34		
	95.87	1292.62	108.08	850.59	205.85		
3803 1902	95.87	549.84	126.13	225.1	106.21		
5340	95.84	63.81	20.12	345.77	185.52		
	95.84	474.84	63.39	220.32	127.88		
11404	95.79	418.88	70.91	173.42	97.17		
5481	95.79	127.56	9.08	76.26	27.33		
4014	95.76	113.7	13.56	235.54	98.27		
13336	95.73	279.83	32.19	161.14	47.69		
23311	95.73	1105.87	94.65	582.94	225.95		
2729		77.92	12.56	174.14	62.83		
16184 173	95.6 95.55	321.68	77.18	111.75	80.53		

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TABLE 572: C	PA	ž* :		LY LOLDOU KOMOLI Temprod	Nomey Docket 44921-5093-01-WC Document No. 1935328.1		
Timopoint(S):	0 10 <u>18</u>						
dadiia	LDA_Score	Tox Meen	TOX_SD	NowLox [Noew	NonTox_SD		
20188	95.52	90.59	11.88	197.76	86.75		
730	95.5	22.32	1.87	46.5	36.75		
7936	95.26	30.51	2.08	53.18	17.85		
22282	94.91	53.07	5.52	94.39	29.7		
1620	94.91	76.11	5.81	128.03	54.9		
23047	94.78	20.65	1.74	37.72	15.03		
25507	94.7	35.38	7.64	80.16	43.95		
	94.49	105.07	9.11	69.26	36.62		
11840 1283	94.46	37.16	4.76	102.56	52.44		
	94.28	30.71	6.02	72.59	29.14		
20450	94.28	24.65	3.63	23.96	19.34		
2746	94.12	89.2	6.31	166.54	132.76		
18981	94.12	43.35	10.72	102.24	50.73		
1719	94.09	25.11	2.35	41.74	13.07		
18227	94.04	106.12	6	68.88	31.42		
21104		22.96	0.93	25.22	15.43		
209	94.04	38.28	12.47	93.58	34.44		
9092	93.91	641.41	32.27	826.38	223.34		
18867	93.64 93.51	22.92	3.87	46.92	21.81		
1241		37.14	11.24	76.55	22.5		
17110	93.43	101.33	9.45	168.13	88.83		
4683	93.43	25.25	2.88	48.15	27.27		
6601	93.4	23.16	5.04	51.26	19.17		
25805	93.3	101.11	12.46	158.16	36		
16653	93.24	57.45	13.99	114.85	48.83		
17439	93.22	26.58	3.94	47.7	13.41		
23293	93.19	34.49	5.31	64.35	20.12		
8207	93.14	52.99	3.62	85.25	36.56		
1914	93.14	44.37	3.98	88.57	53.72		
25707	93.11	36.21	4.13	55.86	16.25		
15573	93.06		12.77	96.77	37.55		
826	93.03	152.42	5	64.12	24.26		
4292	93	34.66	2.55	95.36	29.63		
16263	92.98	84.73	6.96	88.33	32.6		
20373	92.98	53.95		145.43	57.8		
23826	92.93	94.27	1.71	36.69	21.31		
23302	92.87	43.51	3.93	40.68	13.3		
18883	92.74	24.09	115	1186.76	461.24		
17764	92.69	1657.6	28.74	883.92	394.46		
20701	92.58	603.05	85.74	1189.03	285.05		
25479	92.55	1592.53		84.92	30.78		
19238	92.45	50.15	6.3	93.88	45.91		
9126	92.42	46.46	6.75	78.1	26.9		
17976	92.34	40.43	12.4	85.73	29.06		
1375	92.32	53.48	5.77	390.96	143.52		
20784	92.24	589.17	42.47	114.02	53.58		
20283	92.16	50.37	12.41		56.62		
1143	92.1	49.08	11.87	96.96	41.81		
24392	91.81	52.5	11	101.15	22.79		
15610	91.76	23.38	7.97	53.7	31.25		
14926	91.73	40.32	9.96	86.49	17.67		
25754	91.6	21.19	2.5	39.72			



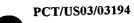
		-9	34-		
TABLE 572: C	PA	128	A00	omey Decket 449	<u>921-5033-01-WO</u>
imepoint(s)	E E E M O S	11 T		Dogumei	nt No. 1935323.1
<u>අ</u> ට්ල්ල්	LDA Secro	Tox Mean:	Tox SD:	MeeM kollwoll	DE KOTWON
dentifier		200	54.05	833.35	196.16
6922	91.55	1104.21	16.41	149.2	74.94
20236	91.36	68.89	5.71	57.55	25.48
389	91.31	28.61	106.68	679.77	159.28
229	91.2	931.81	11.31	262.08	53.25
1624	91.07	203.55	9.94	79.21	37.41
16332	91.04	39.42		21.62	11.53
16825	91.04	35.83	8.73	139.15	43.01
24473	91.04	92.38	8.24		27.59
16108	91.04	173.14	7.06	140.36	262.69
16205	91.02	725.37	118.18	1099.72	133.43
21915	90.99	759.26	80.93	564.61	28.89
17577	90.96	31.71	9.67	72.29	
25343	90.94	35.44	8.05	70.71	30.5
24621	90.94	41	7.36	73.88	28.41
2643	90.89	26.15	5.54	51.02	20.81
25216	90.89	25.75	4.45	52.69	36.06
10980	90.83	20.78	7.05	47.51	19.94
14925	90.83	193.95	25.99	323.81	105
17206	90.78	42.9	9.6	79.16	26.01
24757	90.75	46.07	10.04	77.86	31.85
16924	90.7	330.54	72.13	188.19	110.76
24	90.62	23.27	7.38	52.69	25.07
	90.59	64.83	10.37	30.22	58.33
15097 976	90.57	21.19	4.73	38.49	15.85
	90.54	22.06	2.05	30.92	19.92
24430	90.54	28.2	7.68	55.87	39.49
16383	90.51	35.21	13.55	83.74	39.46
24869	90.51	24.75	10.1	72.07	43.23
11839		76.08	9.9	119.79	44.6
9074	90.51	66.86	4.27	61.06	101.26
15185	90.38	66.18	13.15	122.46	46.55
18897	90.28	70.82	8.07	106.24	29.47
2356	90.28		5.06	54.93	22.13
3928	90.28	28.23	36.59	1150.73	216.85
18618	90.14	1292.25		50.27	28.14
17649	90.04	21.9	3.61	67.6	50.26
20854	90.01	31.79	4.85	81.28	27.05
2070	90.01	45.04	8.46		79.12
16912	90.01	221.66	21.16	303.16	15.06
3783	89.98	20.05	5.91	40.16	162.98
16768	89.96	544.26	29.95	494.82	16.12
442	89.9	20.59	3.46	37.22	10.12



ABLE 5AA.	CPA J			iomey Dockei 44 Docume	ney Docket 44921=5033-014W0 Document No. 1935328.1		
imepoint(S):	6thrs.						
dentifier sist	LDA Score :		Tox_SD	MOONTOX_MOON			
1968	99.66	336.13	5.88	154.33	63.23		
050	99.42	100.04	5.64	28.38	21.7		
3231	99.21	382.85	49.17	122.87	53.82		
434	98.86	815.52	40.4	394.11	132.33		
9467	98.83	963.65	78.28	439.31	162.93		
5847	98.73	117.99	17.88	22.43	32.95		
18337	98.6	315.9	43.13	156.61	101.32		
9514	98.25	1625.14	124.57	935.34	219.48		
2866	98.17	783.55	140.13	118.19	180.78		
13746	98.09	58.47	5.72	162.03	69.53		
14740	97.91	251.1	42.02	92.06	56.78		
16043	97.85	65.23	5.34	131.11	45.88		
7618	97.75	366.94	73	146.38	58.39		
4032	97.72	225.35	46.24	93.86	33.44		
7639	97.69	482.34	97.28	276.54	68.37		
8305	97.64	281.02	23.78	132.68	83.1		
11463	97.59	61.05	6.38	130.46	52.77		
15551	97.51	212.76	8.45	327.45	67.4		
26379	97.48	32.66	3.64	79.32	39.73		
15387	97.38	330.99	11.81	521.41	121.08		
14463	97.35	128.68	14.4	57.53	30.83		
19993	97.24	834.02	110.46	397.43	186.02		
22092	97.24	195.7	21.08	103.42	33.5		
22239	97.19	89.8	6.76	40.58	25.26		
16509	97.11	195.88	40.57	70.08	47.32		
6342	97.03	100.36	12.46	234.31	80.47		
11514	96.98	356.8	31.13	220.75	53.99		
11813	96.95	65.04	8.21	23.62	16.34		
7282	96.95	85.49	23.62	28.9	16.14		
6647	96.87	952.01	106.22	524.25	162.71		
14419	96.77	29.11	3.32	62.1	23.9		
10369	96.74	302.69	27.14	175.06	59.32		
14844	96.69	105.77	26.25	273.9	87.14		
19992	96.66	1058.37	103.5	621.86	218.14		
10637	96.56	100.18	9.48	198.87	66.32		
14662	96.53	95.36	9.99	176.13	49.95		
9391	96.42	423.3	9.9	601.29	149.1		
10805	96.34	69.88	8.09	28.65	19.93		
22981	96.29	370.75	48.03	195.08	67.46		
	96.29	141.4	10.43	66.67	42.65		
3912	96.24	212.48	55.64	74.57	47.43		
16199 15713	96.21	27.93	0.74	42.68	23.4		
	96.18	527.26	117	267.03	108.03		
22380	96.18	182.57	7.24	307.66	102.75		
16609	96.18	503.31	122.16	238.04	92.28		
4449	96.13	590.95	73.32	347.49	100.8		
21454		116.46	23.06	26.8	44.19		
10641	96.1	309.46	45.16	95.94	83.94		
2860	96.08	1149.91	100.8	714.57	206.69		
16910	96.05	279.76	35.52	164.4	44.88		
22436 5038	96.05 96.03	868.99	125.61	408.26	165.84		

Timepoint()	SAA: CPA##### Inn(s): Chris		58		:mt No. 1934
ldendifier GT&C	LDA Seom	Tox_Mean	Tox_SD	MOONTOX MOON	Klowie
18925	96	20.76	10.18	111.16	53.99
5246	95.97	259.18	20.49	174	37.86
5624	95.97	144.44	43.05	461.94	196.46
11782	95.92	38.48	8.47	89.15	31.4
21150	95.89	199.42	28.46	43.82	130.34
1902	95.87	549.84	126.13	225.1	106.21
5340	95.84	63.81	20.12	345.77	185.52
5481	95.79	418.88	70.91	173.42	97.17
4014	95.76	127.56	9.08	76.26	27.33
2729	95.73	1105.87	94.65	582.94	225.95
23311	95.73	279.83	32.19	161.14	47.69
13336	95.73	113.7	13.56	235.54	98.27
8143	95.71	170.23	41.48	36.73	104.73
20845	95.71	101.81	19.04	244.45	113.42
17455	95.71	58.94	16.19	167.12	68.1
	95.71	59.53	6.3	118.67	45.83
22294	95.68	71.81	10.84	154.47	62.84
19375	95.65	140.69	25.48	252.98	59.02
24273	95.65	77.92	12.56	174.14	62.83
16184		119.96	9.09	205.1	64.49
14007	95.57	321.68	77.18	111.75	80.53
173	95.55	418.64	112.72	116.67	121.67
19258	95.52		11.88	197.76	86.75
20188	95.52	90.59	1.87	46.5	36.75
730	95.5	22.32	187.1	978.96	235.48
11708	95.5	1570.75	109.4	368.91	279.54
2161	95.47	718.79	29.11	392.61	106.35
22037	95.47	567.62		56.98	45.71
10008	95.44	46.79	1.57	540.06	130.54
18679	95.44	314.94	30.16	91.87	36.98
11255	95.44	43.35	6.45	137.15	89.51
3172	95.42	379.58	108		86.25
9571	95.36	102.94	24.96	258.74	96.55
11021	95.31	112.36	16.22	260.23	25.17
5662	95.31	100.36	9.13	55.73	15.01
17890	95.28	66.54	20.91	33.49	193.84
8817 17771	95.28	534.09	26.54	796.95	829.79
17771	95.26	459.5	39.93	1474.61	
5561	95.26	635.86	54.55	410.29	115.15
7936	95.26	30.51	2.08	53.18	17.85
8710	95.23	99.02	32.46	24.8	34.56
3791	95.2	123	19.41	225.78	55.92
22476	95.18	797.35	122.65	464.58	134.58
11588	95.18	158.03	13.52	90.91	35.29
5073	95.1	219.4	24.53	96.08	77.65
17343	95.07	141.9	41.79	41.44	49.31
7106	95.02	162.46	51.13	40.3	44.28
23542	94.99	411.48	75.6	220.51	81.08
45171		401.02	57.08	254.06	284.5
15171 1620	94.91	76.11	5.81	128.03	54.9
	94.91	53.07	5.52	94.39	29.7
22282		20.65	1.74	37.72	15.03
23047	94.78	120.00			
•					

			957-		1000 F000 6A W	
Were save	CPA 6 Me			iomey Docket 44221-5033-01-W Document No. 1935328.		
Hee	LDA Score	Tox Mean	Tox_SD ::	Meen seinen	KonTox_SD	
lentifier :			7.64	80.16	43.95	
5507	94.7	35.38	9.11	69.26	36.62	
1840	94.49	105.07		102.56	52.44	
283	94.46	37.16	4.76	72.59	29.14	
0450	94.28	30.71	6.02	23.96	19.34	
746	94.28	24.65	3.63	166.54	132.76	
8981	94.12	89.2	6.31	102.24	50.73	
719	94.12	43.35	10.72	41.74	13.07	
8227	94.09	25.11	2.35	68.88	31,42	
21104	94.04	106.12	6	25.22	15.43	
209	94.04	22.96	0.93		34.44	
9092	93.91	38.28	12.47	93.58	223.34	
18867	93.64	641.41	32.27	826.38	21.81	
1241	93.51	22.92	3.87	46.92	22.5	
17110	93.43	37.14	11.24	76.55	88.83	
4683	93.43	101.33	9.45	168.13		
6601	93.4	25.25	2.88	48.15	27.27	
25805	93.3	23.16	5.04	51.26	19.17	
16653	93.24	101.11	12.46	158.16	36	
17439	93.22	57.45	13.99	114.85	48.83	
23293	93.19	26.58	3.94	47.7	13.41	
8207	93.14	34.49	5.31	64.35	20.12	
1914	93.14	52.99	3.62	85.25	36.56	
25707	93.11	44.37	3.98	88.57	53.72	
15573	93.06	36.21	4.13	55.86	16.25	
	93.03	152.42	12.77	96.77	37.55	
826	93	34.66	5	64.12	24.26	
4292	92.98	84.73	2.55	95.36	29.63	
16263		53.95	6.96	88.33	32.6	
20373	92.98	94.27	7.56	145.43	57.8	
23826	92.93	43.51	1.71	36.69	21.31	
23302	92.87	24.09	3.93	40.68	13.3	
18883	92.74	1657.6	115	1186.76	461.24	
17764	92.69	603.05	28.74	883.92	394.46	
20701	92.58		85.74	1189.03	285.05	
25479	92.55	1592.53	6.3	84.92	30.78	
19238	92.45	50.15	6.75	93.88	45.91	
9126	92.42	46.46	12.4	78.1	26.9	
17976	92.34	40.43	5.77	85.73	29.06	
1375	92.32	53.48		000.00	143.52	
20784	92.24	589.17	72.71	- 144 00	53.58	
20283	92.16	50.37			56.62	
1143	92.1	49.08	11.87		41.81	
24392	91.81	52.5	11	101.15	22.79	
15610	91.76	23.38	7.97	53.7	31.25	
14926	91.73	40.32	9.96	86.49	17.67	
25754	91.6	21.19	2.5	39.72	196.16	
16922	91.55	1104.21	54.05	833.35		
20236	91.36	68.89	16.41	149.2	74.94	
889	91.31	28.61	5.71	57.55	25.48	
229	91.2	931.81	106.68	679.77	159.28	
1624	91.07	203.55	11.31	262.08	53.25	
16332	91.04	39.42	9.94	79.21	37.41	



				Violiney Docket 449	21-5033-01-WO
TABLE SAA:					nt No. 1935928.1
<u> Timepoin((S):</u>	O MB		To the second second		
GEGG Mandifier	LDA Score	Tox_Mean	Tox_SD	Nowloss Ween.	NonTox_SD .
16825	91.04	35.83	8.73	21.62	11.53
24473	91.04	92.38	8.24	139.15	43.01
16108	91.04	173.14	7.06	140.36	27.59
21915	90.99	759.26	80.93	564.61	133.43
17577	90.96	31.71	9.67	72.29	28.89
25343	90.94	35.44	8.05	70.71	30.5
24621	90.94	41	7.36	73.88	28.41
2643	90.89	26.15	5.54	51.02	20.81
25216	90.89	25.75	4.45	52.69	36.06
10980	90.83	20.78	7.05	47.51	19.94
14925	90.83	193.95	25.99	323.81	105
17206	90.78	42.9	9.6	79.16	26.01
24757	90.75	46.07	10.04	77.86	31.85
16924	90.7	330.54	72.13	188.19	110.76
24	90.62	23.27	7.38	52.69	25.07
976	90.57	21.19	4.73	38.49	15.85
24430	90.54	22.06	2.05	30.92	19.92
16383	90.54	28.2	7.68	55.87	39.49
	90.51	35.21	13.55	83.74	39.46
24869 11839	90.51	24.75	10.1	72.07	43.23
9074	90.51	76.08	9.9	119.79	44.6
	90.38	66.86	4.27	61.06	101.26
15185	90.28	66.18	13.15	122.46	46.55
18897 2356	90.28	70.82	8.07	106.24	29.47
3928	90.28	28.23	5.06	54.93	22.13
18618	90.14	1292.25	36.59	1150.73	216.85
17649	90.04	21.9	3.61	50.27	28.14
20854	90.01	31.79	4.85	67.6	50.26
20854	90.01	45.04	8.46	81.28	27.05
16912	90.01	221.66	21.16	303.16	79.12
3783	89.98	20.05	5.91	40.16	15.06
16768	89.96	544.26	29.95	494.82	162.98
	89.9	20.59	3.46	37.22	16.12
				44.89	14.65
				158.7	55.28
				59.27	28.22
20402 25322 16839	89.88 89.85 89.85	26.04 84.09 29.32	5.63 22.98 9.43	44.89 158.7	55.28

TABLE 588:	DICLOFENA	3	NOW	10y.Docket4492	X1-5033-01-WO	
rimgoin((s): 24, hrs				<u>Document No. 1995323.1</u>		
GEGC Gentifier		Tox_Meen	Tox_SD	Novijeka je		
2248	99.42	123.05	20.63	276.37	64.08	
22512	99.18	336.76	228.52	30.43	59.64	
14081	99.18	750.44	470.01	42.44	119.33	
22514	99.02	552.77	366.47	52.29	74.71	
18465	99.02	696.39	23.92	275.39	190.6	
6431	98.97	1162.87	697.58	184.89	232.1	
18580	98.97	957.57	165.01	224.79	140.2	
14504	98.94	1105.51	793.3	141.66	169.98	
23555	98.89	215.07	62.04	28.99	30.81	
13353	98.86	99.16	10.35	285.39	60.5	
3452	98.86	194.02	36.2	31.77	32.37	
22513	98.86	6348.24	2457.86	25.17	731.18	
21445	98.86	146.46	45.47	20.44	49.88	
19703	98.83	38.21	5.5	111.44	38.67	
25052	98.83	1017.44	639.62	31.88	130.45	
23889	98.81	54.47	14	181.08	60.56	
4444	98.81	42.8	23.25	618.7	352.58	
20803	98.81	70.55	7.85	286.63	114.33	
24237	98.81	911.16	255.19	186.41	102.92	
7225	98.78	719.26	93.75	342.63	93.48	
17281	98.73	201.68	20.99	629.02	191.28	
1809	98.7	3248.17	2400.05	128.8	721.62	
22515	98.65	3274.06	1504.56	123.05	365.16	
7697	98.62	123.53	16.25	451.92	149.95	
20529	98.62	1526.01	706.95	129.08	178.59	
11966	98.57	159.04	4.79	295.17	95.77	
14600	98.57	313.62	64.89	116.49	54.82	
4026	98.54	957.89	143.85	373.03	129.82	
17913	98.52	92.83	15.81	195.84	44.19	
21281	98.46	116.9	18.8	307.3	79.38	
20698	98.46	3100.88	519.76	894.92	436.82	
22522	98.44	111.57	20.12	248.85	63.35	
1561	98.44	2089.87	444.45	870.4	215.28	
21660	98.44	4788.18	968.74	1744.98	724.08	
12577	98.44	1074.93	280.47	156.76	140.13	
25290	98.38	157.38	13.62	50.51	74.77	
6532	98.38	260.11	19.09	140.84	43.61	
9166	98.33	130.71	46.97	28.83	18.32	
11904	98.31	160.67	12.68	60.38	43.62	
21740	98.31	2324.58	720.55	735.41	291.35	
5197	98.25	665.08	91.17	332.53	86	
1175	98.23	72.7	15.21	631.74	347.72	
11553	98.23	263.42	25.11	92.62	46.25	
22598	98.2	2883.49	1095.79	993.37	345.97	
18994	98.2	57.38	2.69	29.85	12.42	
699	98.2	1237.14	187.92	610.41	155.87	
26320	98.15	144.01	56.59	23.9	32.81	
11720	98.15	1489.98	359.38	743.47	267.56	
16809	98.15	130.18	28.14	29.63	25.5	
21657	98.12	1770.79	258.03	750.1	290.74	
	100.12			222.01	60.98	

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ABLE 5BB:	DICLOFENAC			rey Docket 4492	<u> </u>	
imepoint(S):	24, hrs	7.3.0		DOGRWEUG	No. 1935020.1	
	449	Tox Means	Tox: SD	MEEM_KOTMON	NonTox_SD :	
		627.32	163.76	31.87	119.86	
221	98.12	62.91	17.76	225.9	90.16	
265	98.09	5465.43	775.66	1968.13	947.45	
854	98.09 98.09	350.06	81.49	51.73	57.86	
20354	98.07	45.3	15.15	208.16	81.81	
939	98.07	5969.98	386.71	1653.18	1653.8	
5189	98.07	2289.3	197.25	1041.02	391.42	
3479	98.07	480.18	173.39	149.92	76.01	
3522	98.07	6728.75	1010.26	2461.72	1089.81	
1850	98.07	1463.42	232.84	590.66	210.37	
19 16367	98.04	304.75	182.47	1419.78	542.72	
1969	98.04	1755.88	638.34	261.33	250.1	
11203	98.01	68.58	2.09	42.4	18.09	
2161	98.01	1595.75	274.89	367.24	274.12	
6018	97.99	749.11	182.64	5848.41	3949.32	
24249	97.99	428.32	12.89	1446.45	1263.42	
24249 7784	97.96	40.67	11.95	121.82	50.8	
4191	97.96	258.34	4.33	183.79	78.42	
22030	97.96	7883.99	135.84	8120.43	4261.97	
	97.93	40.15	4.6	97.1	31.57	
11959	97.93	603.36	352.07	90.42	99.17	
2310	97.91	177.49	38	77.19	109.51	
22321	97.88	2576.2	241.31	1370.88	388.51	
563	97.88	870.99	206.61	322.35	110.36	
5110	97.85	262.26	14.27	158.75	62.78	
24082	97.85	151.27	16.77	320.59	110.78	
6862	97.85	71.15	12.44	194.07	64.18	
4084	97.83	63.68	31.09	238.36	64.78	
23321	97.83	559.61	125.07	284.83	82.89	
3504		649.04	133.72	191.79	217.17	
26133	97.8	831.74	70.75	1604.42	413.81	
9842		648.61	122.28	157.32	138.92	
10659	97.8	1271.59	344.57	489.91	168.45	
14481	97.78	852.43	123.48	346.14	135.56	
20	97.78 97.78	383.1	140.99	126.87	88.36	
2555		7492.5	1443.96	2555	1370.84	
3292	97.78	246.93	38.56	112.87	50.48	
20605	97.75	1276.81	260.98	694.08	136.26	
309	97.75	399.67	66.24	201.11	56.2	
15284	97.75	3144.79	753.44	1199.84	591.08	
17340	97.75	103.78	16.34	33.84	21.73	
19411	97.72	448.09	14.54	318.06	60.33	
19082	97.7	175.18	13.53	102.88	33.13	
8597	97.67	2490.8	624.91	879.77	386.8	
20701	97.67	204.07	8.62	112.17	51.53	
11596	97.64	657.08	84.96	204.22	158.01	
4951	97.64		3.72	78.9	23.21	
10320	97.62	36.54 4643.75	1399.8	1637.06	815.45	
412	97.62	84.44	0.49	87.19	27.36	
	10 / 56	184 44	リリ・サブ	101.10		
6296 20889	97.56 97.54	435.07	184.77	155.58	72.49	



				200 BOCK A 1/166	04_36660_64_000	
ABUE SEB:	DICLOFENA	79	TO BY	ncy Docket 44921-5033-01-WC Document No. 1935323.1		
fimepoint(S):	24, hrs		<u> </u>	Document	l des recens	
HUCC dendifier =	LDA_Score	Tox_Mean	Tox_SD	MOON TO THOSE	NonTox_SD	
	97.51	120.9	29.9	261.09	59.61	
3569	97.46	292.15	101.58	792.75	196.26	
6726 55	97.46	105.31	49.11	41.74	26.6	
55	97.4	2982.73	459.97	1475.19	463.5	
558	97.4	175.4	32.45	65.04	132.7	
3869	97.4	99.16	6.61	197.15	61.13	
450	97.38	1564.26	321.91	807.52	193.29	
3097	97.35	175.05	58.91	708.56	219.76	
1977	97.33	62.93	7.26	177.97	66.66	
1978		42.85	0.76	22.12	19.76	
5112	97.3	68.7	64.18	607.34	298.88	
20707	97.3	1229.29	290.23	368.96	220.83	
6519	97.27		1.46	62.46	20.61	
6446	97.27	28.54	505.82	1593.05	373.48	
622	97.22	2725.41	33.24	455.42	117.76	
4314	97.17	215.14	3.52	26.46	13.62	
15115	97.17	49.63		235.15	688.31	
23868	97.14	579.71	92.07	556.77	145.98	
23322	97.14	185.8	85.55	27.5	16.14	
2153	97.14	59.02	10.93		45.93	
2853	97.11	121.1	21.77	57.69	259.71	
24228	97.09	1920.8	552.93	977.26	351.03	
21014	97.06	418.99	61.15	1043.77	47.67	
23301	97.06	92.56	16.56	188.16	86.65	
8210	97.06	405.39	124.68	126.29	251.25	
15626	97.06	2124.33	290.87	1329.46		
20114	97.03	64.45	6.01	27.02	26.71	
19392	97.03	2795.11	688.74	1455.54	349.41	
20298	96.98	637.18	8.37	508.65	152.64	
3604	96.98	42.06	4.01	80.53	22.91	
5384	96.98	131.54	29.81	27.29	61.5	
16366	96.95	182.94	101.39	798.85	304	
16198	96.93	194.54	41.59	93.11	37.06	
21707	96.93	206.79	62.29	40.94	52.29	
18541	96.93	1513.68	54.25	1076.93	225.43	
10306	96.9	684.54	148.28	343.87	103.05	
4198	96.9	1755.06	186.43	1089.27	230.7	
25691	96.9	1243.83	80.1	887.18	306.88	
16520	96.88	3617.88	707.67	1783.61	608.39	
1641	96.85	237.07	33.58	110.38	51.88	
18611	96.8	1883.04	397.42	1139.82	540.71	
4133	96.74	132.22	38.36	375.36	112.11	
17530	96.74	54.11	22.11	256.81	108.06	
9134	96.72	324.43	15.37	473.65	107.28	
	96.66	42.49	2.35	20.33	14.62	
24263	96.66	77.16	11.72	161.63	58.63	
1540		1601.08	72.37	1043.5	312.68	
3431	96.66	62.44	22.75	194.15	65.15	
12848	96.61	78.18	7.85	43.74	16.04	
871	96.61	212.24	140.67	1277.88	438.73	
13088 15612	96.58 96.56	100.23	6.66	445.31	327.96	



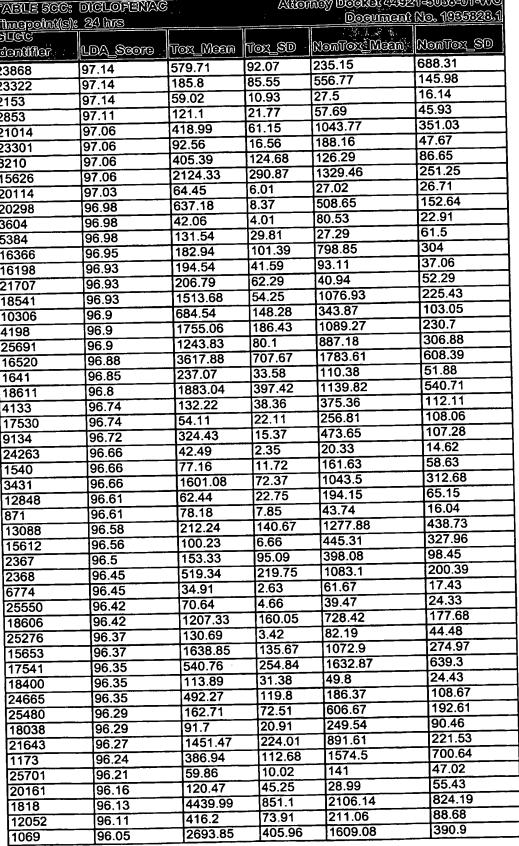
PCT/US03/03194

Thragoint(s):	Table sec: Diclofenae Timgoin((s): 24 his		, de . d		
lderiller, GUSS		Tox_Meen	Tox_SD		Kontox_S
2248	99.42	123.05	20.63	276.37	64.08
14081	99.18	750.44	470.01	42.44	119.33
18465	99.02	696.39	23.92	275.39	190.6
6431	98.97	1162.87	697.58	184.89	232.1
19703	98.83	38.21	5.5	111.44	38.67
20803	98.81	70.55	7.85	286.63	114.33
4444	98.81	42.8	23.25	618.7	352.58
1809	98.7	3248.17	2400.05	128.8	721.62
14600	98.57	313.62	64.89	116.49	54.82
11966	98.57	159.04	4.79	295.17	95.77
4026	98.54	957.89	143.85	373.03	129.82
17913	98.52	92.83	15.81	195.84	44.19
20698	98.46	3100.88	519.76	894.92	436.82
22522	98.44	111.57	20.12	248.85	63.35
6532	98.38	260.11	19.09	140.84	43.61
9166	98.33	130.71	46.97	28.83	18.32
5197	98.25	665.08	91.17	332.53	86
11553	98.23	263.42	25.11	92.62	46.25
18994	98.2	57.38	2.69	29.85	12.42
16809	98.15	130.18	28.14	29.63	25.5
11720	98.15	1489.98	359.38	743.47	267.56
1221	98.12	627.32	163.76	31.87	119.86
4439	98.12	502.34	119.99	222.01	60.98
21657	98.12	1770.79	258.03	750.1	290.74
20354	98.09	350.06	81.49	51.73	57.86
3265		62.91	17.76	225.9	90.16
	98.09	1463.42	232.84	590.66	210.37
19	98.07	6728.75	1010.26	2461.72	1089.81
1850	98.07	2289.3	197.25	1041.02	391.42
6479	98.07		15.15	208.16	81.81
2939	98.07	45.3			542.72
16367	98.04	304.75	182.47	1419.78	274.12
2161	98.01	1595.75	274.89	367.24	
11203	98.01	68.58	2.09	42.4	18.09
24249	97.99	428.32	12.89	1446.45	1263.42
6018	97.99	749.11	182.64	5848.41	3949.32
22030	97.96	7883.99	135.84	8120.43	4261.97
4191	97.96	258.34	4.33	183.79	78.42
7784	97.96	40.67	11.95	121.82	50.8
11959	97.93	40.15	4.6	97.1	31.57
4084	97.85	71.15	12.44	194.07	64.18
6862	97.85	151.27	16.77	320.59	110.78
24082	97.85	262.26	14.27	158.75	62.78
3504	97.83	559.61	125.07	284.83	82.89
23321	97.83	63.68	31.09	238.36	64.78
10659	97.8	648.61	122.28	157.32	138.92
	97.8	831.74	70.75	1604.42	413.81
9842 2555	97.78	383.1	140.99	126.87	88.36
20	97.78	852.43	123.48	346.14	135.56
14481	97.78	1271.59	344.57	489.91	168.45
17340	97.75	3144.79	753.44	1199.84	591.08
15284	97.75	399.67	66.24	201.11	56.2
1. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	101.10	1000.01	1	1	
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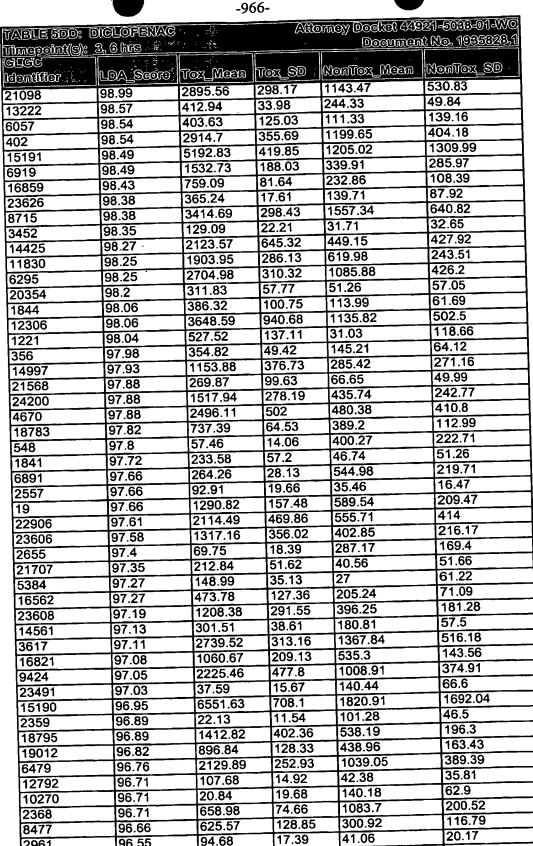


				- 0 -0.000	X 6000 M WA
rimepoin((S):	DICLOFENAC 24 hrs		S. March	may Docket 4499 Document	11695923.1 No. 1985923.1
G.T.G.C.	3.00	Tox_Mean	Toz_SD:	MOONTOX_MOON	MonTox_SD
309	97.75	1276.81	260.98	694.08	136.26
20605	97.75	246.93	38.56	112.87	50.48
9082	97.7	448.09	14.54	318.06	60.33
20701	97.67	2490.8	624.91	879.77	386.8
3597	97.67	175.18	13.53	102.88	33.13
1951	97.64	657.08	84.96	204.22	158.01
112	97.62	4643.75	1399.8	1637.06	815.45
10320	97.62	36.54	3.72	78.9	23.21
5296	97.56	84.44	0.49	87.19	27.36
9583	97.56	299.68	83.41	61.1	99.67
3817	97.56	1208.25	71.46	795.38	193.32
20889	97.54	435.07	184.77	155.58	72.49
6825	97.54	220.78	18.83	427.45	116.42
12108	97.54	162.64	23.68	354.51	99.65
21209	97.51	409.26	138.72	83.36	83.88
6366	97.51	634.09	146.11	274.67	103.36
1690	97.51	333.9	55.29	150.91	49.41
16706	97.51	341.19	41.09	183.25	51.87
23569	97.51	120.9	29.9	261.09	59.61
15652	97.51	2207.48	158.31	1501.42	366.17
8215	97.48	898.23	238.43	386.94	135.31
18239	97.46	125.92	19	31.14	28.12
155	97.46	105.31	49.11	41.74	26.6
16726	97.46	292.15	101.58	792.75	196.26
19412	97.43	747.4	71.56	387	117.83
21871	97.43	595.81	105.03	323.19	79.41
358	97.4	2982.73	459.97	1475.19	463.5
23869	97.4	175.4	32.45	65.04	132.7
6189	97.38	434.7	248.73	3932.55	2204.54
4450	97.38	99.16	6.61	197.15	61.13
8097	97.38	1564.26	321.91	807.52	193.29
21977	97.35	175.05	58.91	708.56	219.76
3773	97.35	279.96	56.93	67.59	60.5
5111	97.35	686.4	173.48	235.43	134.49
10532	97.35	570.1	71.47	279.06	93.25
1431	97.33	28.55	23.44	433.11	188.55
22619	97.33	710.18	106.2	299.88	114.53
11438	97.33	147.39	15.6	67.58	27.21
11322	97.33	1129.97	93.13	701	170.55
10269	97.33	3302.71	386.33	2041.79	390.93
8794	97.33	2165.18	720.69	1099.96	281.4
22746	97.3	707.53	186.64	277.13	131.57
25112	97.3	42.85	0.76	22.12	19.76
20707	97.3	68.7	64.18	607.34	298.88
16446	97.27	28.54	1.46	62.46	20.61
24200	97.27	1227.62	173.04	438.65	250.36
16519	97.27	1229.29	290.23	368.96	220.83
11934	97.25	140.68	16.52	76.25	22.82
23422	97.25	82.48	7.53	46.51	18.73
5622	97.22	2725.41	505.82	1593.05	373.48
15115	97.17	49.63	3.52	26.46	13.62

3/064624		-96	54-		PC1/US03/03
TABLE SCC:	DICLOFENAC			may Docket 4492	x1-5038-01-WO
vimepoint(s)	: 24 hrs		: :		No. 1985328.1
ellec Mandfler	LDA Scote	Tox_Mean	Tox_SD	NonTox Mem	MonTox_SD
23868	97.14	579.71	92.07	235.15	688.31
23322	97.14	185.8	85.55	556.77	145.98
2153	97.14	59.02	10.93	27.5	16.14
2853	97.11	121.1	21.77	57.69	45.93
21014	97.06	418.99	61.15	1043.77	351.03
23301	97.06	92.56	16.56	188.16	47.67
8210	97.06	405.39	124.68	126.29	86.65
15626	97.06	2124.33	290.87	1329.46	251.25
20114	97.03	64.45	6.01	27.02	26.71
20298	96.98	637.18	8.37	508.65	152.64
3604	96.98	42.06	4.01	80.53	22.91
5384	96.98	131.54	29.81	27.29	61.5
16366	96.95	182.94	101.39	798.85	304
16198	96.93	194.54	41.59	93.11	37.06
21707	96.93	206.79	62.29	40.94	52.29
18541	96.93	1513.68	54.25	1076.93	225.43
10306	96.9	684.54	148.28	343.87	103.05
	96.9	1755.06	186.43	1089.27	230.7
4198	96.9	1243.83	80.1	887.18	306.88
25691	96.88	3617.88	707.67	1783.61	608.39
16520	96.85	237.07	33.58	110.38	51.88
1641	96.8	1883.04	397.42	1139.82	540.71
18611	96.74	132.22	38.36	375.36	112.11
4133	96.74	54.11	22.11	256.81	108.06
17530	96.72	324.43	15.37	473.65	107.28
9134		42.49	2.35	20.33	14.62
24263	96.66	77.16	11.72	161.63	58.63
1540	96.66	1601.08	72.37	1043.5	312.68
3431	96.66	62.44	22.75	194.15	65.15
12848	96.61	78.18	7.85	43.74	16.04
871	96.61	212.24	140.67	1277.88	438.73
13088	96.58	100.23	6.66	445.31	327.96
15612	96.56	153.33	95.09	398.08	98.45
2367	96.5	519.34	219.75	1083.1	200.39
2368	96.45	34.91	2.63	61.67	17.43
6774	96.45	70.64	4.66	39.47	24.33
25550	96.42	1207.33	160.05	728.42	177.68
18606	96.42		3.42	82.19	44.48
25276	96.37	130.69	135.67	1072.9	274.97
15653	96.37	1638.85	254.84	1632.87	639.3
17541	96.35	540.76	31.38	49.8	24.43
18400	96.35	113.89	119.8	186.37	108.67
24665	96.35	492.27	72.51	606.67	192.61
25480	96.29	162.71	72.51	240.54	90.46



,						
	2	Aftomey Docket 44921-5033-01-WO Document No. 1935328.1				
	·	Marina S. S. Kill	10000 mass - bal	1000 10000_000		
LDA Score	Tox_Mean	TOX_SD.	NonTox_Ween	NonTox_SD :		
	46.68	19.65	236.3	129.2		
	412.42	130.5	163.03	97		
	106.98	12.5	224.9	72.74		
	2669.42	378.25	1382.32	466.93		
	165.29	41.33	382.07	96.93		
95.92	201.9	63.94	73.68	49.91		
	24 hrs LDA Score 96 95.97 95.95 95.95 95.95	New New	24 hrs 10x Mean 10x SD 96 46.68 19.65 95.97 412.42 130.5 95.95 106.98 12.5 95.95 2669.42 378.25 95.95 165.29 41.33	24 hrs Tex_Mean Tex_SD NonVex_Mean 96 46.68 19.65 236.3 95.97 412.42 130.5 163.03 95.95 106.98 12.5 224.9 95.95 2669.42 378.25 1382.32 95.95 165.29 41.33 382.07		



108.64

719.66

345.63

96.55

96.55

2961

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-967-		

TABLE SOD: DICLOFENAC			A 10 mey Doglar 44221-5033-91-WO			
Timegoin((s)): 3, 6 like			<u> </u>			
CLCC ldonMior	LDV Score	Tox_Mean	Tox_SD :	Monijo, Men.	BE KOTOON	
3773	96.52	237.12	61.33	67.32	60.27	
17664	96.5	715.67	141.01	279.32	160.36	
17950	96.36	195.3	21.06	106.91	40.34	
14776	96.36	52.62	7.91	148.14	49.23	
16327	96.28	236.77	64.26	544.9	157.57	
1639	96.28	101.27	17.82	197.14	45.79	
7913	96.13	312.36	54.3	165.09	71.72	
15103	96.05	134.3	3.56	179.38	33.07	
22840	96.02	1649.81	308.3	873.65	258.97	
12946	96.02	155.12	26.49	349.58	99.66	
12088	95.83	241.33	35.14	119.28	53.51	
17800	95.78	40.88	10.48	102.12	36.29	
20161	95.78	100.16	34.79	28.88	55.44	
15189	95.78	5938.56	990.57	1644.15	1642.84	
25317	95.73	2601.23	361	1379.88	464.15	
7451	95.7	1878.35	262.08	1137.68	307.82	
8368	95.62	43.09	29.16	192.84	79.45	
23230	95.59	164.32	20.46	302.08	105.02	
17564	95.49	314.92	17.82	493.73	137.7	
11021	95.46	82.39	25.14	260.59	96.22	
21574	95.41	533.56	84.01	985.01	271.75	
23349	95.3	82.47	6.75	132.74	33.79	
21679	95.28	24.4	6.35	61.71	24.1	
22733	95.22	63.55	12.91	26.38	20.47	
6918	95.22	518.65	16.4	416.5	384.38	
24219	95.2	742.54	85.54	379.34	187.82	
15606	95.14	394.1	34.7	611.57	139.67	
5451	95.09	378.74	18.2	270.07	89.54	
23369	94.9	83.29	25.57	227.13	80.12	
15170	94.88	78.6	28.28	196.67	56.39	
21368	94.8	81.82	12.05	174.81	54.32	
13557	94.77	356.74	47.35	636.66	160.37	
4383	94.75	156.27	23.64	83.9	33.37	
21062	94.72	76.05	16.15	24.89	77.95	
3722	94.69	726.67	105.31	395.48	144.35	
3730	94.67	3264.3	637.18	1641.3	693.25	
16561	94.64	393.63	76.06	227.68	69.2	
26335	94.64	2858.06	627.98	1130.13	748.06	
1114	94.59	817.1	46.37	566.08	206.94	
959	94.56	44.1	4.28	21.21	14.97	
10918	94.48	276.78	35.51	161.42	60.59	
8237	94.45	170.84	35.21	90.4	35.69	
6598	94.45	379.04	52.96	182.85	84.47	
8725	94.35	68.91	10.95	23.29	25.02	
1877	94.35	374.31	61.37	697.52	185.52	
2193	94.35	89.18	16.09	42.41	29.51	
10958	94.35	76.5	10.79	41.87	16.04	
11840	94.32	32.38	3.98	69.51	36.62	
5719	94.32	21.26	22.19	86.48	33.42	
15755	94.24	446.61	57.29	741.64	180.47	
12422	94.24	42.86	4.56	68.97	21.6	
12422	134.24	172.00	17.00	100.01	<u> 1 → · · · · </u>	

F	TABLE 500: D	CLOFENAC		AWO	mey Docket 449	21-5093-0
1	Thronoling(IS)): 3	3M 3 L			Documen	<u> </u>
	elec Joniffer	LDA Scoro	Tox_Mean	lox_20	Nontiox Meeu	NonTex_{
		94.21	449.89	•	383.88	432
L	10248	94.19	52.62	9.25	25.86	25.23
L	1805	94.19	2725.65	331.2	1449.2	630.73
L	228	94.16	384.45	12.49	485.4	121.74
	6013	94.03	3000.23	187.33	1899.84	625.62
ŀ	16135	94	5451.45	291.82	3555.2	2539.97
	23300	94	124.15	13.1	254.63	97.85
	23368	93.92	24	7.28	76.35	35.27
	12010	93.9	59.33	4.75	106.17	37.5
	18302	93.76	404.35	116.32	146	137.28
	1404	93.71	23.16	6.66	64.75	30.9
		93.52	415.08	82.79	775.09	202.2
	1876		2375.51	97.48	1559.9	1004.11
	17787	93.47 93.47	34.87	8.04	69.71	21.06
	18402		136.62	9.03	188.86	35.57
	15188	93.44			215.85	65.85
	960	93.39	130.81	14.13	556.56	126.38
	18723	93.31	364.82	40.26		545.92
	1904	93.31	513.91	65.51	976.01	1260.97
	1804	93.26	4964.54	605.41	2595.22	
	18564	93.15	220.08	37.71	382.3	96.96
	17379	93.13	229.33	24.92	117.99	71.05
	23348	93.13	47	3.97	75.54	22.33
	21827	93.1	111.01	11.85	164.08	37.68
	13092	92.97	42.78	38.01	221.01	123.49
	14591	92.94	32.03	7.91	70.16	24.41
	16130	92.83	5184.54	390.69	3525.46	2339.12
	15675	92.81	284.38	35.01	449.15	187.1
	25563	92.73	883.55	158.59	1406.91	309.32
	15017	92.6	5560.91	358.68	3971.97	2710.22
	15426	92.3	170.4	21.13	266.54	62.97
v	23569	92.3	172.2	24.29	261.17	59.74
	15936	92.25	48.19	11.55	24.69	17.52
	16123	92.23	161.58	42.01	82.27	68.22
			8708.17	642.14	5353.63	5001.54
	16401	92.17	56.5	9.41	101.21	34.36
	10530	92.14	933.17	99.46	668.68	277.14
	16150	92.09	6079	548.16	3223.82	1796.75
	6478	92.09		70.94	221.17	143.8
	8641	92.04	435.2		2614.05	1219.9
And the second	21013	92.04	2865.74	139.93		16.31
	1843	92.02	79.5	14.81	29.38	4394.45
ings of self-	17109	92.01	7214.62	625.72	4950.32	
	21917	91.97	342.09	108.81	74.09	63.39
e de la estada de la composição de la comp La composição de la composição dela composição de la composição d	20168	91.95	343.75	132.92	52.24	72.77
	12423	91.91	94.66	17.41	168.85	72.45
	2367	91.83	258.09	34.72	398.15	98.83
	23045	91.8	221.05	18.12	163.93	54.31
and the state of the same	355	91.79	176.62	21.06	64.55	37.78
		91.77	25.65	10.24	63.69	23.22
	15980 18301	91.75	301.7	71.49	147.3	94.31
		_1		0.46	144.77	54.12
	19942	91.69	194.61	8.46	177.77	1397.25

and the second second second second second second



TABLE SDD: C	DOLOFENAC		A	Docket 44E	21-5033-91-WO 6 No. 1935323.1
Timepoin((S):	<u> </u>	ſ	ır————	1	
CCCC Condition	LDA Score	Tox_Mean	Tox_SD_	NonTox_Moon	NonTox_SD
22567	91.61	111.14	13.97	178.29	48.4
	91.56	349.67	23.57	264.44	91.66
			105.34	797.85	503
			4.6	101.63	31.77
	-		23.68	284.05	62.76
				29.5	25.35
			8.28	127.78	36.34
21653 18675 1350 22910 16809	91.50 91.51 91.43 91.32 91.31 91.24	1228.45 65.04 188.79 110.62 86.67	105.34 4.6 23.68 32.46	797.85 101.63 284.05 29.5	503 31.77 62.76 25.35

				Deb0000 000	on 6000 on W6
TABLE FIÈ: Timegoin((S))	DICLOFINA ; 3, 6 hrs	20			21-5055-41-440 } No. 1985923.1
(GI CGC	LDV-Zeolo	Tox_Mean	Tox_SD	Noutoz Mew	
13222	98.57	412.94	33.98	244.33	49.84
6057	98.54	403.63	125.03	111.33	139.16
14425	98.27	2123.57	645.32	449.15	427.92
1221	98.04	527.52	137.11	31.03	118.66
21568	97.88	269.87	99.63	66.65	49.99
548	97.8	57.46	14.06	400.27	222.71
2557	97.66	92.91	19.66	35.46	16.47
6891	97.66	264.26	28.13	544.98	219.71
5384	97.27	148.99	35.13	27	61.22
23608	97.19	1208.38	291.55	396.25	181.28
14561	97.13	301.51	38.61	180.81	57.5
16821	97.08	1060.67	209.13	535.3	143.56
19012	96.82	896.84	128.33	438.96	163.43
6479	96.76	2129.89	252.93	1039.05	389.39
10270	96.71	20.84	19.68	140.18	62.9
12792	96.71	107.68	14.92	42.38	35.81
8477	96.66	625.57	128.85	300.92	116.79
2961	96.55	94.68	17.39	41.06	20.17
3773	96.52	237.12	61.33	67.32	60.27
17664	96.5	715.67	141.01	279.32	160.36
17950	96.36	195.3	21.06	106.91	40.34
1639	96.28	101.27	17.82	197.14	45.79
	96.28	236.77	64.26	544.9	157.57
16327	96.13	312.36	54.3	165.09	71.72
7913	96.05	134.3	3.56	179.38	33.07
15103	95.83	241.33	35.14	119.28	53.51
12088	95.78	100.16	34.79	28.88	55.44
20161	95.73	2601.23	361	1379.88	464.15
25317	95.62	43.09	29.16	192.84	79.45
8368	95.49	314.92	17.82	493.73	137.7
17564		82.47	6.75	132.74	33.79
23349	95.3	24.4	6.35	61.71	24.1
21679	95.28	518.65	16.4	416.5	384.38
6918	95.22	63.55	12.91	26.38	20.47
22733	95.22	742.54	85.54	379.34	187.82
24219	95.2	378.74	18.2	270.07	89.54
5451	95.09		25.57	227.13	80.12
23369	94.9	83.29	12.05	174.81	54.32
21368	94.8	81.82	23.64	83.9	33.37
4383	94.75	156.27	16.15	24.89	77.95
21062	94.72	76.05	627.98	1130.13	748.06
26335	94.64	2858.06	76.06	227.68	69.2
16561	94.64	393.63		21.21	14.97
959	94.56	44.1	4.28 35.51	161.42	60.59
10918	94.48	276.78			84.47
6598	94.45	379.04	52.96	182.85	35.69
8237	94.45	170.84	35.21	90.4	16.04
10958	94.35	76.5	10.79	41.87	29.51
2193	94.35	89.18	16.09	42.41	185.52
1877	94.35	374.31	61.37	697.52	25.02
8725	94.35	68.91	10.95	23.29	33.42
5719	94.32	21.26	22.19	86.48	100.42



128.32

2339.12

187.1

3/064624		-9	71-		PC1/US03/031
				mey Docket 449	21-5000-01-000
Time oint(s):	DICLOFENA : 3,6 hrs			Document of the contract of th	3 No. 1935323.1
CLCC Contilor===	LDA LS core	NOX_MOON	Tox_SD .	NonTox_Meen	NonTox_SD :
15755	94.24	446.61	57.29	741.64	180.47
12422	94.24	42.86	4.56	68.97	21.6
3725	94.19	142.26	41.16	44.4	53.55
10248	94.19	52.62	9.25	25.86	25.23
228	94.16	384.45	12.49	485.4	121.74
22251	94.08	153.02	21.22	95.25	38.99
6252	94.03	175.57	30.66	369.52	149.64
23300	94	124.15	13.1	254.63	97.85
16135	94	5451.45	291.82	3555.2	2539.97
18004	93.98	100.14	19.83	47.04	31.05
23368	93.92	24	7.28	76.35	35.27
8917	93.9	121.68	25.68	42.47	42.63
23005	93.9	191.35	31.62	124.41	86.42
12010	93.9	59.33	4.75	106.17	37.5
14404	93.82	825.25	223.47	315.66	277.71
	93.76	404.35	116.32	146	137.28
18302		506.47	62.44	299.87	115.44
22619	93.76	7567.09	496.35	4348.63	2005.16
14459	93.76			64.75	30.9
1404	93.71	23.16	6.66	84.83	66.71
11251	93.55	176.33	26.91		202.2
1876	93.52	415.08	82.79	775.09	
18402	93.47	34.87	8.04	69.71	21.06
17787	93.47	2375.51	97.48	1559.9	1004.11
15188	93.44	136.62	9.03	188.86	35.57
23512	93.42	485.53	59.23	810.99	237.25
22230	93.39	198.57	14.63	144.75	34.07
960	93.39	130.81	14.13	215.85	65.85
5886	93.37	854.6	81.19	562.59	170.54
18172	93.37	91.28	14.8	43.94	39.92
18723	93.31	364.82	40.26	556.56	126.38
1904	93.31	513.91	65.51	976.01	545.92
1804	93.26	4964.54	605.41	2595.22	1260.97
2163	93.23	191.66	34.02	104.84	65.44
18564	93.15	220.08	37.71	382.3	96.96
2897	93.13	82.39	18.82_	44.53	25.25
7362	93.13	499.71	119.92	939.41	279.43
17379	93.13	229.33	24.92	117.99	71.05
23348	93.13	47	3.97	75.54	22.33
7583	93.1	278.42	90.42	50.57	124.21
6720	93.1	183.72	57.33	31	97.86
21827	93.1	111.01	11.85	164.08	37.68
18205	93.05	471.05	43.67	340.16	72.47
12301	93.02	236.82	42.03	137.61	66.66
19427	93.02	5521.57	389.76	3976.69	2476
21466	92.99	7958.56	343.83	6529.42	2984.48
13092	92.97	42.78	38.01	221.01	123.49
5396	92.94	142.73	45.03	64.88	74.66
14591	92.94	32.03	7.91	70.16	24.41
7003	02.04	192 30	55.08	307.26	128 32

183.39

284.38

5184.54

55.08

35.01

390.69

397.26

3525.46

449.15

16130

15675

7003

92.86

92.83

गि∕ाश हि ब्रह्मह॰	DICLOFENA	3	$\Delta \Omega$	may Docket 449	21,57000-01,000
Timeroings)		9	معادد		} No. 1925323.1
	. en o me			6086000000	3 17.000 0.806.00.300.00
ldeniller,	LDA_Score .			NonTox_Mean .	
25563	92.73	883.55	158.59	1406.91	309.32
15017	92.6	5560.91	358.68	3971.97	2710.22
15426	92.3	170.4	21.13	266.54	62.97
23569	92.3	172.2	24.29	261.17	59.74
15936	92.25	48.19	11.55	24.69	17.52
16123	92.2_	161.58	42.01	82.27	68.22
16401	92.17	8708.17	642.14	5353.63	5001.54
10530	92.14	56.5	9.41	101.21	34.36
16150	92.09	933.17	99.46	668.68	277.14
6478	92.09	6079	548.16	3223.82	1796.75
8641	92.04	435.2	70.94	221.17	143.8
21013	92.04	2865.74	139.93	2614.05	1219.9
17109	92.01	7214.62	625.72	4950.32	4394.45
21917	91.97	342.09	108.81	74.09	63.39
20168	91.95	343.75	132.92	52.24	72.77
12423	91.91	94.66	17.41	168.85	72.45
2367	91.83	258.09	34.72	398.15	98.83
23045	91.8	221.05	18.12	163.93	54.31
15980	91.77	25.65	10.24	63.69	23.22
18301	91.75	301.7	71.49	147.3	94.31
19942	91.69	194.61	8.46	144.77	54.12
22567	91.61	111.14	13.97	178.29	48.4
21653	91.56	349.67	23.57	264.44	91.66
18675	91.51	1228.45	105.34	797.85	503
1350	91.43	65.04	4.6	101.63	31.77
22910	91.32	188.79	23.68	284.05	62.76
16809	91.31	110.62	32.46	29.5	25.35
15186	91.24	86.67	8.28	127.78	36.34
9423	91.23	1899.72	494.08	810.91	290.76
20713	91.16	940.06	150.25	717.94	521.48
24718	91.14	577.26	44.11	750.4	172.87
15630	91.11	21.95	3.32	37.86	12.78
3016	91.06	3883.9	162.24	2791.81	1521.04
21407	90.99	147.55	60.36	50.81	27.56
15242	90.98	29.43	3.66	46.26	13.3
6109	90.98	5084.76	427.43	3583.04	2268.92
14498	90.98	190.73	21.56	293.51	74.29
18770	90.95	337.23	27.45	466.95	106.33
11938	90.9	834.77	83.98	1108.07	201.05
13547	90.84	44.69	4.41	72.34	27.8
20744	90.83	1481.65	317.99	343.77	294.93
12193	90.79	85.94	12.35	128.44	28.13
24766	90.79	21.28	2.26	39.74	21.98
16871	90.74	36.82	2.87	57.18	23.7
826	90.71	52.61	7.67	97.1	37.58
4012	90.68	2248.17	171	2438.05	1162.53
9929	90.63	448.54	48.38	673.08	182.35
243	90.63	41.59	3.77	61.29	24.31
16217	90.63	599.86	45.03	450.16	151.55
17306	90.53	3646.9	140.28	2594.74	1274.48
4185	90.5	5947.25	549.24	4088.41	2983.78
		· · · · · · · · · · · · · · · · · · ·	<u> </u>		<u> </u>

TABLE SZZ: Timepoini(S)	DICLOFENA		Aice	may Docket 449 Documen	21-5033-01-W0 { No. 1935323.1
[6][[6]C		Tox_Moan	TOX_SD	MonTox_Mean	
20938	90.47	487.93	29.41	612.77	105.12
	90.47	487.93 3193.3	29.41 338.4	3087.63	2061.18
20938 4010 4213				1 - 1 - 1 - 1	

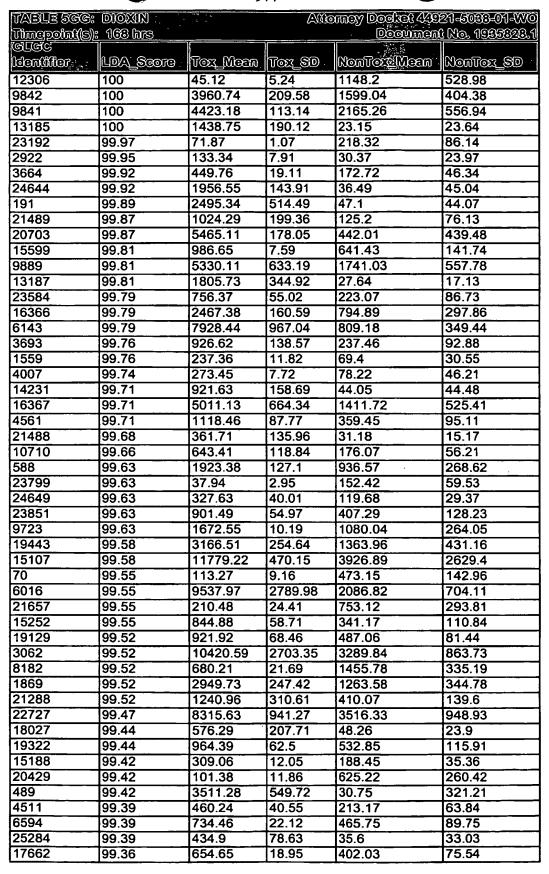
والمدوة فيستد يككن الأعلاج ووعم الويوات الراكات

TABLE SFF: (Timepoint(s):		第一 四月第1 章 五 第 章	a service of	may Docket 4491 Document	21-5093-01-WO } No. 1935323.1
identifor :: · · ·	LDV-Zeolo	Tox_Ween .	Tox_SD	NonTox_Meen	NonTox_SD
14595	99.81	326.64	5.25	67.73	82.28
354	99.79	92.36	0.22	82.21	152.61
1857	99.68	135.38	34.61	22.97	156.76
20715	99.63	2716.49	163.16	380.46	421.28
18687	99.58	3600.76	172.19	657.37	578.39
20713	99.55	3608.94	312.55	714.29	508.05
4207	99.5	185.94	8.55	527.67	274.65
23274	99.47	402.83	6.49	611.73	121.31
22416	99.47	437.5	23.89	146.45	101.89
7393	99.42	74.98	0.29	45.23	35.58
2457	99.39	962.87	38.12	251.21	150.93
8527	99.29	296.29	2.22	160.76	177.64
26109	99.23	1616.96	208.74	145	258.03
16807	99.1	6098.25	623.59	2326.3	989.13
14267	99.1	2612.63	146.68	1188.41	382.61
23699	99.1	1669.23	186.12	641.84	305.74
6919	99.05	313.36	1.17	345	296.14
15580	99.02	4010.96	141.66	2244.71	628.1
3943	98.99	40.62	0.2	39.44	20.59
16901	98.99	215.2	3.21	339.04	84.81
18138	98.97	7745.05	249.87	4546.56	1453.1
23183	98.94	515.77	26.78	215.61	90.85
8856	98.94	96.1	3.45	47.93	15.64
20714	98.91	3334.71	868.91	564.34	693.87
5602	98.91	1266.07	120.13	206.09	208.63
18686	98.81	4181.68	704.04	702.56	597.85
18742	98.81	1158.53	154.91	344.23	186.12
4271	98.78	512.28	68.14	59.26	134.04
240	98.76	82.31	0.59	114.6	41.82
16148	98.76	3131.87	592.64	1033.38	371.51
22851	98.76	69.88	1.07	112.97	55.9
20925	98.76	2528.69	381.39	416.44	433.34
4272	98.7	326.83	48.56	33.64	74.6
15577	98.68	3113.86	39.97	1900.42	671.98
23130	98.68	366.67	2.8	524.09	146.28
1858	98.65	243.5	90.09	24.58	181.75
15085	98.62	3316.99	396.59	1428.45	429.04
15408	98.62	625.53	11.49	292.03	164.72
4196	98.6	247.43	44.95	86.13	93.63
1960	98.6	98.18	0.45	77.83	30.22
18293	98.6	3200.02	349.15	1368.4	440.5
4011	98.57	4856.75	731.97	1813.13	670.11
18125	98.54	879.85	16.6	576.01	159.83
3431	98.49	1471.97	17.51	1044	313.19
5213	98.46	626.54	2.92	541.16	185.69
17339	98.44	201.93	7.24	855.88	471.89
6409	98.39	192.76	5.07	108.77	47.06
16275	98.39	5342.33	45.26	3432.65	2260.08
21975	98.33	182.16	2.46	268.53	82.01
21872	98.28	105.6	9.42	186.83	41.67
10887		65.35			32.92
1,0007	98.28	და.აა	1.5	106.07	192.92

		-97	5-		
	SER MANGAN ::		A CONTROL	may Docket 449	21-5033-01-WO
Maggini(S):	DIFLUNISAL M bas			Document	} No. 1935328.1
STGC IIMAMINI	743 WB		(S.)		
ortifier -	LDA_Score	Tox_Meen	TOX_SD 🐉	Novilox Integr	Moniox_SD
2604	98.28	3212.42	609.6	1027.7	464.38
21341	98.28	1507.43	72.03	855.62	302.78
21354	98.28	2463.17	381.13	422.38	398.02
15582	98.23	13240.99	1092.99	5708.51	2856.56
18072	98.23	57.09	0.78	33.1	24.95
16703	98.23	2323.05	177.21	1167.43	382.89
19099	98.2	122.48	1.45	83.93	33.96
17758	98.15	2134.3	578.84	360.49	368.41
2210	98.15	3413.1	319.9	1990.77	430.41
20711	98.15	1058.07	208.05	134.19	202.08
24665	98.12	50.77	8.77	187.24	109.51
17847	98.12	1109.04	68.03	704.75	149.14 562.03
6380	98.12	3422.14	327.69	1761.85	404.55
23698	98.12	1633.49	392.24	356.69	670.38
15579	98.09	3551.99	355.67	1675.76	
15848	98.07	2280.83	100.39	1329.5	349.44
21355	98.07	1996.5	627.15	298.92	276.7
22958	98.07	79.51	0.45	83.02	58.87
14070	98.04	180.41	0.94	171.45	49.28
28	98.04	502.98	13.94	804.95	268.31
11633	98.01	322.01	33.88	77.91	76.39
21750	98.01	400.65	54.98	155.78	70.9
1728	97.99	484.45	19.95	249.91	114.02
2799	97.96	287.89	7.32	492.41	225.66
14763	97.96	1776.92	110	567	402.88
26032	97.94	103.14	30.76	1130.68	604.66
16190	97.91	1387.18	179.63	757.23	213.67
8931	97.88	68.35	1.01	48.48	28.85
16039	97.88	142.52	3.84	233.51	67.42
16215	97.8	408.88	21.59	778.84	177.05
15383	97.78	201.11	2.12	136.83	51.87
6623	97.78	116.56	0.77	115.47	42.41
9772	97.78	60.78	0.54	73.76	39.92
4133	97.72	295.72	3.82	374.97	112.6
25500	97.72	78.04	3.85	155.25	51.57
10754	97.7	130.1	9.34	40.7	57.5
21010	97.7	1495.14	115.56	675.45	295.81
4012	97.67	6489.94	1063.65	2430.81	1149.27
15992	97.62	607.51	16.87	406.64	211.47
18671	97.62	90.07	3.42	39.25	40.3
19393	97.59	379.37	60.17	798.76	189.68
2811	97.59	333.35	12.18	191.71	79.66
23282	97.56	298.84	10.22	442.19	89.33
17728	97.56	4193.46	58.07	2479.83	1319.44
8917	97.54	174.7	22.84	42.6	42.58
21730	97.51	538.03	232	218.83	73.46
	97.51	4423	676.48	2271.55	713.2
16701	97.51	469.77	38.23	266.26	66.2
16521	97.43		395.32	668.36	274.72
16150		588.84	57.54	325.11	126.47
18958	97.41	223.12	21.4	499.2	170.08

		-9/			
ABLE SFF: [NIFLUNISAL		(XXX)	may Docket 449	21-5033-01-440
imapoint(s):				, Dogumen	<u> </u>
गालद		Tor Moss	Test Sep 2	Novijox Nov	NonTox_SD
	LDA SCOTO		30.16	623.63	173.66
	97.41	288.7	9.97	685.54	244.67
5777	97.27	448.38	66.63	1181.05	301.13
0984	97.17	1726.78	9.31	296.14	83.97
9335	97.14	164.87	149.67	1349.34	445.46
5124	97.11	2460.11	24.42	320.53	127.27
9391	97.09	87.1	34.01	536.03	129.67
1575	97.06	300.48	3.51	69.74	31.21
559	97.01	21.25	12.21	66.81	28.77
844	96.96	133.02	112.45	1158.95	617.6
793	96.88	1868.73	15.64	391.66	106.99
973	96.88	201.75	5.73	131.21	61.04
20802	96.88	39.21	36.69	1190.74	285.23
25479	96.85	786.55	67.73	121.61	87.18
22602	96.77	373.46	437.67	1570.92	604.8
17554	96.66	3215.53	7.08	342.64	91.48
23486	96.61	218.26	90.03	260.86	110.37
22603	96.56	598.4	71.52	844.92	185.31
24537	96.53	450.32	172.33	1186.67	355.89
25064	96.51	2088.31	318.41	4208.95	2875.34
25319	96.48	8538.83	17.04	596.96	333.69
20600	96.45	315.58	5.09	151.82	45.55
11611	96.43	87.75	502.98	1646.16	619.49
15125	96.43	3495.72	141.09	996.65	291.76
20983	96.4	1624.54	97.18	1186.61	460.31
17764	96.4	2068.19	3.12	108.85	61.23
16416	96.37	62.11	10.02	297.38	89.15
382	96.32	188.08	189.77	2045.22	727.16
17807	96.29	3536.06	18.11	356.77	119.14
19018	96.27	181.03	20.2	191.66	87.35
16546	96.21	343.62	4.9	97.81	92.64
1399	96.21	28.91	7.78	68.03	38.91
397	96.11	121.65	97.03	604.95	197.6
16767	96.06	1098.65	5.67	167.88	106.31
18578	96.06	46.9	22.69	435.07	216.75
20931	96	88.28	9.75	201.73	116.28
25501	95.98	56.97	2.43	65.09	38.41
355	95.98	22.14 116.68	16.48	46.58	38.2
18315	95.95		10.67	248.94	92.08
16450	95.95	103.94	217.49	339.47	186.15
20555	95.95	886.45	185.14	3588.66	2474.3
21152	95.95	6830.97	53.76	1870.04	689.67
10949	95.92	2718.83	59.41	1102.66	503.38
10623	95.87	1794.44	212.62	598.63	283.8
15409	95.84	1460.42	9.83	138.38	72.95
25814	95.82	32.25	113.07	499.67	128.91
25070	95.82	865.15	349.51	574.18	982.99
12157	95.79	1472.37	2.44	108.49	43.46
15187	95.79	65.46	48.81	609.2	205.56
24535	95.74	226.85	9.38	646.91	151.6
9905	95.69	768.97	1.73	78.19	27.49
4395	95.61	50.4	1.73	170.13	

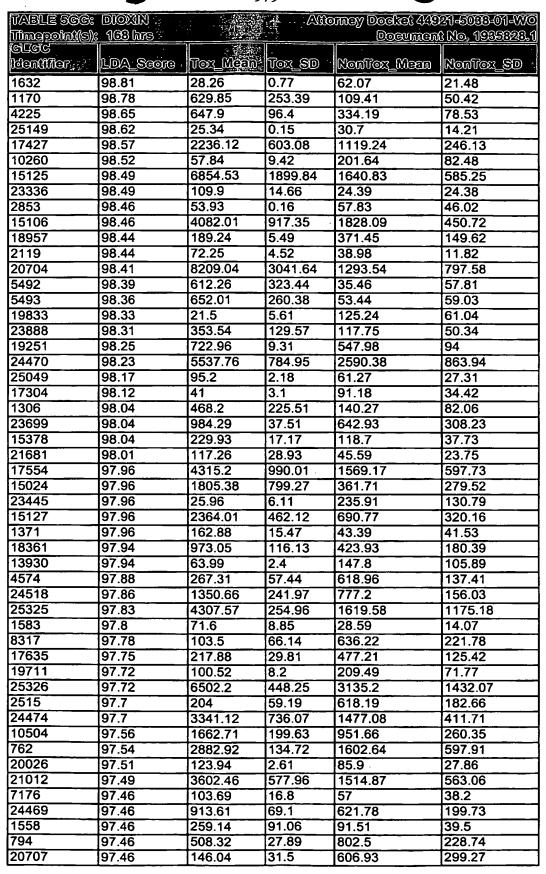






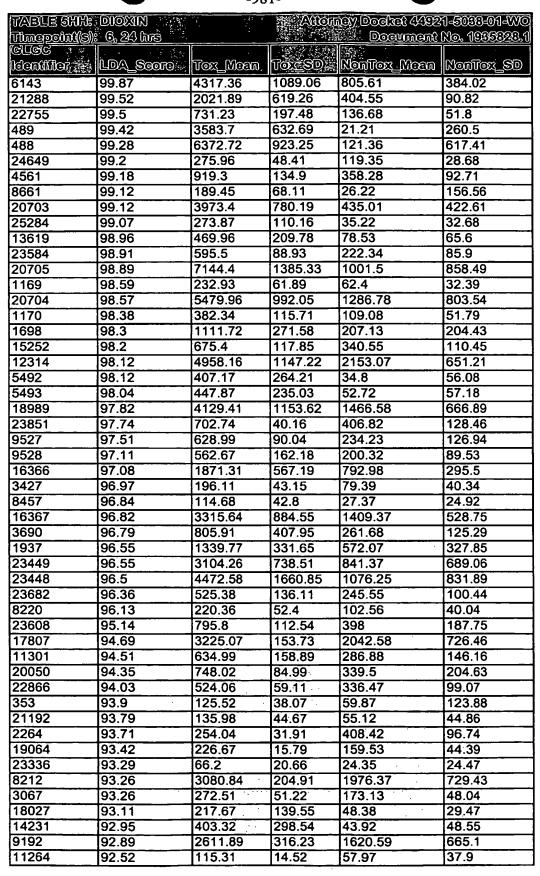
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TABLE SCC:	DIOXIN 163 bis			may Docket 449 Document	21-5083-01-009 } No. 1985028-1
G C G C	LDA Score	'	Tox_SD		NonTox_SD
ldentifier		42.35	8.43	144.72	47.92
179	99.34	4122.68	998.88	1179.22	336.82
13563	99.34		7.22	235.86	84.78
293	99.34	36.87 3595.94	914.71	1141.15	344.76
16305	99.31	113.62	15.3	34.42	15.97
6121	99.29	192.12	21.52	804.44	238.33
3365	99.29		71.03	26.6	156.55
8661	99.26	224.85 1172.51	25.16	610.85	157.06
699	99.26		5.31	146.34	52.63
23520	99.23	250.96	270.32	736.36	169.63
4245	99.23	1992.81	2758.4	3718.75	1008.01
17359	99.23	11372.36		164.49	43.22
16307	99.23	213.34	0.8	825.34	378.93
20430	99.21	90.52	19.8	34.5	47.99
24341	99.18	74.78	5.07	118.8	41.13
15098	99.18	42.84	1.4	287.9	73.75
6628	99.15	634.88	78.78	308.23	102.83
16780	99.15	1362.14	513.45	240.86	77.45
23320	99.15	532.99	37.28	141.84	58.66
25725	99.13	724.78	271.51		33.11
14149	99.13	40.54	1.35	89.86	88.27
21468	99.13	57.17	0.83	27.9	38.82
20669	99.1	254	16.47	127.12	664.43
12314	99.1	5617.22	749.84	2159.45	652.38
488	99.07	8688.94	2485.17	134.23	38.54
16905	99.05	166.94	11.9	69.25	111.74
16781	99.05	1700.4	746.5	326.9	29.31
3488	99.05	133.89	7.23	60.03	102.5
4918	99.05	477.88	19.29	206.95	90.15
22713	99.02	72.88	3.44	230.08	79.49
18525	99.02	495.81	69.06	202.68	852.84
20705	98.99	11263.92	2621.54	1011.22	134.75
8594	98.97	1013.91	50.86	544.16	204.62
1698	98.97	1686.86	259.61	208.61	31.03
16018	98.94	96.76	8.44	47.74	301.35
21740	98.94	393.75	21.16	739.32	
2581	98.94	26.93	3.01	89.88	32.33
15126	98.94	4704.33	738.51	1270.37	521.78
21051	98.94	52.38	1.52	168.9	87.58
14495	98.91	1168.01	309.82	321.92	106.49
409	98.91	157.03	2.52	102.42	57.39
2354	98.91	2565.91	493.93	816.22	282.15
1169	98.91	442.56	178.26	62.52	30.34
18867	98.89	1974.42	508.83	824.06	218.05
3697	98.89	963.19	110.37	426.22	134.46
17324	98.86	116.94	11.64	378.69	117.57
16364	98.84	643.42	143.53	178.43	86.44
23628	98.84	615.8	45.67	326.81	85.75
8719	98.84	50.1	0.66	81.9	34.05
8215	98.84	1082.88	133.38	386.91	134.74
15124	98.81	4496.25	860.65	1346.1	428.82
18989	98.81	6527.42	1960	1469.82	658.61

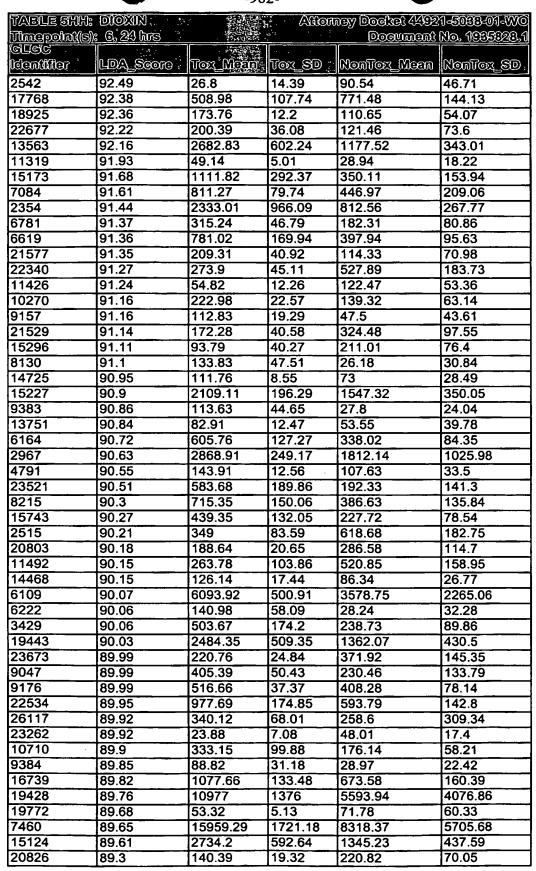




-980-

117765	137.43	1400			
47765	97.43	409.77	27.82	885.74	344.25
ldonifier	FRANCES OF				
Promy Military	LDA Score	TOX_MOON	II (1000 SD)		Inames Ten
(G) [G) C				NonTox_Mean	Warrier Co
Timegoint(S)	100 mp	1	1		
				DOCUMEN	<u>} No. 1935323.1</u>
TABLE 566:	RIBRADIA		2000		സം ക്കളാളം വ
E	(2000) (N)		√ ₩6	moy Docket 449	211450333340114WQ1
					54 5666 64 000





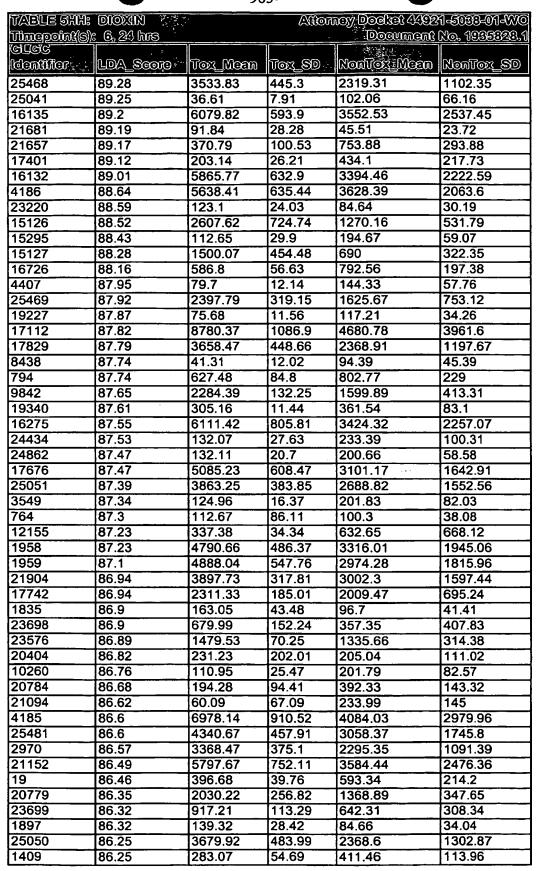
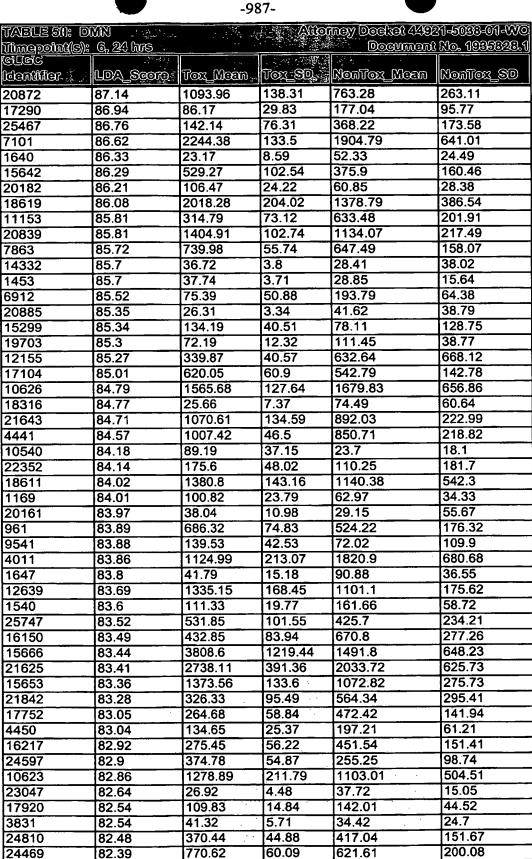


TABLE SHH:	DIOXIN SE		.∵	poy Dockot 4402	1-5093-01-WO
Timepoint(s):	6,24 hrs				No. 1935328.1
(G. T. G. C.				F. 4	
ldentifier	LDV Score	Lox Meen	iox Sd	WEEKT TO LUCK	NonTox_SD
19252	85.99	330.82	38.53	520.83	190.2
16130	85.91	5670.73	927.47	3523.39	2336.88
17148	85.8	6068.76	805.91	3825.99	2485.79
15718	85.77	44.87	10	72.76	30.53
24420	85.75	1988.24	191.34	1528.34	574.77
745	85.72	26.49	1.34	26.85	12.99
17472	85.7	4352.42	609.97	2564.44	1598.12
12192	85.52	286.13	57.2	192.18	51.78
25252	85.51	112.36	44.05	220.57	94.93
14983	85.48	6883.32	1215.13	4024.13	3461.55
17787	85.35	2655.76	444.29	1558.71	1002.63
818	85.3	5380.67	628.86	3411.17	2156.46
15274	85.08	53.18	10.3	83.71	27.08
24235	85.07	505.73	113.52	329.1	169.28
4212	85.01	6376.04	787.98	4055.65	2672.48
18867	84.97	1189.1	213.55	824.34	222.08
17062	84.95	69.11	11.87	114.71	47.85

			, J -		
TABLE SII: D			Affor	mey Docket 4492	
Timepoint(s):	6, 24 hirs -	2 (3)	·	Document	No. 1935323.1
klendijer - "	LDA_Score	negM_xoT	Ton_SD :	NonTox_Mean	NonTox_SD
10611	99.23	260.37	72.4	23.98	38.98
20755	98.46	376.86	78.86	54.53	60.24
7324	98.38	457.11	129.36	92.35	83.29
12873	98.3	407.94	77	114.93	67.27
20082	98.2	186.17	43.62	40	43.7
20757	98.09	1163.72	405.06	271.12	115.22
20449	98.06	83.53	20.65	40.61	104.49
21275	97.93	570.18	165.66	204.68	90.03
3090	97.45	275.65	74.39	141.14	39.01
25705	97.24	1290.52	178.77	741.1	195.7
15301	97.19	91.6	25.54	25.71	129.29
15300	96.66	421.39	88.59	231.58	229.6
16427	95.99	81.11	13.6	223.4	81.95
6155	95.91	106.94	23.89	275.99	110.88
1650	95.44	118.02	29.48	256.09	75.05
16426	95.38	180.15	33.39	404.43	119.96
19230	95.14	414.35	132.54	200.5	113.44
22681	95.06	322.74	96.22	158.17	361.42
17239	94.93	662.68	105.52	447.81	102.34
23445	94.82	31.51	22.16	236.45	130.54
18943	94.53	616.56	97.37	370.31	114.49
17541	94.48	2931.46	420.37	1625.04	635.87
12745	93.79	69.9	14.85	40.07	23.9
10109	93.71	1234.99	52.48	1046.73	223.89
20481	93.58	40.6	9.74	97.31	35.1
25550	93.47	78.27	16.65	39.37	24.25
23928	93.37	71.3	26.48	144.71	37.67
21228	93.31	78.48	17.26	167.64	61.75
23115	93.18	450.71	117.99	253.66	142.87
16823	93.13	423.93	50.59	753.84	216.05
11274	92.7	183.86	45.89	308.91	67.56
16824	92.06	103.69	44.85	263.55	99.01
14594	91.73	176.08	53.81	46.07	37.76
9196	91.64	140.71	29.23	274.89	87.41
10695	91.61	378.58	37.87	252.95	155.23
1654	91.56	101.41	24.76	205	61.93
20705	91.51	327.76	109.86	1030.44	949.55
14424	91.39	349.64	162.38	91.56	282.7
22929	91.32	689.87	130.29	1242.24	788.78
3657	91.31	118.24	51.59	378.52	136.92
24234	91.27	204.32	25.16	146.78	122.16
22476	91.24	270.33	52.51	466.29	135.25
1037	91.23	77.54	10.71	39.36	37.3
8860	91.22	565.01	111.13	361.06	137.37
17097	91.08	147.73	30.16	66.94	46.59
22677	90.57	279.58	106.61	121.13	72.8
7184	90.51	427.1	151.85	144.47	69.17
15098	90.39	64.64	15.43	118.91	41.13
19710	90.34	133.76	18.3	240.26	107.59
11150	90.34	61.64	22.65	178.91	93.15
26184	90.33	582.38	179.83	278.07	79.64
	<u> </u>	<u> </u>	•		



TABLE 51: D Timogoin((s):		Altomay Doeles 44921-5033-01-WO Doeument No. 1935323.1			
kanninar Katak	LDV Zocoto	Tox_Meen	Tox_SD	Menjozijnem	NonTox_SD
23048	90.31	408.77	34.44	315.57	61.65
8494	90.26	103.62	25.77	192.52	70.38
20735	90.21	284.86	70.69	189.51	132.51
7784	89.99	72.74	14.56	121.86	50.88
1431	89.86	275.65	56.58	432.92	189.36
23776	89.76	33.3	24	135.64	69.41
16518	89.73	1195.51	200.43	771.59	339.07
40	89.7	200.35	21.2	363.96	186.44
11547	89.54	197.93	53.7	344.87	111.06
2131	89.53	45.39	25.7	120.14	29.79
16938	89.45	1899.98	471.54	1366.33	273.44
1900	89.3	164.49	44.57	335.2	146.94
4588	89.23	21.91	5.28	42.45	24.88
18252	89.17	2218.64	327.68	1501.46	500.37
18636	89.12	4123.05	577.24	2650.68	1037.55
21796	89.12	149.5	23.05	104.57	58.07
1644	88.92	68.48	23.27	158.32	52.66
8950	88.69	106.48	8.09	153.07	49.07
18624	88.69	874.22	156.06	600.12	236.24
25632	88.69	31.5	11.37	129.14	294.02
3367	88.61	769.16	143.81	532.38	199.52
1928	88.51	206.8	22.17	292.67	97.04
20703	88.46	135.17	53.54	451.31	483.11
17054	88.4	1579.04	60.14	1397.18	302.49
24431	88.36	123.48	49.47	63.66	151.45
21523	88.35	76.66	19.77	41.39	29.92
18750	88.3	275.76	12.87	246.57	72.01
4391	88.16	1232.65	146.3	936.26	222.33
5996	87.98	137.61	25.16	230.1	78.74
19075	87.95	177.45	16.86	141.87	67.27
8240	87.92	133.57	33.3	76.01	57.48
16917	87.9	39.04	16.19	94.24	50.18
4314	87.82	311.47	51.04	455.52	118
23964	87.81	92.91	39.26	184.17	47.24
16073	87.77	74.26	28.35	173.59	76.39
18936	87.74	2250.9	303.58	1613.45	474.33
2809	87.66	40.73	5.43	27.94	24.02
11152	87.65	112.18	30.12	334.65	142.25
6645	87.63	97.65	15.95	141.26	32.41
17175	87.63	735.72	75.51	613.13	171.88
547	87.57	556.61	117.35	373.58	91.18
11353	87.55	87.8	3.69	92.5	34.02
2482	87.51	89.43	50.01	214.96	65.37
6554	87.45	451.7	57.12	611.4	162.44
19105	87.34	932.98	84.45	764.77	185.7
4914	87.27	181.2	169.82	481.83	150.22
1653	87.25	221.08	68.26	387.22	96.06
3916	87.23	1118.61	183.59	1540.3	411.05
15571	87.21	36.15	13.09	136.96	374.23
6911	87.19	97.02	52.48	234.31	74.39
	87.18	102.96	21.36	82.14	152.8



1560.04

2998.04

15667

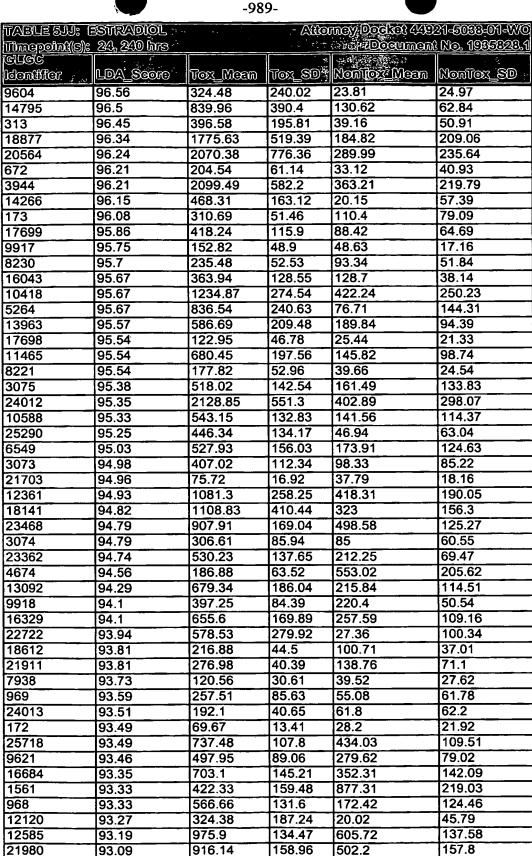
82.38



TABLESI: D Timepoin((s):			ACCO	mey Docket 449f Document	21-5093-01-WO No. 1935323.1
GEGG GEGG	LDA_Score:	Tox_Meein	Tox_SD	NonTox_Meen	NonTox_SD
20448	82.34	72.6	21.45	42.76	74.17
1753	82.3	561.45	72.44	440.41	172.36
17105	82.19	1122.82	102.4	982.97	354.51
16780	82.17	228.22	30.02	310.25	112.33
23854	82.1	576.74	63.35	452.11	150.57
21064	82.09	71.37	7.22	64.12	25.19
7064	82.06	402.56	67.08	334.93	202.12

12313

93.03

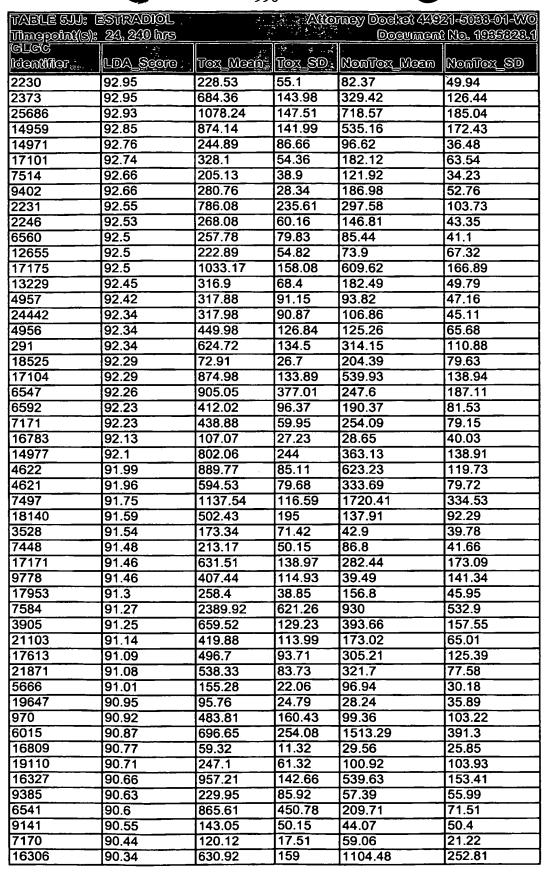


422.1

664.19

3729.49





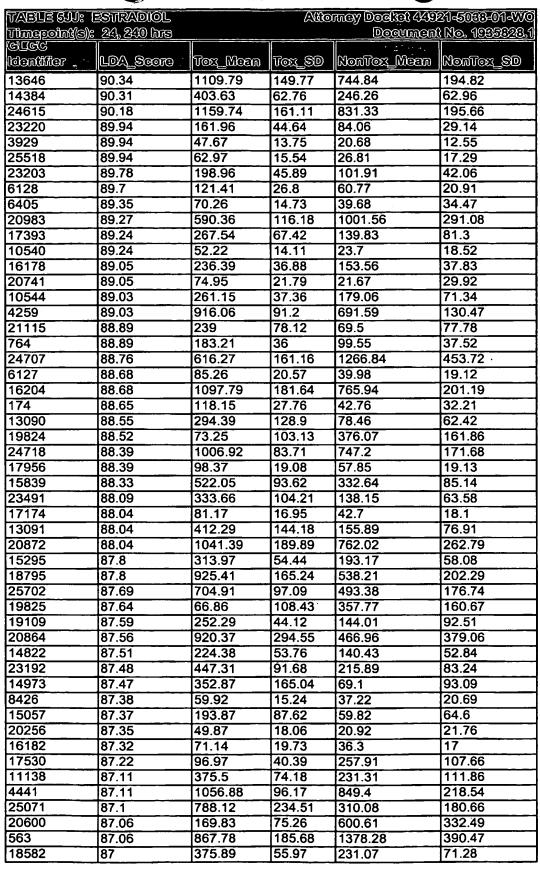


TABLE 5.U: ESTRADIOL Timogoin((s): 24, 240 hrs				may Docket 449 Document	
	4.5. 1.46	Tox_Meen	Tox_SD:	Nonvox Meen	NonTox_SD ;
17502	86.87	154.76	47.87	82.76	50.09
20998	86.76	691.22	190.72	1252.21	333.81
24771	86.66	726.23	155.97	1111	316.73
3902	86.65	212.25	49.14	127.34	39.19
16285	86.6	51.39	16.14	21.84	11.72
1867	86.57	921.57	146.81	627.71	163.29
4090	86.57	871.98	102.21	604.17	151.53
20601	86.55	351.5	152.17	974.6	456.91

TABLE SXX:	ESTRADIOL		Atto	may Docket 449	21-5033-01-WO
Timepoin((s):	24, 240 hrs		:	Document	No. 1935923.1
	LDA_Scoro	Tox_Moan	Tox_SD	NonTox_Noon	NonTox_SD
9604	96.56	324.48	240.02	23.81	24.97
14795	96.5	839.96	390.4	130.62	62.84
313	96.45	396.58	195.81	39.16	50.91
20564	96.24	2070.38	776.36	289.99	235.64
3944	96.21	2099.49	582.2	363.21	219.79
173	96.08	310.69	51.46	110.4	79.09
9917	95.75	152.82	48.9	48.63	17.16
8230	95.7	235.48	52.53	93.34	51.84
5264	95.67	836.54	240.63	76.71	144.31
10418	95.67	1234.87	274.54	422.24	250.23
16043	95.67	363.94	128.55	128.7	38.14
8221	95.54	177.82	52.96	39.66	24.54
17698	95.54	122.95	46.78	25.44	21.33
10588	95.33	543.15	132.83	141.56	114.37
21703	94.96	75.72	16.92	37.79	18.16
23468	94.79	907.91	169.04	498.58	125.27
16329	94.1	655.6	169.89	257.59	109.16
9918	94.1	397.25	84.39	220.4	50.54
21911	93.81	276.98	40.39	138.76	71.1
7938	93.73	120.56	30.61	39.52	27.62
969	93.59	257.51	85.63	55.08	61.78
24013	93.51	192.1	40.65	61.8	62.2
172	93.49	69.67	13.41	28.2	21.92
968	93.33	566.66	131.6	172.42	124.46
21980	93.09	916.14	158.96	502.2	157.8
12313	93.03	422.1	664.19	3729.49	1819.18
2230	92.95	228.53	55.1	82.37	49.94
25686	92.93	1078.24	147.51	718.57	185.04
14959	92.85	874.14	141.99	535.16	172.43
14971	92.76	244.89	86.66	96.62	36.48
17101	92.74	328.1	54.36	182.12	63.54
7514	92.66	205.13	38.9	121.92	34.23
2231	92.55	786.08	235.61	297.58	103.73
2246	92.53	268.08	60.16	146.81	43.35
17175	92.5	1033.17	158.08	609.62	166.89
6560	92.5	257.78	79.83	85.44	41.1
4957	92.42	317.88	91.15	93.82	47.16
4956	92.34	449.98	126.84	125.26	65.68
17104	92.29	874.98	133.89	539.93	138.94
18525	92.29	72.91	26.7	204.39	79.63
6547	92.26	905.05	377.01	247.6	187.11
7171	92.23		 		
	92.23	438.88	59.95 96.37	254.09	79.15
6592 14977	92.23	412.02 802.06	244	190.37	81.53
4622				363.13	138.91
	91.99	889.77	85.11	623.23	119.73
4621	91.96	594.53	79.68	333.69	79.72
18140	91.59	502.43	195	137.91	92.29
3528	91.54	173.34	71.42	42.9	39.78
7448	91.48	213.17	50.15	86.8	41.66
9778	91.46	407.44	114.93	39.49	141.34
17171	91.46	631.51	138.97	282.44	173.09

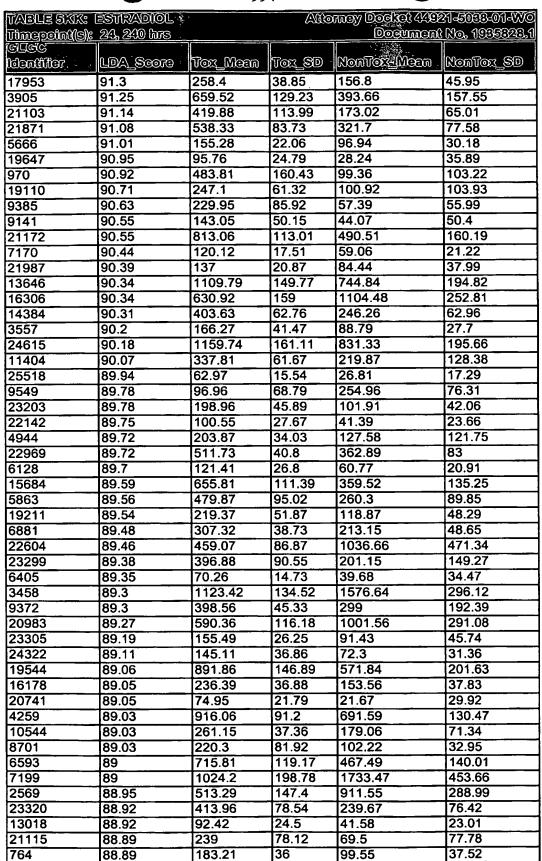


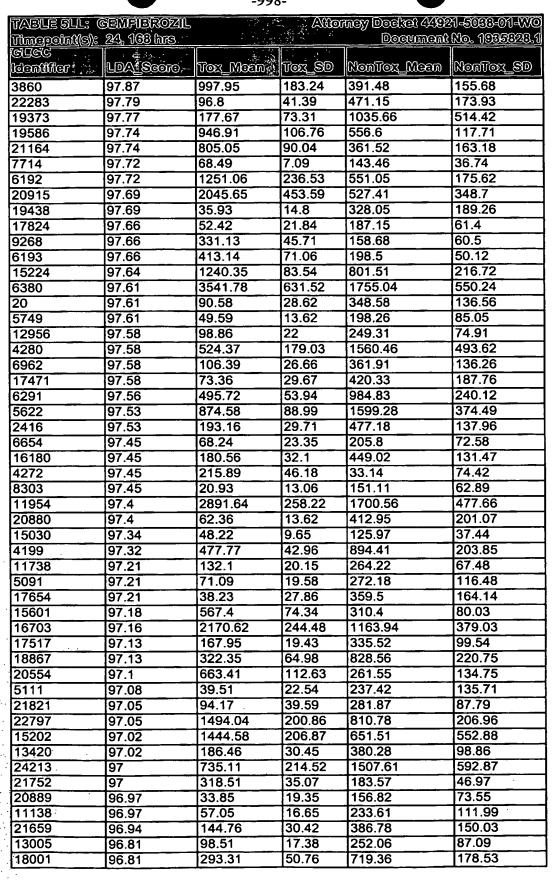




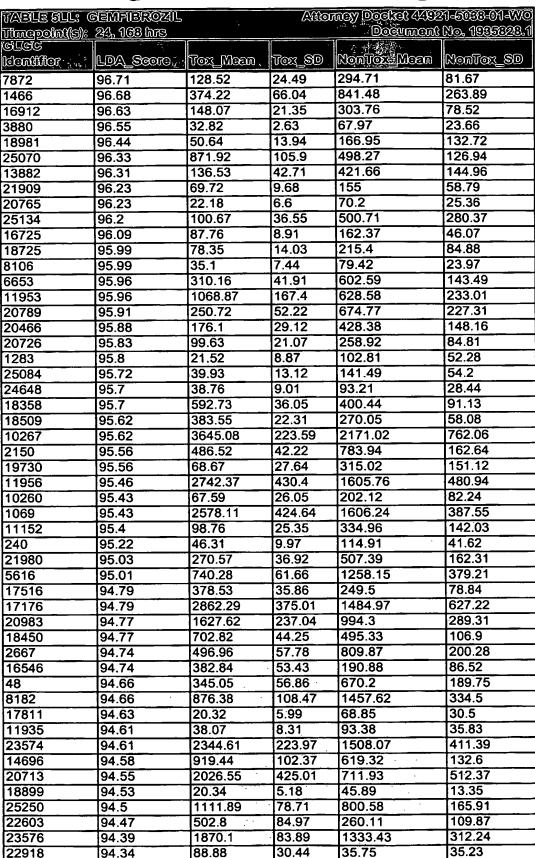
TABLE SXX: (
Timopoint(s):	24, 240 hrs	Document No. 1935323.1				
CHCC Identifier	LDA_Scoro	Tox_Meen		Monifox Mean	NonTox_SD :	
6127	88.68	85.26	20.57	39.98	19.12	
16204	88.68	1097.79	181.64	765.94	201.19	
174	88.65	118.15	27.76	42.76	32.21	
13090	88.55	294.39	128.9	78.46	62.42	
24718	88.39	1006.92	83.71	747.2	171.68	
17956	88.39	98.37	19.08	57.85	19.13	
15839	88.33	522.05	93.62	332.64	85.14	
17174	88.04	81.17	16.95	42.7	18.1	
13091	88.04	412.29	144.18	155.89	76.91	
20872	88.04	1041.39	189.89	762.02	262.79	
18795	87.8	925.41	165.24	538.21	202.29	
25702	87.69	704.91	97.09	493.38	176.74	
19109	87.59	252.29	44.12	144.01	92.51	
20864	87.56	920.37	294.55	466.96	379.06	
14822	87.51	224.38	53.76	140.43	52.84	
23192	87.48	447.31	91.68	215.89	83.24	
14973	87.47	352.87	165.04	69.1	93.09	
8426	87.38	59.92	15.24	37.22	20.69	
20256	87.35	49.87	18.06	20.92	21.76	
16182	87.32	71.14	19.73	36.3	17	
17530	87.22	96.97	40.39	257.91	107.66	
11138	87.11	375.5	74.18	231.31	111.86	
4441	87.11	1056.88	96.17	849.4	218.54	
25071	87.1	788.12	234.51	310.08	180.66	
20600	87.06	169.83	75.26	600.61	332.49	
563	87.06	867.78	185.68	1378.28	390.47	
18582	87	375.89	55.97	231.07	71.28	
17502	86.87	154.76	47.87	82.76	50.09	
20998	86.76	691.22	190.72	1252.21	333.81	
24771	86.66	726.23	155.97	1111	316.73	
3902	86.65	212.25	49.14	127.34	39.19	
16285	86.6	51.39	16.14	21.84	11.72	
1867	86.57	921.57	146.81	627.71	163.29	
4090	86.57	871.98	102.21	604.17	151.53	
25039	86.55	514.51	175.16	979.57	310.7	
4222	86.55	649.32	61.74	493.24	211.92	
763	86.55	57.45	13.65	27.28	17.95	
20601	86.55	351.5	152.17	974.6	456.91	
16205	86.49	1510.63	228.6	1094.77	260.32	
13520	86.44	227.09	44.64	109-61	87.22	
17586	86.44	329.91	73.86	223.15	70.21	
9620	86.44	710.72	110.06	531.44	111.24	
18180	86.39	42.27	8.45	23.41	11.06	
14353	86.36	46.85	5.35	37.25	21.8	
15136	86.34		176.15	585.63	293.13	
		866.19	29.38	108.16	36.38	
17123	86.33	166.01	164.97	975.51	266.72	
12312	86.18	626.54	43.17	229.71	51.23	
24628	86.17	324.07			46.78	
17590	86.17	149.63	20.51	105.95		
15654	86.14	550.7	120.95	322.51	146.66	
5351	86.04	795.4	108.5	590.62	117.27	

TABLE SKK: ESTRADIOL Timepoin((s)): 24, 240 hrs			Afformey Docket 44921-5033-91-000 Document No. 1985323.1		
CHCC Centifier = 3	LDA_Score	Tox_Mean	Tox_SD :	MOONTOX_MOON	NonTox_SD
18539	85.99	263.14	51.82	145.61	68.05
15838	85.98	278.55	39.3	195.67	39.04
20729	85.98	390.1	76.46	239.28	67.43
18573	85.91	190.93	33.19	132.68	33.63
9241	85.88	240.69	36.12	166.41	44.83
14925	85.82	575.36	129.28	321.05	101.88
23825	85.64	58.4	12.17	37.98	26.01

ត្∧ល្ខេសា ∙ ៤	BEMFIBROZIL			ncy Docket 4492	146881014WO
	24, 163 hrs		by green		No. 1985323.1
GEGG	- 45 27 -		[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
ldendiffer	LDA_Scoro:	Tox_Mean	TOX_SO	MoonTore (Moca)	MonTox_SD
23699	99.47	2609.83	358.43	633.02	272.51
23698	99.36	2915.36	526.82	345.13	361.61
1857	99.2	376.61	125.74	21.27	154.74
20714	99.18	3333.45	744.96	554.04	672.88
1858	99.18	580.52	188.9	21.98	177.26
6479	99.07	152.66	32.23	1048.4	390.92
16150	99.02	1942.74	276.34	663.03	261.15
18687	98.96	3559.7	515.91	646.64	550.87
18647	98.8	124.66	28.39	420.59	146.55
17705	98.78	37.24	7.02	131.68	38.38
16148	98.72	2519.41	339	1028.83	365.54
6431	98.7	30.31	10.04	187.79	238.15
18742	98.67	1239.1	300.55	340.77	176.5
17706	98.65	75.85	15.5	182.62	42.67
18686	98.62	3141.77	399.62	695.15	588.33
17686	98.57	1544.6	145.76	873.61	180.45
21355	98.51	1481.07	192.8	295.35	272.48
14131	98.41	238	85	33.36	29.94
6213	98.38	51.17	8.34	153.05	53.91
6366	98.35	112.39	14.11	276.3	104.32
18293	98.35	3270.42	548.89	1361.22	423.7
10308	98.33	616.18	139.67	1480.3	341.59
9885	98.33	45.36	11.59	297.91	110.56
3279	98.3	1409.57	180.37	695.28	186.92
11363	98.3	122.59	26.84	505.74	172.38
21288	98.27	652.52	59.96	410.11	142.95
22813	98.27	28.35	7.24	114.52	43.88
21354	98.22	2046.25	245.95	417	389.19
12094	98.19	10361.77	904.15	4813.41	1786.49
6477	98.17	938.37	123.68	2271.56	862.5
2316	98.14	29.01	9.84	131.45	52.33
20711	98.14	906.86	155.33	131.56	197.74
25501	98.11	23.71	12.36	202.44	115.91
24458	98.11	275.35	47.25	633.46	153.12
3581	98.11	576.77	63.08	309.21	74.14
2683	98.11	107.58	23.12	350.89	114.4
15740	98.11	209.22	35.17	980.35	339
22522	98.09	490.14	82.77	247.28	61
20715	98.09	2091.79	423.29	375.09	412.81
21832	98.09	580.54	288.43	2778.47	1003.27
20001	98.06	1577.58	169	949.56	194.85
17758	98.06	1713.59	355.87	356.13	362.28
4576	98.06	23.1	8.95	186.15	78.03
17770	98.01	222.81	24.69	574.98	219.89
8500	98.01	712.67	203.07	3270.19	1161.43
6066	97.98	67.81	16.14	284.38	127.76
22947	97.98	88.95	24.24	298.36	78.27
16131	97.95	497.97	110.75	2040.39	930.01
18644	97.93	588.78	172.34	2185.59	805.18
760	97.9	139.13	42.17	792.84	407.71
17142	97.9	124.27	49.45	681.38	310.59



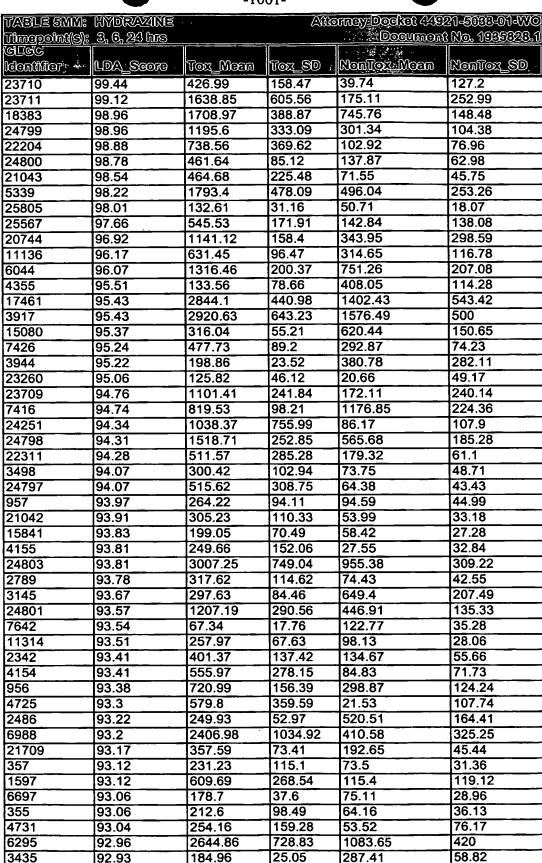




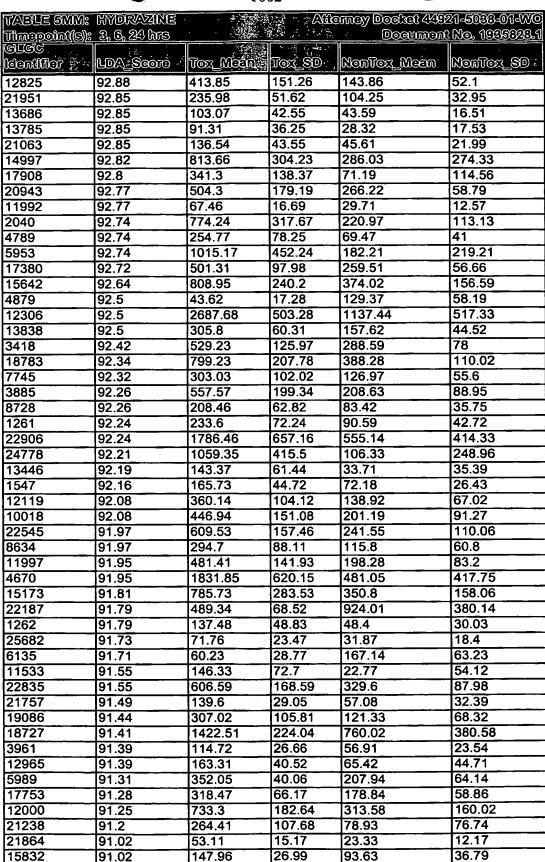


-1000-

TABLE ELL: (Timopoint(S):			Affor	mey Docket 4492 Document	1-5033-01-WO No. 1935323.1
GLGC		Tox Meen :	Iox So	Noulox Mosu	NonTox_SD
20925	94.31	1630.61	481.84	413.35	432.2
17431	94.18	67.68	23.76	164.26	59.49









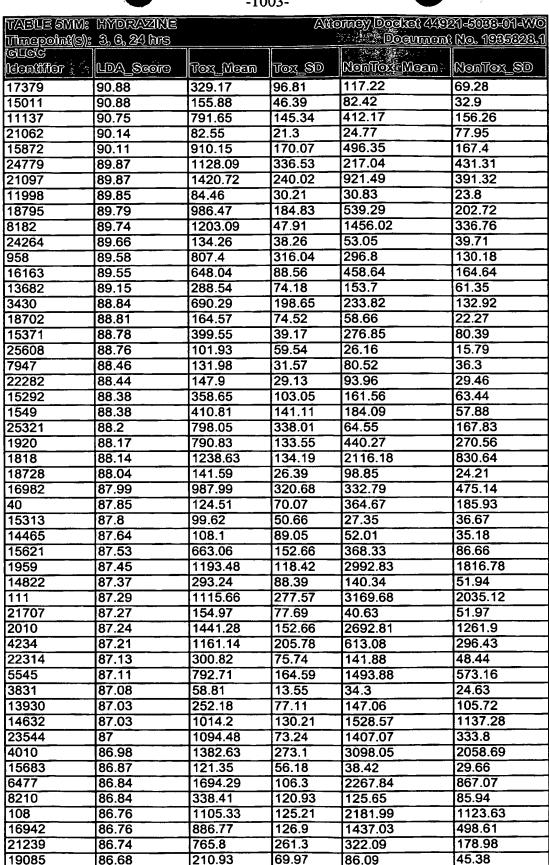


TABLE SMM: Timepoin(s):			Atte	omey Docket 449 Documen	21-5053-01-WO } No. 1935223.1
granginar 🗼	LDA-Score	Tox_Mean	Tox_SD	NonTox_Meen	Montox_SD
1798	86.68	1484.39	174.76	2804.34	1336.11
23491	86.66	67.14	20.87	140.44	66.74
22860	86.63	118.74	38.34	54.3	23.7
8211	86.52	1188.67	125.17	2378.65	1113.31
1853	86.52	1338.93	193.22	2982.14	1637.61
2968	86.44	1151.48	133.67	2449.68	1262.65
4012	86.44	1414	214.2	2443.23	1160.81
17306	86.36	1382.22	224.07	2606.3	1273.84
14981	86.34	1141.57	161.43	3446.36	2312.72



TABLE SIM:	INDOMETHA	GIN	AMO	may Dockot 4402	
Timepoint(s):		· 			No. 1935828.1
CLCC IdonMilar	LDA_Score	Tox_Mean	TOX_SD	Meen To Thom	NonTox_SD
20864	99.76	22.07	8.1	473.18	380.52
17500	99.76	174.03	33.42	28.03	42.3
15503	99.71	707.2	157.43	61.75	41.85
635	99.55	356.02	104.81	1579.4	481.32
17281	99.55	77.18	25.65	630.46	189.09
5687	99.52	45.22	12.45	224.58	66.95
25525	99.5	291.2	107.36	1352.98	361.99
15504	99.47	863.83	283.47	41.6	61.95
21414	99.42	1352.84	131.93	114.58	156.26
634	99.39	432.57	121.45	1538.18	416.47
22514	99.39	744.68	197.84	50.41	64.45
6431	99.39	1733.91	415.59	180.39	214.32
2088	99.34	174.83	69.74	34.94	23.17
16366	99.34	93.95	42.5	800.53	302.18
6200	99.34	1517.47	437.52	67.7	98.35
2012	99.34	433.93	109.02	64.15	36.03
14504	99.34	1218.06	151.51	139.14	164.06
16367	99.31	164.6	117.46	1422.75	539.55
19469	99.31	149.18	32.53	478.15	112.46
19444	99.31	562.59	270.42	35.95	70.52
22512	99.28	660.51	290.11	28.4	42.93
2013	99.28	186.78	42.25	22.86	21.27
22522	99.23	81.82	24.3	249.27	62.78
4892	99.2	2302.4	1160.31	132.97	256.35
23005	99.2	620.21	76.08	122.59	80.13
14081	99.2	1288.65	640.74	38.65	86.88
6541	99.18	412.63	39.8	215.12	104.04
6143	99.18	122.62	42.4	823.43	449.41
15207	99.18	303.17	40.71	74.03	39.9
1893	99.18	266.77	71.14	31.12	27.82
8317	99.18	110.89	21.93	637.6	220.45
9583	99.15	416.77	51.01	60.09	97.66
15029	99.15	176.23	42	1588.92	516.45
8273	99.15	388.63	151.29	42.51	25.01
21285	99.12	1018.03	350.87	98.52	156.99
4933	99.1	418.95	103.33	2049.11	736.07
24589	99.07	529	248.49	54.24	44.27
155	99.07	180.93	33.27	41.29	25.2
18580	99.07	1267.38	310.49	221.92	126.09
3121	99.02	171.84	59.51	821.21	247.16
12606	98.99	161.66	41.16	742.66	237.27
18890	98.96	162.68	53.68	752.65	355.55
17369	98.96	430.65	73.83	119.15	44.67
4011	98.94	509.46	121.38	1823.51	676.9
14330	98.94	942.7	237.45	236	118.54
7384	98.91	1780.22	300.89	686.94	245.66
13361	98.91	349.1	47.62	182.6	37.74
15116	98.91	257.21	62.72	85.81	27.62
14185	98.91	1185.42	257.99	313.52	177.82
11426	98.91	350.88	45.99	121.21	51.34
15872	98.91	98.44	36.44	500.46	168.63
13072	190.91	130.77	100.77	1000.70	1.00.00

TABLEEKN:		CIN		may Docket 4492	
Mwasojuka):	49, 72 hrs			Decument	Mo. 1935323.1
Identifier Gues	LDA_Score	Tox_Mean	Tox_SD	NonTox_Meen	NonTox_SD :
7743	98.91	345.67	60.84	110.57	52.5
24237	98.91	912.03	228.83	184.87	96.96
14840	98.89	236.7	44.89	72.02	37.34
9124	98.86	793.91	57.23	375.63	97.89
17684	98.86	92.04	17.94	322.08	87.9
10984	98.86	129.88	64.62	1060.09	302.49
12551	98.86	50.4	10.88	233.66	77.71
17541	98.83	448.67	101.47	1635.58	637.34
22690	98.83	97.78	59.37	653.38	276.46
14881	98.83	415.82	120.83	1707.93	632.16
556	98.83	326.23	26.19	669.91	127.65
9079	98.83	788.75	135.81	310.96	88.92
4636	98.83	435.3	83.64	73.38	124.83
23321	98.83	70.84	11.27	238.71	64.44
16993	98.83	181.67	44.16	1061.5	291.65
20529	98.83	1248.68	268.72	127.3	176.94
20816	98.81	771.64	143.25	245.66	388.61
17499	98.81	148.93	29.77	25.73	89.53
13332	98.81	55.78	8.2	229.78	83.4
14600	98.81	535.82	168.97	115.13	47.39
373	98.78	95.13	34.96	475.37	164.19
6189	98.78	180.55	93.95	3941.06	2199.2
22897	98.75	171.35	48.54	42.52	23.63
43	98.75	142.99	32.74	436.41	130.66
5421	98.75	521.6	96.83	200.28	71.9
21014	98.75	187.37	72.97	1046.08	348.11
2320	98.75	57.11	20.6	305.95	108.38
4914	98.75	72.31	29.34	482.29	149.47
15888	98.73	393.33	60.16	165.93	140.34
3744	98.73	515.5	85.21	189.2	149.68
21947	98.73	132.87	26.87	396.84	97.07
3112	98.7	476.11	98.4	199.28	62.44
15517	98.7	115.84	32.38	32.43	15.57
10055	98.65	94.7	9.27	34.76	28.72
19121	98.65	130.93	38.98	24.05	21.62
19004	98.65	454.67	78.8	147.74	65.62
21074	98.65	920.52	66.01	445.27	138.25
6366	98.65	796.93	120.52	273.22	98.99
699	98.65	1188.89	92.19	609.29	154.22
1995	98.62	114.72	164.94	1945.29	964.02
4026	98.62	925.46	134.15	371.92	127.61
2484	98.59	21.07	11.5	357.2	222.64
12277	98.59	238.39	55.81	32.61	39.1
13523	98.59	542.26	77.21	251.51	74.05
6532	98.59	312.02	38.89	140.36	42.5
2555	98.59	543.06	103.8	125.65	84.95
20523	98.59	397.31	131.77	47.75	64.63
20869	98.57	255.12	72.98	59.6	47.42
21443	98.57	805.71	152.23	325.49	85.92
16809	98.57	165.52	38.18	29.27	24.29
18453	98.57	84.64	17.34	644.76	264.64

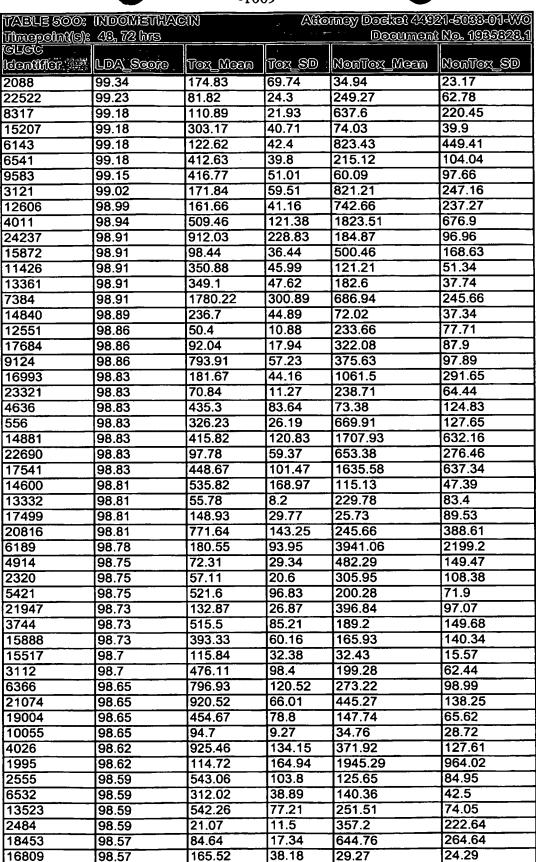
5175 98.54 223.53 69.32 40.02 63.42 22515 98.54 1444.32 389.76 124.13 387.74 20354 98.51 371.97 55.85 51.01 55.74 1827 98.49 72.31 10.06 20.56 18.93 20868 98.49 189.92 59.99 41.52 34.83 19411 98.49 178.07 42.51 33.37 19.72 15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1806.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 36.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 </th <th></th> <th></th> <th>-10</th> <th></th> <th></th> <th></th>			-10			
	Timepoint(s):		Sin 3		•	
22515 98.54 1444.32 389.76 124.13 387.74 20354 98.51 371.97 55.85 51.01 55.74 1827 98.49 72.31 10.06 20.56 18.93 20868 98.49 189.92 59.99 41.52 34.83 19411 98.49 178.07 42.51 33.37 19.72 15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 6540.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 368.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 15071 98.38 55.58 6.19 30.71 24.21<	deatifier decec	LDA_Score	Tox_Meen	Tox_SD	NOOTOX_MOEA	NonTox_SD
20354 98.51 371.97 55.85 51.01 55.74 1827 98.49 72.31 10.06 20.56 18.93 20868 98.49 189.92 59.99 41.52 34.83 19411 98.49 178.07 42.51 33.37 19.72 15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 368.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 10071 98.38 85.86 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04	5175	98.54	223.53	69.32	40.02	63.42
1827	22515	98.54	1444.32	389.76	124.13	387.74
20868 98.49 189.92 59.99 41.52 34.83 19411 98.49 178.07 42.51 33.37 19.72 15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 582.49 135.61 221.08 57.4 4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 247.39 32.73 32.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 39.96<	20354	98.51	371.97	55.85	51.01	55.74
19411 98.49 178.07 42.51 33.37 19.72 15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 96.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 88597 98.35 250.46 49.87 102.41 31.77 20783 98.35 246.49 170.24 13.77	1827	98.49	72.31	10.06	20.56	18.93
15185 98.49 218.02 62.85 60.41 100.75 17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 99.35 250.46 49.87 102.41 31.77 20783 98.35 236.65 77.37 51.51 38.96 10016 98.33 792.81 211.28 29.91 112.09 16048 98.33 154.07 30.86 32.24 29.86	20868	98.49	189.92	59.99	41.52	34.83
17693 98.46 55.17 11.57 211.14 128.01 9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 66.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 58.58 6.19 30.71 24.21 17377 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.6 77.37 51.51 38.96 10016 98.33 792.81 211.28 29.91 112.09 16048 98.33 176.11 63.21 172.15 51.53 <td>19411</td> <td>98.49</td> <td>178.07</td> <td>42.51</td> <td>33.37</td> <td>19.72</td>	19411	98.49	178.07	42.51	33.37	19.72
9842 98.46 640.71 77.24 1606.87 410.98 10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 86.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 2505 98.44 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 163.83 15.75 72.94 32.13 14003 98.3 13.78 9.08 157.09 102.34 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 12.21 17289 99.22 1080.73 108.75 377.99 183.97 16519 98.22 1274.29 22.32 36.92 131.83 14.87 274.82 87.76 1658 98.22 1274.29 22.32 36.93 17.85 40.83 20.5 12.63 1	15185	98.49	218.02	62.85	60.41	100.75
10015 98.43 319.83 48.32 138.08 50.73 17257 98.43 191.55 56.09 40.38 31.83 31.73 31.71 31.77 3	17693	98.46	55.17	11.57	211.14	128.01
17257 98.43 191.55 56.09 40.38 31.83 2005 98.43 86.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.35 250.46 49.87 102.41 31.77 20783 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 376.11 63.21 172.15 51.53 4227 98.33 154.07 30.86 32.24 29.86 9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 </td <td>9842</td> <td>98.46</td> <td>640.71</td> <td>77.24</td> <td>1606.87</td> <td>410.98</td>	9842	98.46	640.71	77.24	1606.87	410.98
2005 98.43 86.81 18.58 20.19 12.65 4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 236.5 77.37 15.15 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 176.07 30.86 32.24 29.86 9223 98.3 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04	10015	98.43	319.83	48.32	138.08	50.73
4439 98.43 582.49 135.61 221.08 57.4 2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.27 247.13 55.44 104.88 31.2	17257	98.43	191.55	56.09	40.38	31.83
2505 98.41 162.62 66.27 755.53 189.25 10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 152.07 30.86 32.24 29.86 9223 98.3 31.78 9.08 157.09 102.34 18038 98.3 31.78 9.08 157.09 102.34 18038 98.3 31.78 9.08 157.09 102.34 <td>2005</td> <td>98.43</td> <td>86.81</td> <td>18.58</td> <td>20.19</td> <td>12.65</td>	2005	98.43	86.81	18.58	20.19	12.65
10071 98.38 58.58 6.19 30.71 24.21 17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 792.81 211.28 29.91 112.09 16048 98.33 792.81 211.28 29.91 112.09 16048 98.33 154.07 30.86 32.24 29.86 9223 98.3 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 163.83 15.75 72.94 32.13 14003 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 779.98 28.38 20.5 12.63 </td <td>4439</td> <td>98.43</td> <td>582.49</td> <td>135.61</td> <td>221.08</td> <td>57.4</td>	4439	98.43	582.49	135.61	221.08	57.4
17377 98.38 247.39 32.73 73.21 49.04 8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 31.78 9.08 157.09 102.34 18038 98.3 31.78 9.08 157.09 102.34 18038 98.27 247.13 55.44 104.88 31.2 </td <td>2505</td> <td>98.41</td> <td>162.62</td> <td>66.27</td> <td>755.53</td> <td>189.25</td>	2505	98.41	162.62	66.27	755.53	189.25
8597 98.35 250.46 49.87 102.41 31.77 20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 163.83 157.57 72.94 32.13 14003 98.3 163.83 157.57 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 14219 98.22 1060.73 108.75 377.99 183.97	10071	98.38	58.58	6.19	30.71	24.21
20783 98.35 236.5 77.37 51.51 38.96 10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 163.83 15.75 72.94 32.13 14003 98.3 163.83 15.75 72.94 32.13 14003 98.3 163.83 15.75 72.94 32.13 14003 98.3 163.83 15.75 72.94 32.13 14003 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97	17377	98.38	247.39	32.73	73.21	49.04
10016 98.33 271.85 40.63 91.73 47.86 1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 17258 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 <td>8597</td> <td>98.35</td> <td>250.46</td> <td>49.87</td> <td>102.41</td> <td>31.77</td>	8597	98.35	250.46	49.87	102.41	31.77
1221 98.33 792.81 211.28 29.91 112.09 16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9923 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 78.98 28.38 20.5 12.63 24219 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41	20783	98.35	236.5	77.37	51.51	38.96
16048 98.33 376.11 63.21 172.15 51.53 7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 131.83 14.87 274.82 87.76 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15	10016	98.33	271.85	40.63	91.73	47.86
7427 98.33 154.07 30.86 32.24 29.86 9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83	1221	98.33	792.81	211.28	29.91	112.09
9223 98.3 328.74 141.18 88.51 39.55 1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 145.59 44.27 804.82 225.28 <td>16048</td> <td>98.33</td> <td>376.11</td> <td>63.21</td> <td>172.15</td> <td>51.53</td>	16048	98.33	376.11	63.21	172.15	51.53
1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 <td>7427</td> <td>98.33</td> <td>154.07</td> <td>30.86</td> <td>32.24</td> <td>29.86</td>	7427	98.33	154.07	30.86	32.24	29.86
1572 98.3 163.83 15.75 72.94 32.13 14003 98.3 31.78 9.08 157.09 102.34 18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 <td>9223</td> <td>98.3</td> <td>328.74</td> <td>141.18</td> <td>88.51</td> <td>39.55</td>	9223	98.3	328.74	141.18	88.51	39.55
18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129	1572	98.3	163.83	15.75	72.94	32.13
18038 98.3 64.36 15.87 249.99 90.04 17258 98.27 247.13 55.44 104.88 31.2 12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129	14003	98.3	31.78	9.08	157.09	102.34
12797 98.27 78.98 28.38 20.5 12.63 24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6	18038	98.3	64.36	15.87	249.99	90.04
24219 98.22 1060.73 108.75 377.99 183.97 16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 <t< td=""><td>17258</td><td>98.27</td><td>247.13</td><td>55.44</td><td>104.88</td><td>31.2</td></t<>	17258	98.27	247.13	55.44	104.88	31.2
16519 98.22 1274.29 222.32 366.94 216.58 17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36	12797	98.27	78.98	28.38	20.5	12.63
17382 98.22 131.83 14.87 274.82 87.76 17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.	24219	98.22	1060.73	108.75	377.99	183.97
17480 98.22 163.32 52.34 68.15 33.41 16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8<	16519	98.22	1274.29	222.32	366.94	216.58
16416 98.2 271.85 91.29 108.09 60.15 1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8<	17382	98.22	131.83	14.87	274.82	87.76
1700 98.17 301.86 72.09 83.5 41.83 21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.0	17480	98.22	163.32	52.34	68.15	33.41
21012 98.14 495.25 96.3 1522.52 566.27 794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62	16416	98.2	271.85	91.29	108.09	60.15
794 98.14 145.59 44.27 804.82 225.28 21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.4	1700	98.17	301.86	72.09	83.5	41.83
21657 98.12 1345.86 71.6 749.74 292.41 18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93	21012	98.14	495.25	96.3	1522.52	566.27
18988 98.09 30.38 13.56 223.34 129.63 20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	794	98.14	145.59	44.27	804.82	225.28
20879 98.09 43.74 30.64 625.47 269.64 23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	21657	98.12	1345.86	71.6	749.74	292.41
23322 98.06 175.17 55.47 557.6 145.02 13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	18988	98.09	30.38	13.56	223.34	129.63
13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	20879	98.09	43.74	30.64	625.47	269.64
13283 98.01 183.6 63.4 902.59 271.24 13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	23322		175.17	55.47	557.6	145.02
13499 97.98 157.44 31.79 50.5 36.82 14882 97.96 354.04 130.14 1304.22 413.04 2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	13283	98.01		63.4	902.59	271.24
2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	13499	97.98	157.44	31.79	50.5	36.82
2853 97.96 129.41 20.44 57.52 45.82 1262 97.93 173.78 34.84 48.39 29.8 23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	14882	97.96	354.04	130.14	1304.22	413.04
23044 97.93 334.36 75.68 152.38 55.27 9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	2853		129.41	20.44	57.52	45.82
9125 97.9 1110.1 130.53 634.63 135.06 14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	1262	97.93	173.78	34.84	48.39	29.8
14384 97.9 512.02 67.81 246.63 62.43 154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	23044	97.93	334.36	75.68	152.38	55.27
154 97.9 418.22 115.55 165.54 59.93 10887 97.9 29.6 7.88 106.33 32.62	9125	97.9	1110.1	130.53	634.63	135.06
10887 97.9 29.6 7.88 106.33 32.62	14384	97.9	512.02	67.81	246.63	62.43
	154	97.9	418.22	115.55	165.54	59.93
1841 97.88 275.92 85.51 46.56 50.38	10887	97.9	29.6	7.88	106.33	32.62
	1841	97.88	275.92	85.51	46.56	50.38

WO 03/064624

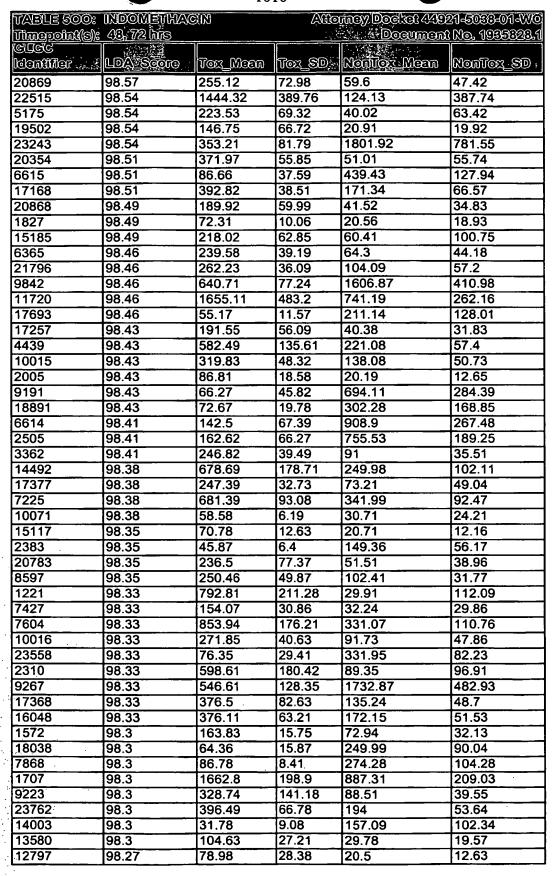
PCT/US03/03194

-1008-

TABLE 5XX: INDOMETHACIN			Alloi	may Docket 4492	
Timepoin((s): 43, 72 hrs				<u> </u>	<u>No. 1935323.1</u>
G. T. G. C.				4.2	i
ldeniliter, 🗽	LDA_Score :	Tox_Moan .	LOXED L	MOONTOX_MOON	NonTox_SD
1795	97.85	80.33	33.43	535.15	374.1







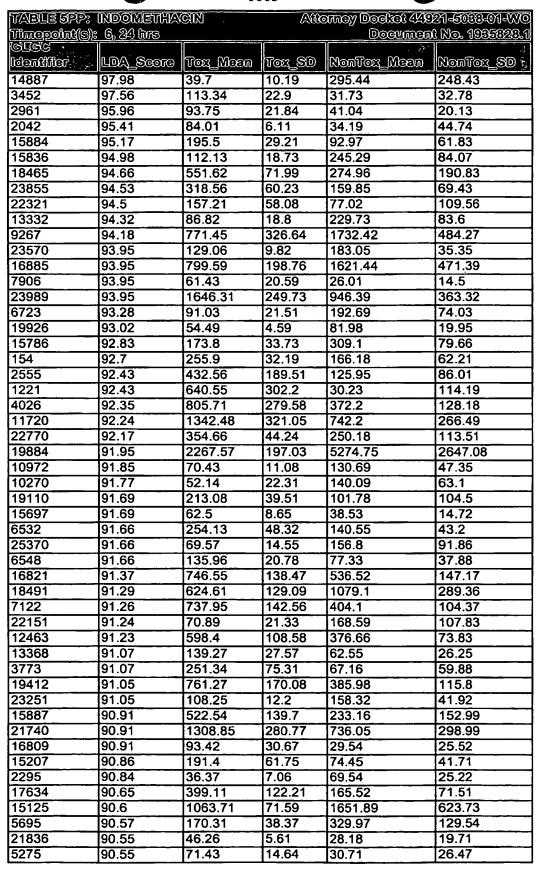


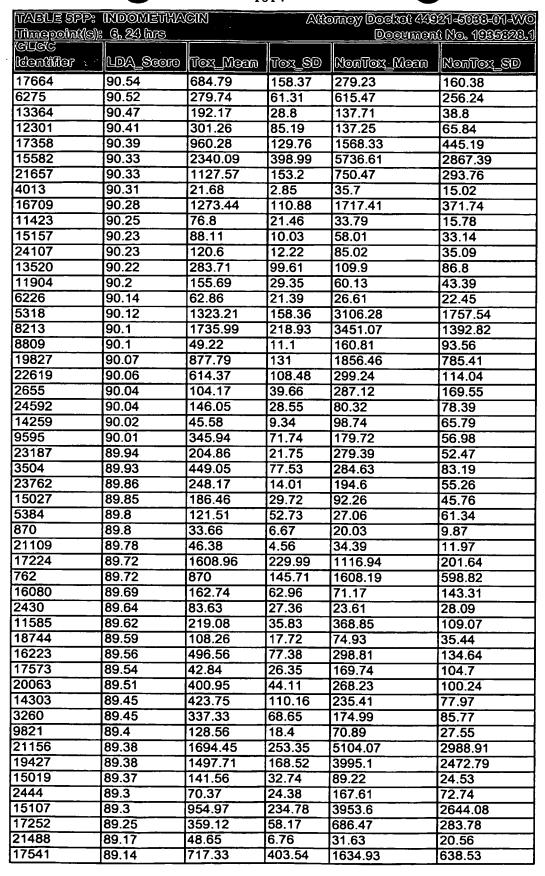
3-01-W0 35323.1 01 SD
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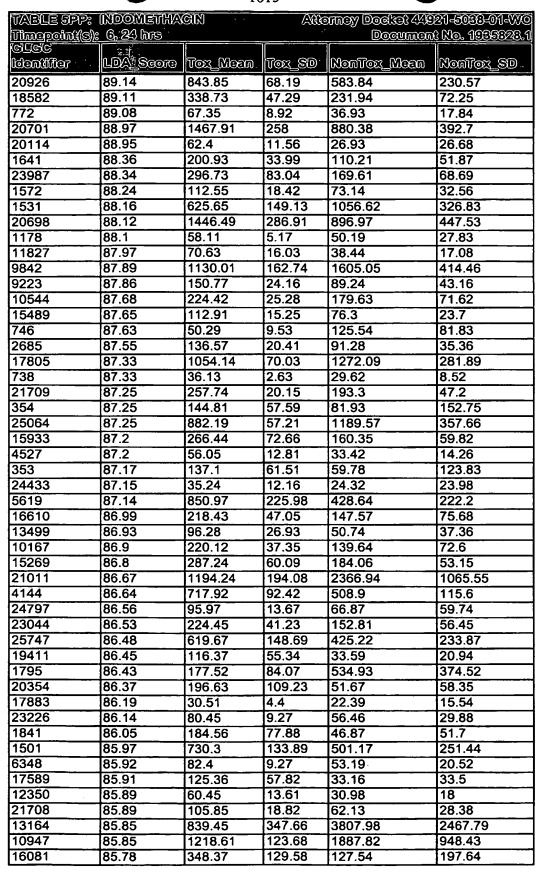
3

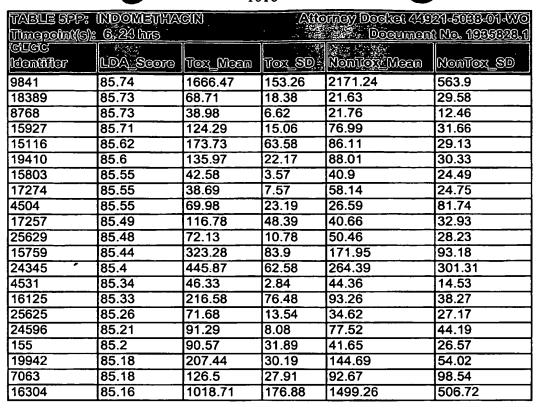
-1012-

TABLE 500: Timepoint(s):	INDOMETHAC 43, 72 his	NIN .	Auc	may Docket 449	21-5068-01-WO No. 1935823.1
(G.T.G.C.	LDA_Score	Tox_Mean	Tox_SD	Nonfox Mean	NonTox_SD
23872	97.11	254.62	73.06	73.96	154.85
4574	97.08	264.2	83.17	619.9	136.28
25777	97.08	347.17	36.34	686.6	244.17









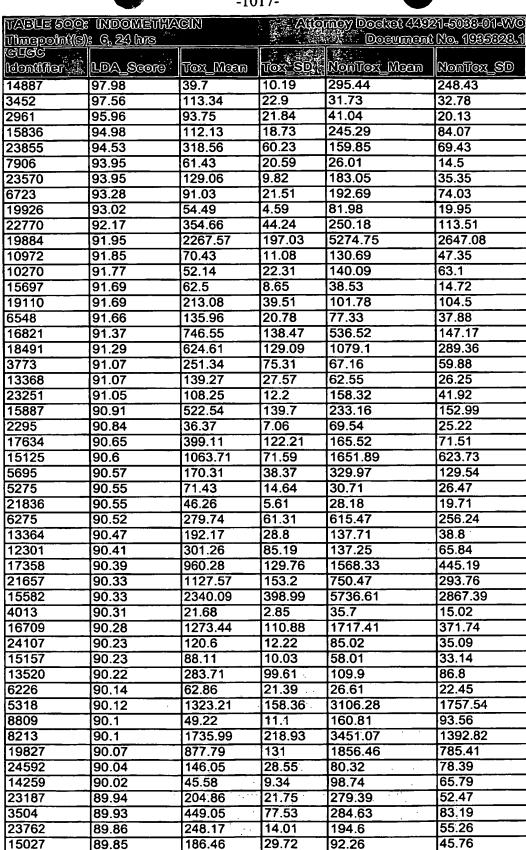
870

89.8

33.66

6.67

20.03





9.87

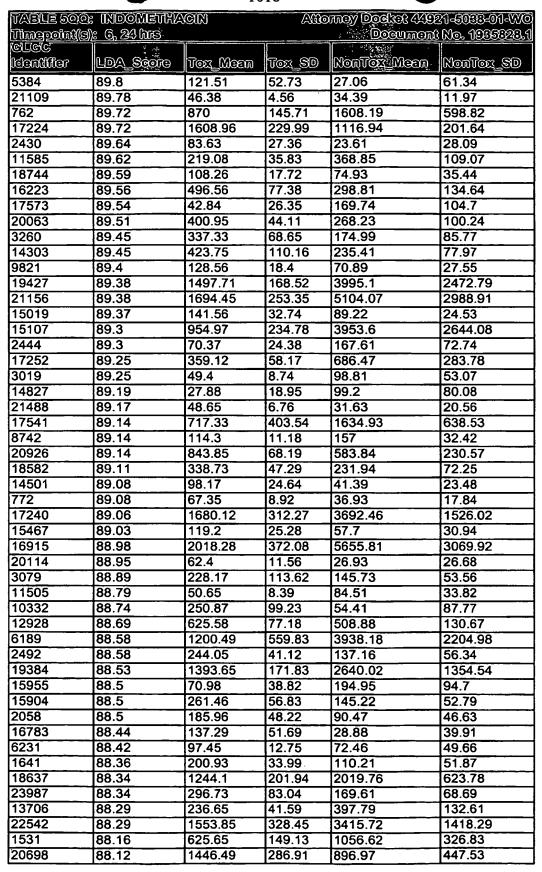
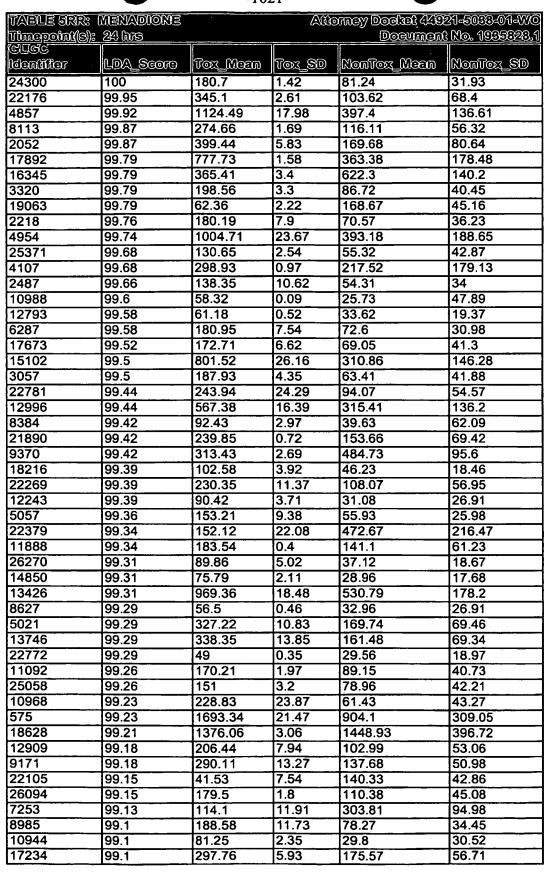
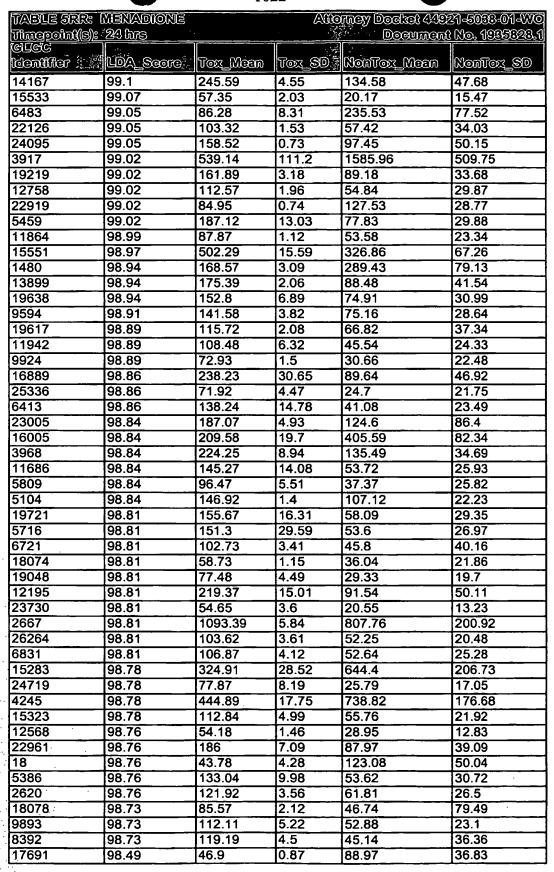
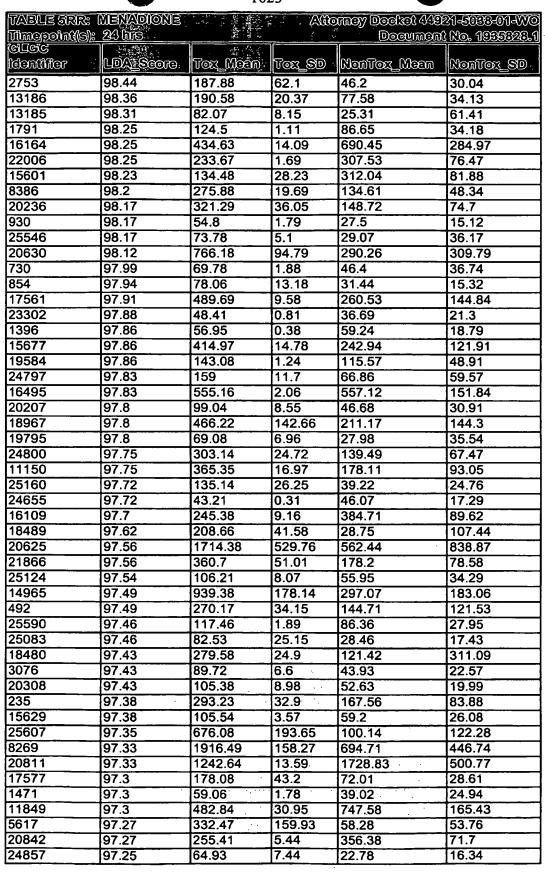


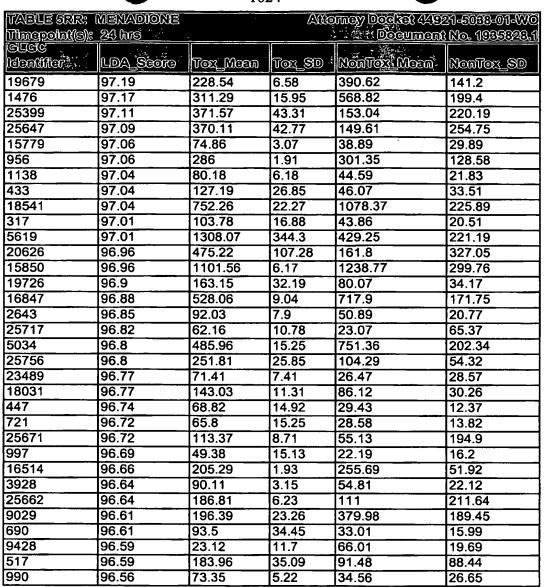
TABLE 500		CIN CIN	OWA	mey.Docket 4492	31-5088-01-WO
Timepoint(s)): 6, 24 hrs		**) Dogumen(
CLCC Idendifor	LDV Seque	Tox_Mean	Tox_SD:	Nontrox Non	NonTox_SD :
1178	88.1	58.11	5.17	50.19	27.83
11827	87.97	70.63	16.03	38.44	17.08
9842	87.89	1130.01	162.74	1605.05	414.46
10544	87.68	224.42	25.28	179.63	71.62
15489	87.65	112.91	15.25	76.3	23.7
746	87.63	50.29	9.53	125.54	81.83
2685	87.55	136.57	20.41	91.28	35.36
17805	87.33	1054.14	70.03	1272.09	281.89
738	87.33	36.13	2.63	29.62	8.52
25064	87.25	882.19	57.21	1189.57	357.66
15933	87.2	266.44	72.66	160.35	59.82
4527	87.2	56.05	12.81	33.42	14.26
353	87.17	137.1	61.51	59.78	123.83
24433	87.15	35.24	12.16	24.32	23.98
5619	87.14	850.97	225.98	428.64	222.2
16610	86.99	218.43	47.05	147.57	75.68
13499	86.93	96.28	26.93	50.74	37.36
10167	86.9	220.12	37.35	139.64	72.6
15269	86.8	287.24	60.09	184.06	53.15
21011	86.67	1194.24	194.08	2366.94	1065.55
4144	86.64	717.92	92.42	508.9	115.6
24797	86.56	95.97	13.67	66.87	59.74
23044	86.53	224.45	41.23	152.81	56.45
25747	86.48	619.67	148.69	425.22	233.87
19411	86.45	116.37	55.34	33.59	20.94
17883	86.19	30.51	4.4	22.39	15.54
23226	86.14	80.45	9.27	56.46	29.88
1841	86.05	184.56	77.88	46.87	51.7
1501	85.97	730.3	133.89	501.17	251.44
6348	85.92	82.4	9.27	53.19	20.52
17589	85.91	125.36	57.82	33.16	33.5
12350	85.89	60.45	13.61	30.98	18
21708	85.89	105.85	18.82	62.13	28.38
13164	85.85	839.45	347.66	3807.98	2467.79
10947	85.85	1218.61	123.68	1887.82	948.43
9841	85.74	1666.47	153.26	2171.24	563.9
8768	85.73	38.98	6.62	21.76	12.46
15927	85.71	124.29	15.06	76.99	31.66
15116	85.62	173.73	63.58	86.11	29.13
15803	85.55	42.58	3.57	40.9	24.49
17274	85.55	38.69	7.57	58.14	24.75
17257	85.49	116.78	48.39	40.66	32.93
25629	85.48	72.13	10.78	50.46	28.23
15759	85.44	323.28	83.9	171.95	93.18
24345	85.4	445.87	62.58	264.39	301.31
4531	85.34	46.33	2.84	44.36	14.53
25625	85.26	71.68	13.54	34.62	27.17
24596	85.21	91.29	8.08	77.52	44.19
155	85.2	90.57	31.89	41.65	26.57
19942	85.18	207.44	30.19	144.69	54.02
7063	85.18	126.5	27.91	92.67	98.54

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Elimbogomini		Sun .	CARRO.	_	
(Q.CQ.C -	6 0 5 23-3 000 5	1	ì	n recenives we	No. 1935323.1
ldeniiio:	LDA Score	Tox Mean	TOX_SD	NonTox_Meen	NonTox_SD
16304	85.16	1018.71	176.88	1499.26	506.72
21039	85.08	99.44	21.32	239.59	180.51
9541	85.08	124.15	44.41	72.06	109.95
8597	85.07	144.07	20.56	102.84	33.19
21707	85.07	152.81	70.83	40.76	52.2
8212	85.02	1243.19	145.66	1984.57	731.41
17908	84.89	121.64	35.63	72.53	116.7
15558	84.86	403.8	67.32	309.7	117.24
21076	84.84	50.29	5.48	40.21	16.58
15259	84.83	173.67	39.01	101.51	55.77
17995	84.78	1096.43	199.3	1700.15	651.94
20464	84.78	1368.16	149.82	1782.69	560.41
10623	84.71	558.28	150.08	1106.36	503.43
912	84.71	444.45	52.53	353.86	126.43
4011	84.65	1065.84	236.96	1821.55	680.32
14347	84.63	1231.25	156.22	1744.22	515.78
20449	84.59	80.01	96.05	40.6	104.34
24897	84.57	20.87	8.46	44.28	16.55
18327	84.56	101.34	33.54	44.4	26.98
25676	84.54	152.77	32.89	96.72	43.31
11203	84.53	86.52	27.79	42.24	17.81
16221	84.49	87.05	12.61	62.94	28
14353	84.43	57.65	12.97	37.24	21.71
19584	84.38	189.94	25.96	115.26	48.7

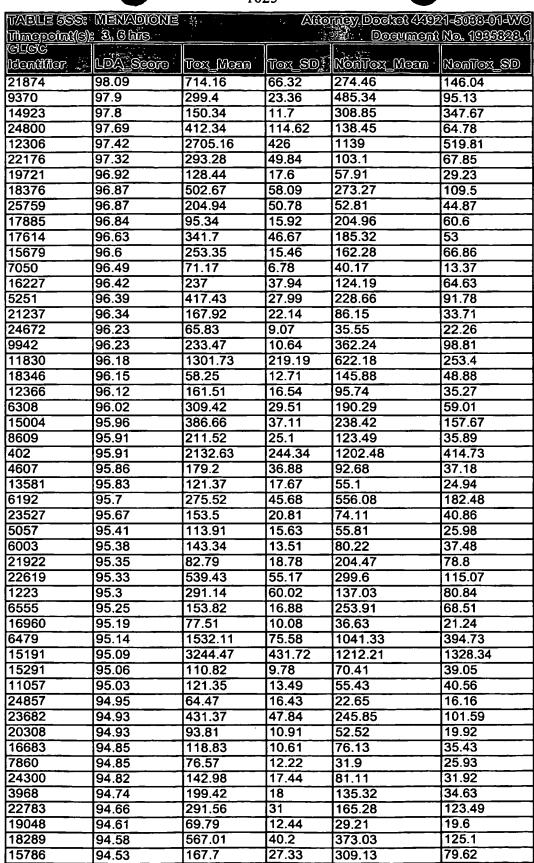














Timepoint(s): 3, 6 hrs Text Mean Text SD Nontfort Mean Nontfort Mean	
2329 94.53 408.53 39.92 217.64 99.54 11631 94.5 318.94 82.68 141.5 76.24 25756 94.45 233.48 36.77 103.91 53.94 13027 94.45 85.08 8.75 176.1 57.93 16109 94.42 238.15 26.31 385.19 89.34 6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
11631 94.5 318.94 82.68 141.5 76.24 25756 94.45 233.48 36.77 103.91 53.94 13027 94.45 85.08 8.75 176.1 57.93 16109 94.42 238.15 26.31 385.19 89.34 6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
25756 94.45 233.48 36.77 103.91 53.94 13027 94.45 85.08 8.75 176.1 57.93 16109 94.42 238.15 26.31 385.19 89.34 6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
13027 94.45 85.08 8.75 176.1 57.93 16109 94.42 238.15 26.31 385.19 89.34 6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
16109 94.42 238.15 26.31 385.19 89.34 6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
6598 94.42 381.42 57.54 182.73 84.32 13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
13377 94.32 1409.07 68.91 954.34 331.58 20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
20450 94.32 130.43 20.38 72.2 28.95 12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
12974 94.29 194.88 13.16 125.27 46.52 20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
20701 94.29 1366.85 185.45 880.87 393.54 6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
6845 94.24 49.02 4.89 28.18 12.7 4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
4213 94.18 4824.8 285.81 4465.41 3881.05 25546 94.18 68.9 13.48 28.95 36.15	
25546 94.18 68.9 13.48 28.95 36.15	
17455 94.11 280.41 34.66 166.29 67.91	
26313 94.03 116.84 15.3 66.02 35.42	
15776 94.03 311.51 42.17 189.48 82.54	
21917 94.03 152.94 42.24 74.85 65.82	
174 93.92 101.38 15.55 43.2 32.8	
19011 93.92 431.83 92.84 288.68 89.28	
11889 93.87 37.05 3.38 21.77 10.49	
19309 93.87 38.24 26.96 91.59 25.39	
18267 93.87 346.69 66.22 126.28 106.4	
6274 93.84 180.9 14.7 116.03 97.86	
19012 93.84 683.46 84.05 439.74 165.4	
3259 93.84 83.94 51.68 243.18 76.39	
16401 93.81 5672.7 575.16 5366.36 5007.6	
10666 93.79 377.1 36.21 570.86 119.56	
9575 93.79 257.18 44.54 447.09 109.46	
22791 93.79 232.74 44.91 139.38 64.05	
2918 93.76 631.79 59.62 435.55 137.55	
18648 93.71 65.41 7.43 36.53 22.03	
26267 93.71 93.67 9.33 52.82 27.89	
13899 93.6 168.37 20.52 88.23 41.36	
4073 93.57 95.92 16.77 251.33 144.2	
5263 93.55 254.49 36.09 450.62 127.69	-
3537 93.49 256.62 33.83 439.6 116.24	
22981 93.49 312.93 27.91 194.98 67.66	
23674 93.44 53.43 7.81 23.63 17.57	
1959 93.41 3101.5 192.27 2981.8 1820.95	
1409 93.39 228.7 40.31 411.79 113.62	
17334 93.39 311.96 66.11 176.67 86.64	
2566 93.39 31.36 105.72 381.53 176.99	
25325 93.36 1467.89 200.42 1624.58 1181.83	
6304 93.31 66.67 6.46 41.92 20.93	
22294 93.31 193.25 20.42 118.16 45.67	
5993 93.31 51.64 10.75 20.65 16.29	
26349 93.28 209.41 29.13 128.94 54.75	
23770 93.23 89.1 4.24 68.39 20.13	
16963 93.12 5068.31 328.3 4286.61 3539.05	,
15190 93.12 4411.01 697.88 1828.63 1710.94	



TABLE 588: MENADIONE Timepoint(s): 3, 6 hrs			Afformey Docket 44921-5933-91-WO Document No. 1935323.1		
CLCC Condition :	LDA_Scoro	Tox_Mean	Tox_SD	NonTox_Mean	NonTox_SD
6109 ,	90.39	3892.59	421.76	3587.94	2271.51
109	90.36	4267.74	420.11	3932.08	2218.07
1340	90.36	74.4	9.59	52.89	25.2
25805	90.33	101.74	19.82	50.95	18.88
7897	90.31	3855.77	393.93	3453.76	2131.21
1682	90.3	84.93	16.27	45.13	21.22
24219	90.25	593.76	96.63	379.86	188.74
819	90.23	3042.17	168.2	2545.71	1186.25
25607	90.2	419.03	157.7	99.54	122.38
20249	90.2	46.76	7.26	24.84	21.04
575	90.2	1737.56	370.42	901.37	304.79
21123	90.18	640.81	49.15	947.96	279.54
25681	90.15	4723.2	312.96	3800.99	2398.13
20266	90.12	196.98	21.62	135.98	68.99
4590	90.04	22.67	9.97	51.5	26.92

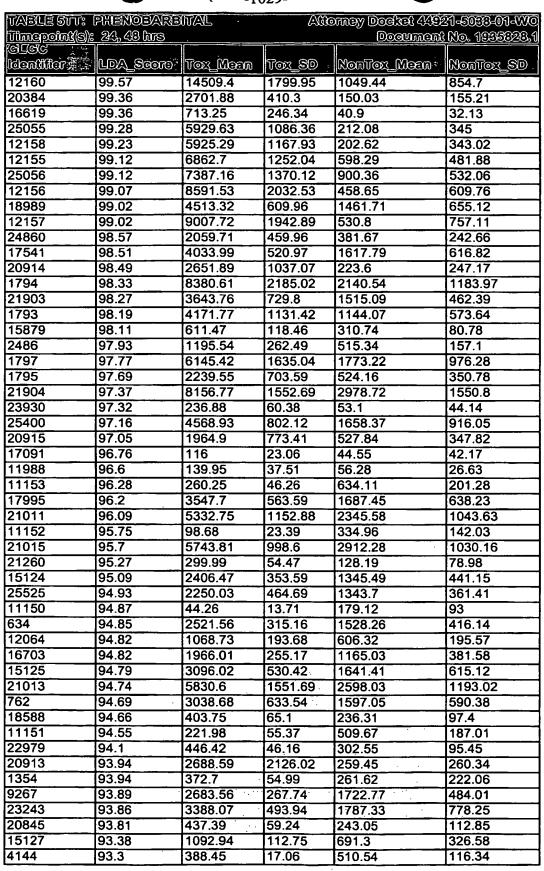


TABLE STT: Timepoint(s):			All C	mey Doctot 4421	21-5033-01-WO
GECC Identifier	LDA Scoro		7.00		NonTox_SD
12556	93.19	471.8	169.24	58.76	95.77
19271	93.15	134.66	35.71	273.31	93.74
7882	93.07	225.07	29.35	81.78	75.73
4312	92.98	521.06	266.69	61.32	146.18
15955	92.88	330.93	30.29	193.64	94.59
635	92.88	2600.97	345.87	1568.77	481.76
20090	92.83	63.15	7.18	109.83	42.39
24112	92.64	2163.88	366.35	1244.91	607.68
12060	92.53	50.55	8.73	91.31	25.79
17705	92.45	82.18	9.37	131.44	38.83
1796	92.37	882.48	338.68	235.11	173.14
5263	92.35	654.46	52.63	448.6	127.54
18939	92	673.45	204.98	202.49	117.42
5968	91.87	1151.84	215.84	708.98	247.14
15166	91.84	415.88	22.37	588.85	137.61
4198	91.68	745.2	83.97	1092.52	231.77
6633	91.6	758.67	172.56	1250.77	331.5
18473	91.52	942.15	242.01	433.28	208.17
8872	91.49	998.09	281.52	491.49	237.66
14957	91.42	77.29	6.42	126.62	46.79
1174	91.29	4791.97	713.92	2379.14	1388.64
13364	91.23	47.42	35.62	138.45	38.39
20707	91.23	1399.02	196.5	601.99	294.44
25725	91.17	270.08	56.84	142.09	63.02
16801	91.15	99.62	9.88	141.59	35.86
4103	91.12	382.3	55.98	198.23	68.92
6524	90.97	546.51	29.95	699.53	141.78
2393	90.91	157.72	41.9	287.6	85.55
3254	90.89	237.54	7.36	257.04	90.92
8212	90.83	3112.17	354.67	1975.03	728.36
5794	90.78	70.25	12.28	123.81	38.5
17740	90.78	4008.33	523.88	2188.6	950.26
5497	90.7	427.99	58.95	643.48	188.3
9032	90.7	823.09	122.31	603.96	158.27
3259	90.67	360.08	39.26	241.8	76.74
3143	90.6	249.63	20.08	355.57	95.49
21039	90.59	720.51	176.04	236.37	176.95
19319	90.54	65.92	11.77	121.34	49.96
23445	90.52	78.1	28.93	236.42	130.77
11830	90.46	377.42	38.91	626.73	257.51
16781	90.44	482.82	105.22	328.26	126.29
4185	90.25	6527.56	558.8	4083.35	2982.46
14811	90.22	106.7	34.71	41.76	24.4
7460	90.14	13903.64	1196.71	8321.17	5716.29
25069	90.06	663.79	261.49	202.92	247.01
17082	90.04	52.62	6.86	89.47	33.8
17766	89.98	689	57.06	487.27	93.09
11755	89.96	2478.27	379.82	1553.49	581.96
16701	89.82	3456.85	244.83	2268.68	714.6
20889	89.8	84.13	16.75	156.56	73.91
4186	89.77	5001.5	445.22	3629.64	2066.56

TABLE STT: 1	PHENOBARB	MAL	e të Me	imey Docket 4492	21-5058-01-00
Timepoint(s):					No. 1935323.1
Identifier GLEC	27 BE	Tox_Mean !	TOX SD	MonTox_Mean	NonTox SD
18990	89.77	75.49	27.67	25.51	57.32
15187	89.64	63.15	9.02	108.66	43.44
1430	89.58	223.43	38.49	90.18	69.26
21038	89.5	733.73	177.68	291.84	201.15
1175	89.23	1449.5	271.46	626.21	343.54
18730	89.16	5379.25	576.87	2887.14	1605.69
26034	89.16	132.89	28.5	52.95	59.9
1853	89.11	5250.77	501.98	2960.48	1633.18
21078	89.08	461.93	70.94	739.71	214.88
5493	89.08	73.21	10.75	54.29	64.32
5496	89.05	317.11	55.78	493.63	155.54
25883	89	3428.03	299.6	2243.39	1051.58
16564	88.92	122.78	23.49	216.29	84.95
17148	88.87	6457.02	555.69	3821.55	2484.2
25705	88.84	562.23	37.31	744.38	198.88
109	88.68	6218.69	454.19	3921.54	2212.43
17805	88.68	1809.45	190.99	1268.19	279.33
20404	88.66	91.37	24.29	205.76	111.45
14534	88.63	8788.22	991.68	4577.37	3851.67
1603	88.62	707.02	82.71	459.07	120.8
8266	88.58	5623.63	609.92	3543.41	2247.9
23709	88.58	75.1	10.72	178.06	250.82
1602	88.55	629.19	74.59	465.64	108.93
20849	88.52	90.37	10.03	138.46	47.97
17147	88.47	5523.31	565.78	3199.37	1951.71
17507	88.42	302.34	20.96	428.45	115.23
18640	88.23	115.7	10.2	159.23	38.33
13088	88.12	1836.55	198.73	1272.65	440.08
17109	88.1	9993.09	1565.35	4933.15	4382.67
23069	88.02	21.58	2.62	33.26	11.81
16274	87.96	6083.51	623.66	4084.4	2900.74
7101	87.94	2763.75	445.77	1901.67	637.97
17092	87.88	126.68	17.28	80.55	46.53
18899	87.86	30.42	4.35	45.83	13.43
2969	87.75	3421.75	431.08	2127.84	1026.48
20899	87.73	46.49	3.88	69.46	24.5
26047	87.69	178.16	55.21	69.79	72.09
15165	87.57	80.94	12.71	124.84	34.8
22025	87.51	4570.37	649.96	2688.89	1734.91

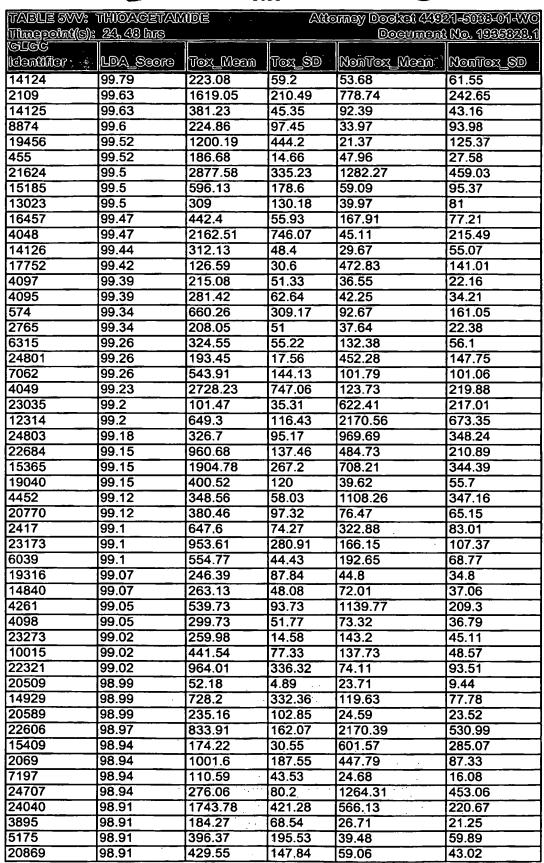
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		1	·	Document	<u> </u>
CLCC Identifier	LDA_Seoig	Tox_Meen	Tox_SD:	Koulox Meeu	MonTox_SD
20744	98.81	992.11	49.01	346.88	302.63
17050	98.28	379.56	51.02	189.11	45.94
13369	98.2	313.84	29.32	166.05	41.94
19412	98.04	632.66	26.83	387.12	118.38
21709	97.85	308.7	21.56	193.31	46.99
22513	97.67	714.42	622.68	36.75	791.9
18389	97.67	108.22	18.24	21.62	29.4
6919	97.67	1115.56	206.3	342.91	293.47
21063	97.54	146.26	45.53	45.87	22.56
8210	97.51	439.87	119.86	126.05	86.09
6060	97.48	320.41	14.26	497.63	113.5
12704	97.48	3225.2	738.25	1537.63	371.36
19472	97.46	953.71	72.93	581.75	129.12
6079	97.35	108.49	8.34	60.79	91.63
21980	97.32	1002	119.49	504.82	160.92
21209	97.27	374.82	146.99	83.28	83.82
12306	97.22	2938.32	781.9	1141.7	521.75
24427	97.16	173.63	19.02	108.43	25.14
20728	97.11	422.01	24.13	263.13	83.97
13166	97.06	303.12	88.37	85.31	66.01
633	97.03	856.71	47	1338.05	288.02
16762	97.01	97.61	6.27	59.29	86.96
24200	96.95	1448.31	479.01	437.64	246.76
21062	96.85	100.66	28.74	24.9	77.86
344	96.82	2969.83	492.02	1274.65	554.2
6236	96.74	252.53	70.23	951.24	409.13
23606	96.71	989.3	166.6	405.17	222.93
22729	96.66	319.68	12.19	182.4	79.86
15558	96.42	589.95	181.9	309.41	116.18
5003	96.4	382.44	32.14	215.43	84.35
7451	96.4	1978.62	261.09	1138.59	308.49
22514	96.34	132.27	49.43	53.14	79.41
17590	96.34	223.78	43.2	106.05	46.42
19513	96.32	307.72	108.08	161.95	46.53
17709	96.29	137.32	33.21	37.84	42.27
5110	96.16	586.14	94.86	322.81	112.64
1991	96.13	57.8	9.91	26.22	15.81
21952	96.1	90.92	14.32	48.78	17.41
24508	96.08	211.47	23.6	112.86	47.28
20435	95.95	64.16	9.79	27.19	14.33
8360	95.92	176.06	5.07	239.49	62.03
2939	95.87	54.55	26.97	208.22	81.78
3709	95.87	38.94	2.34	77.47	35.91
23464	95.81	704.11	117.59	418.74	110.44
12438	95.79	249.67	19.56	138.33	68.02
18715	95.79	358.3	40.15	196.07	76.37
18383	95.71	1135.08	127.59	750.34	166.53
2559	95.71	186.95	25.32	104.46	38.27
373	95.63	227.24	32.46	474.41	165.43
20464	95.6	1095.35	43.55	1782.54	559.52
5579	95.57	257.01	69.72	137.63	47.93



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CLCC CLCCC	LDA_Secto	Lox Mosu"	Tox_SD 😤	NonTox Mean	NonTox_SD &
24152	95.52	67	1.64	89.87	38.21
1286	95.5	183.35	27.33	112.79	27.95
5111	95.39	532.21	128.55	235.59	135.31
19410	95.31	172.82	39.04	88.02	30.15
13420	95.28	654.46	191.67	378.53	98.34
7166	95.23	47.54	94.21	80.42	49.57
16701	95.15	1261.86	136.13	2277.64	717.12
25742	95.12	80.09	17.45	39.46	20.84
3082	95.07	451.48	96.44	259.74	94.84
2514	94.99	1247.26	322.15	547.73	284.03
16533	94.97	800.73	179.26	445.22	130.9
6720	94.89	227.94	50.85	31.13	97.8
2557	94.86	68.59	16.34	35.61	16.81
22927	94.86	64.14	13.24	27.73	17.99
12102	94.73	368.23	93.97	147.04	96.66
12516	94.67	1348.53	187.49	879.19	195.66
12210	94.62	674.98	80.19	318.58	179.59
11152	94.59	646.99	94.91	332.88	141.9
22011	94.59	132.87	21.89	76.56	26.13
23519	94.57	133.17	22.15	77.81	22.23
16398	94.57	839.75	91.42	527.5	137.55
20	94.57	625.39	97.54	346.48	136.85
24204	94.54	111.5	14.67	71.97	20.1
22396	94.49	162.13	27.53	98.98	28.64
1141	94.38	256.36	14	177.05	56.18
1382	94.38	40.43	1.43	37.92	15.32
16703	94.36	585.83	91.17	1170.81	384.69
2569	94.36	251.91	137.3	909.5	288.88
18074	94.17	60.23	9.31	36.02	21.85
20701	94.14	1440.72	250.45	881.7	393.51
5936	94.04	68.8	6.84	23.21	31.36
5131	94.04	435.41	42.67	257.14	90.74
23243	93.93	629.83	152.9	1798.88	784.27
19150	93.93	83.76	13.27	43.56	23.05
21866	93.93	289.08	32.27	178.19	78.76
2242	93.91	4309.63	662.67	2425.76	879.85
6138	93.88	384.76	68.99	227.9	68.41
1084	93.83	49.31	6.12	26.71	14.04
18795	93.8	945.93	140.98	540.82	204.52
5876	93.77	1505.45	97.31	1081.12	389.77
21341	93.72	498.39	73.45	857.6	303.48
2568	93.67	53.46	11.11	141.53	90.79
11166	93.67	272.39	59.51	521.55	148.22
20698	93.67	1371.7	196.62	898.34	448.29
410	93.64	63.01	24.82	186.91	90.68
11197	93.61	189.18	7.01	243.96	56.06
139	93.53	70.22	10.9	41.21	21.5
4407	93.51	205.71	11.21	143.9	57.78
912	93.51	501.96	42.56	353.9	126.25
17062	93.51	220.93	46.01	114.24	47.55
24459	93.4	323.38	55.67	214.05	77.63



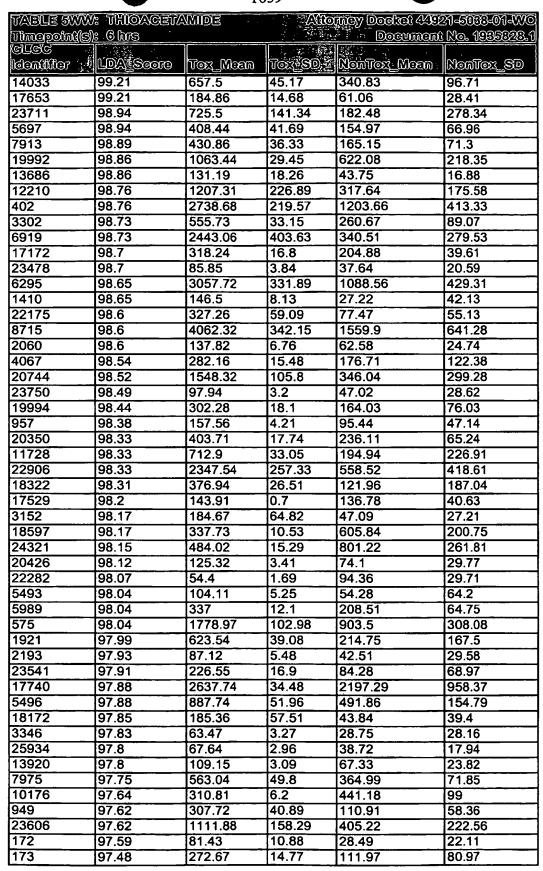
TABLE SUU:	TACRINE	· · · · · · · · · · · · · · · · · · ·	Affe	mey Docket 449	21-5033-01-WO
Timepoint(S):	: SM8			Dogumen	No. 1935328.1
(CLCC (Continor	LDA_Scoro	Tox_Mean	Tox_SD	MEEM_XOTMON	NonTox_SD
4523	93.4	132.26	28.17	63.06	32.11
22314	93.35	241.61	39.08	142.54	49.87
6377	93.27	101.92	8.93	185.61	119.92
15002	93.24	189.83	11.9	141.14	75.67
960	93.22	124.24	17.18	215.73	65.87
5050	93.22	72.57	7.85	48.14	27.95
13646	93.22	964.35	46.75	747.74	197.55
14347	93.16	1160.18	54.48	1743.32	515.67
4349	93.11	59.4	9.99	24.3	17.83
16708	93	615.93	125.51	446.83	94.51
767	92.93	46.98	3.61	27.41	16.65
24862	92.69	306.27	47.3	200.09	58.42
24066	92.66	53.9	7.05	32.6	11.99
15697	92.63	65.64	9.7	38.58	14.74
14953	92.53	522.37	37.45	387.26	80.08
25366	92.4	934.17	30.04	891.92	402.32
25611	92.37	59.69	3.26	42.72	24.51
23543	92.34	868.93	81.11	586.14	160.83
5257	92.34	101.39	22.95	55.82	22.48
1409	92.34	227.42	52.02	411.4	113.81
20793	92.32	158.96	13.55	109.13	30.81
43	92.26	671.9	74.72	434.54	131.34
17433	92.26	260.91	27.83	184.07	54.65
7063	92.24	172.23	64.75	92.62	98.35
9520	92.24	148.15	23.51	90.31	30.29
17517	92.18	493.07	62.8	334.21	99.78
19584	92.16	210.98	33.57	115.36	48.67
4438	92.13	67.98	14.64	38.23	21.03
24205	92.1	160.74	14.55	106.87	34.36
17303	92	53.51	13.3	32.64	13.33
25768	92	210.11	36.07	128.94	42.27
18452	91.97	398.19	128.98	1065.41	457.59
799	91.89	121.66	18.13	258.08	183.73
1700	91.89	147.49	26.83	84.26	44.22
20735	91.89	307.34	83.55	189.6	132.43
5617	91.76	142.38	41.03	58.49	54.93
20935	91.76	295.32	22.28	230.21	42.1
4554	91.73	125.4	23.34	77.21	40.15
15339	91.65	148.59	6.71	124.41	34.48
21708	91.6	107.48	20.06	62.22	28.43
16444	91.49	152.52	7.28	123.3	50.18
14184	91.49	364.58	74.74	196.86	110.06
515	91.49	72.75	9.3	47.46	20.74
17896	91.47	59.18	8.94	112.37	41.42
4339	91.44	201.72	28.66	140.82	39.42
13092	91.44	68.66	27.49	220.65	123.7
2744	91.39	287.61	31.87	207.79	84.44
	1				/



		-10	30-		
TABLE SVV: '		IDE	Affe	nney Docket 449	
Timepoint(s):	24, 43 hrs			Dogument	No. 1935328.1
GTGC GDUILIOL:	LDA_Score	Tox_Meen	Tox_SD	MoonToxi_Mocin	ConTox_SD
23731	98.89	293.68	76.54	131.71	49.58
20587	98.89	437.57	91.43	1017.45	250.54
17480	98.89	201.94	48.87	68.06	33.02
25279	98.89	573.02	130.36	190.9	85.32
2459	98.89	313.18	236.24	26.33	38.53
4491	98.86	564.41	157.03	150.36	57.65
2895	98.86	342.24	50.81	125.44	42.79
18119	98.86	455.08	59.43	177.72	55.14
15012	98.83	229.04	47.87	81.9	58.92
16170	98.83	203.83	59.37	58.96	37.71
17514	98.83	119.01	46.34	531.29	139.51
19407	98.83	1209.07	117	598.87	154.22
13482	98.81	39.09	14.34	170.17	62.14
1460	98.81	1298.65	187.76	282.3	147.04
16813	98.78	102.95	10.12	251.19	65.04
7063	98.78	609.22	144.29	90.91	92.99
10016	98.78	362.99	69.1	91.49	46.31
22607	98.75	249.94	79.92	930.14	237.47
21796	98.75	499.17	133.07	103.3	52.38
6911	98.75	53.72	13.01	234.4	74.16
13317	98.73	132.99	14.51	47.48	31.71
22519	98.73	633.78	111.34	1691.16	425.52
16650	98.73	178.76	37.85	58.5	56.41
10109	98.73	1783.26	105.67	1044.79	219.56
13539	98.7	356.7	51.77	177.05	42.91
1414	98.7	184.02	39.55	41.08	20.94
15258	98.67	985.59	328.35	252.54	133.47
3404	98.67	404.16	91.71	126.3	40
20868	98.67	284.65	99.4	41.25	32.69
12606	98.65	185.44	52.02	742.26	237.79
17680	98.65	1261.07	189.79	410.62	168.29
15888	98.62	436.93	112.38	165.89	140.02
17537	98.62	199.87	28.29	105.68	37.07
5421	98.62	573.42	153.2	200.26	71.05
7262	98.62	1756.3	308.46	565.61	225.13
3090	98.62	289.95	28.26	141.16	39.16
4451	98.59	61.8	27.16	268.23	98.07
2893	98.59	976.57	164.37	420.18	100.83
23013	98.59	557.16	88.62	230.95	68.99
21802	98.59	84.27	11.53	26.95	15.08
16584	98.57	184.55	107.55	22.86	38.52
20771	98.57	201.07	22.61	361.5	72.1
11455	98.57	195.57	56.2	46.02	53.11
23596	98.57	443.56	133.71	1325.62	359.5
4490	98.57	1056.88	347.95	303.22	131.76
2896	98.57	182.71	21.98	67.2	30.68
18165	98.54	58.8	14.89	21.53	10.38
7825	98.54	254.05	33.99	111.16	42.78
16581	98.51	79.68	21.93	25.33	14.43
14121					100.17
	98.49	574.45	62.25	217.5	
238	98.46	297.6	41.62	140.29	46.6

TABLE SVV: '	TIHIOACETAN	103	Affic	mey Docket 449	21-5063-01-00
Timepoint(s):			, , , , , , , , , , , , , , , , , , , ,		1 No. 1935323.1
(G] CGC	1922				
ldeniiier	LDA Score	Tox_Mean	TOX_SD :	NEEDM_XOTROCK	NonTox_SD
19745	98.46	137.4	17.02	50.67	21.56
16148	98.44	433.4	97.61	1038.95	379.87
12118	98.44	1855.09	531.03	263.73	163.1
18068	98.41	124.18	30.54	42.01	13.89
16444	98.38	304.39	74.75	122.7	48.82
20082	98.38	241.26	86.08	39.87	42.8
6912	98.36	50.84	14.35	193.82	64.3
1258	98.36	189.8	37.24	48.72	29.59
3831	98.36	125.11	29.46	34.11	24.01
2005	98.25	80.77	17.62	20.25	12.86
22903	98.2	229.99	38.61	114.18	35.46
1514	98.17	178.75	53.8	53.28	21.7
293	98.17	49.95	18.77	236.23	84.48
1427	98.17	81.09	15.86	28.02	18.51
7064	98.17	1227.38	220.54	331.9	194.28
17255	98.17	57.63	8.67	25.94	11.03
1478	98.14	107.42	31.18	424.29	118.44
9091	98.12	92.08	20.19	23.48	18.72
17502	98.09	279.3	80.84	82.71	49
17157	98.09	93.99	30.18	23.15	16.29
20243	98.09	141.12	18.84	64.38	21.5
24596	98.09	240.62	75.28	76.98	42.84
926	98.06	121.88	35.15	36	21.77
3775	98.06	154.21	46.43	69.04	27
2577	98.04	165.3	12.28	78.03	31.39
20755	98.04	368.9	158.2	54.73	60.37
10503	97.98	214.07	71.53	581.16	127.62
7427	97.98	156.76	45.44	32.3	29.89
13974	97.98	832.49	311.33	226.92	122.72
1479	97.98	73.5	22.42	297.09	94.57
1501	97.96	1643.15	550.04	498.03	240.13
16164	97.96	1010.45	60.66	688.86	284.77
10504	97.96	365.02	93.93	954.97	259.72
17145	97.9	416.32	142.66	1095.63	285.54
20843	97.9	223.81	11.93	116.14	46.18
20872	97.88	1365.47	196.04	762.45	261.25
1382	97.85	105.2	22.24	37.68	14.71
3900	97.85	198.53	77.61	50.2	28.06
25747	97.85	1821.76	709.75	420.97	214.57
4314	97.8	165.23	42.68	455.99	117.03
24811	97.77	300.09	158.01	1508.75	452.88
11454	97.77	310.32	74.93	109.38	56.59
25591	97.77	93.41	26.33	29.71	16.8
16950	97.75	127.28	13.45	50.76	28.32
15700	97.72	111.11	52.17	449.78	122.69
17284	97.72	59.67	19.41	184.78	54.49
17562	97.72	1006.01	174.28	350.43	170.31
21981	97.72	493.33	102.15	1017.07	222.52
457	97.69	367.87	54.5	163.1	64.56
22843	97.69	732	64.09	404.62	116.6
162	97.69	191.46	76.86	53.78	29.44

TABLE 5VV: '		NDE	Año	21-5088-01-WO 1 No. 1985828.1	
GTGC RETGC	LDA_Score	Tox_Moan	Tox_SD:	Mean Confort Mean	MonTox_SD
1809	97.67	677.84	457.09	133.38	741.34
24886	97.64	1945.91	243.11	1194.71	293.98
23309	97.64	123.27	27.22	44.34	20.28
17727	97.64	66.47	21.69	26.14	9.81



TABLESWW: THIOACETAMIDE Thropoin(s): 6 ins (CLCC SEE		Afformery Poetet 44921-5063-01-We Document No. 1985828.1			
	LDA Seoro	Tox_Moon	Tox_SD 🖟	Meen)	NonTox_SD
19143	97.48	835.62	74.9	457.19	141.76
2261	97.46	96.06	15.71	32.65	21.47
18727	97.46	1451.99	42.38	762.41	382.24
24166	97.46	496.34	5.85	374.73	102.01
18301	97.46	466.85	88.21	147.28	93.63
3925	97.46	457.08	9.64	817.58	303.37
2825	97.43	77.42	2.35	43.84	32.85
18302	97.43	721.15	177.54	145.87	135.6
17844	97.4	271.49	9.18	182.97	93.69
6698	97.38	74.93	3.59	48.72	14.81
21856	97.35	21.23	6.23	92.03	48.03
6297	97.35	388.09	52.22	215.96	59.88
6927	97.33	707.5	66.6	399.23	121.27
10369	97.3	307.41	25.82	175.12	59.36
21708	97.27	118.43	4.79	62.22	28.41
5952	97.25	303.32	45.57	106.72	106.58
4674	97.25	127.41	50.69	550.43	207.09
1440	97.25	87.43	3.87	49.47	21.5
25467	97.25	573.12	11.17	366.83	173.81
347	97.17	43.49	1.63	25.09	15.28
3526	97.17	103.07	7.02	170.13	45.01
23268	97.17	148.43	4.87	231.59	65.24
25066	97.14	281.73	16.19	158.83	65.39
23305	97.14	188.34	17.21	91.84	45.85
15267	97.14	80.97	7.26	38.37	16.47
16025	97.11	111.36	15.79	49.55	25.83
13009	97.06	236.49	40.71	118.74	45.99
23273	97.06	236.23	21.37	143.44	45.43
18303	97.06	3010.9	700.83	843.77	661.03
21467	97.06	2398.88	33.26	1604.12	770.42
16769	97.03	225.38	8.31	125.56	62.1
13282	97.03	303.53	3.16	224.72	78.2
24722	97.01	507.33	27.79	823.73	217.06
3114	96.98	96.51	5.93	57.04	28.69
13678	96.98	82	5.95	34.39	23.32
2486	96.98	322.56	8.42	519.36	165.18
9029	96.9	261.18	4.55	379.94	189.57
15644	96.88	2072.1	206.07	1368.64	388.7
10053	96.88	119.32	25.76	37.53	29.92
1877	96.85	390.68	29.09	696.8	186.01
23272	96.85	568.08	34.76	356.77	89.85
9775	96.82	415.24	84.96	129.82	108.28
4063	96.82	317.93	43.41	80.5	101.28
7961	96.77	48.48	3.88	22.74	14.19
20649	96.77	2616.76	245.94	1501.89	429.3
18343	96.77	274.86	3.44	226.41	52.47
5138	96.77	82.11	3.48	135.56	52.22
2569	96.77	443.32	42.77	908.74	290.05
25087	96.74	234.24	17.89	98.66	75.52
15679	96.74	332.61	37.51	162.36	66.6
1264	96.72	4840.33	136.28	4274.31	3339.21

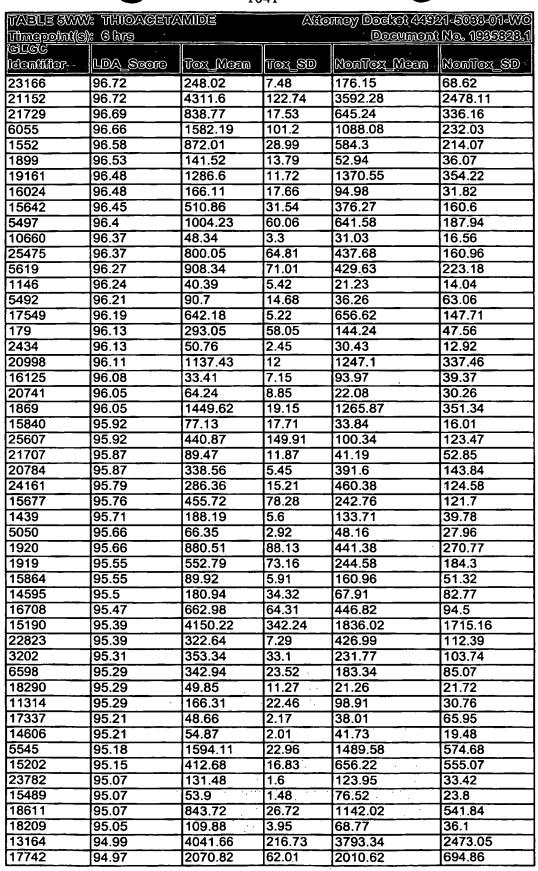
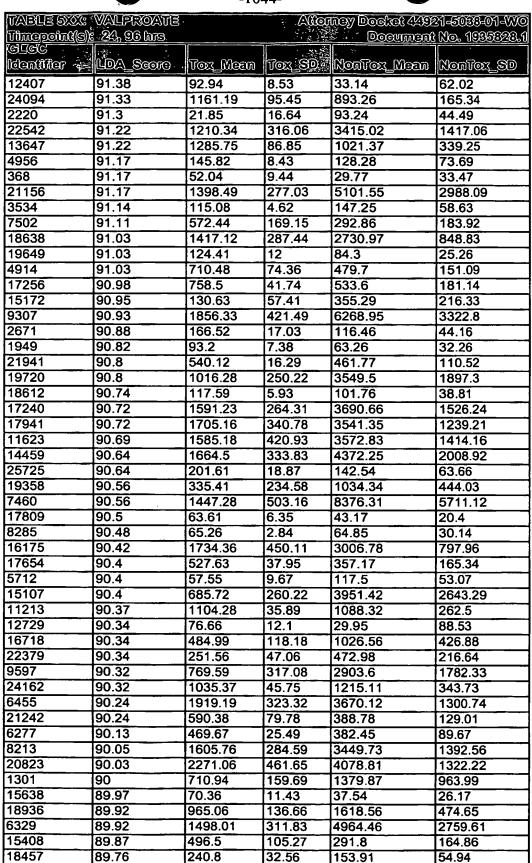


TABLE SWW: THIOXCETAMDE Timepoing(s): 6 bis			A	omey Docket 449 Documen	21-5093-01-WC t No. 1995923.1
ldonillor 🐉		Tox_Moen	Tox_SD	NonTox_Mean	NonTox_SD
15191	94.94	3269.16	461.53	1217.54	1330.78
5232	94.92	139.31	8.96	254.75	89.75
25529	94.89	49.13	8.01	21.73	13.23
12052	94.84	334.46	24.61	211.24	89.04
15613	94.81	503.45	47.38	1181.78	811.56
17379	94.81	276.94	40.14	118.12	70.96
958	94.81	453.27	39.94	299.45	137.37
17613	94.78	387.9	14.41	306.86	126.56
8592	94.78	264.37	9.68	376.87	132.8
8269	94.73	1731.24	296.01	694.46	446.84
25430	94.73	853.41	25.21	619.73	179.59
22862	94.73	166.89	67.9	454.93	165.51
25705	94.7	582.13	11.24	743.76	198.88
11260	94.7	166.95	11.81	96.22	39.99
9424	94.68	1294.97	49.61	1013.46	383.65

			+3-		
TABLIZ SXXX: Timegoint(S)X	24, 93 hrs	- 1 p	Alioi	nay Docket 4492 Document	21-5099-91-WO No. 1995:22.1
CECC CECTIFIE	LDV Score	Tox_Moen:	Tex_SD	NonTox_Meen	NonTox_SD
23698	98.01	864.57	65.18	356.84	407.18
18958	96.87	569.08	66.29	324.63	126.12
17758	96.05	669.19	104.13	362.17	375.48
20715	94.69	946.4	153.83	382.07	430.47
20711	94.67	402.29	88.77	134.67	205.03
12698	94.62	163.34	13.48	76.21	235.64
18742	94.48	550.44	80.52	344.76	188.73
5887	94.46	164.28	47.66	68.45	138.61
14450	94.38	188.2	15.06	102.8	51.9
16721	94.27	408.48	63.51	259.65	73.63
5465	94.22	1185.16	117.95	776.33	205.36
21094	94.14	511.07	89.17	232.22	144.38
22604	93.98	1957.85	349.17	1027.72	469.57
14937	93.74	195.36	28.59	119.35	36.98
18637	93.66	1062.08	136.08	2019.61	623.11
16768	93.61	708.87	45.34	494.16	162.55
12829	93.37	535.03	45.99	379.35	90.31
17289	93.34	223.5	29.48	124.16	77.25
26109	93.32	478.76	128.18	146.1	264.1
19613	93.24	2484.11	155.65	1860.71	485.38
24372	93.21	220.5	21.54	140.4	43.76
14887	93.16	101.8	8.43	294.94	248.64
18687	93.08	1073.99	196.89	660.51	590.16
14191	93.08	116.01	14.38	68.03	26.34
18686	93.05	1263.89	201.14	706.02	613.73
19433	92.79	231.66	53.54	107.01	119.22
6345	92.76	351.14	46.93	230.34	62.46
25412	92.73	29.28	7.08	68.98	31.68
9192	92.6	808.14	104.63	1627.81	666.43
2140	92.57	163.54	17.96	92.56	59.3
18780	92.44	87.19	4.42	62.98	25.42
5316	92.36	140.52	56.6	342.33	116.25
3362	92.15	39.32	11.72	91.85	36.85
12964	92.12	388.64	33.77	236.19	94.18
18636	92.07	1077.28	301.99	2662.77	1037.67
17992	92.07	144.02	35.41	77.48	53.64
20846	91.99	1508.64	204.46	2740.07	862.43
15637	91.99	112.28	17.02	74.85	25.76
21842	91.96	724.51	39.31	562.74	295.62
6107	91.94	141.47	25.19	92.73	56.32
10157	91.86	914.83	66.38	644.19	210.59
	91.86	866.2	77.34	604.77	198.12
	91.83	1219.63		2469.03	845.35
	91.75	120.06	7.34	91.08	45.87
	91.75	551.97	21.82	459.49	122.37
	91.59	278.55	37.16	181.8	121.4
	91.59	148.41	21.26	86.16	93.88
	91.51	815.06	116.69	529.94	172.12
	91.49		844.23	4872.17	2250.97
	91.46	20.12		34.7	21.52
16420	91.43	702.05	35.62	557.06	113.3

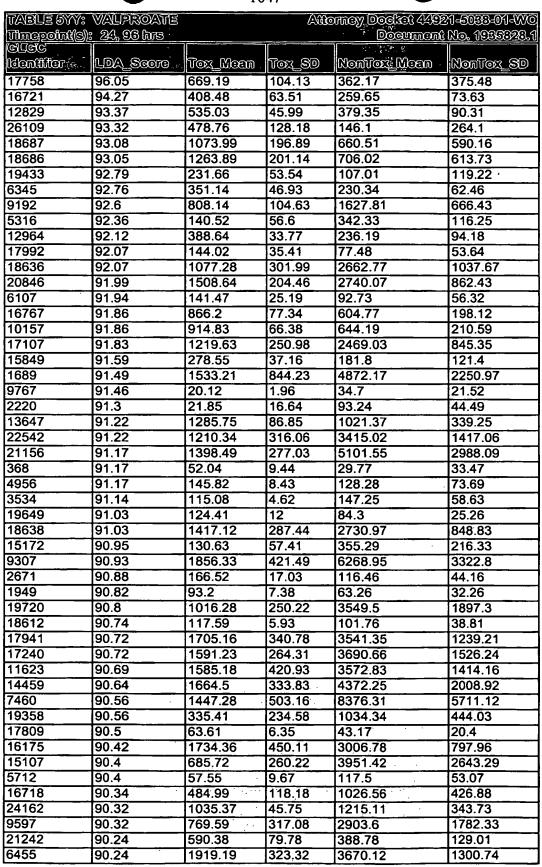






Timepoint(S)	VALPROATE 24, 93 hrs			ney Docket 442 Document	
GEGG	LDALSéciro	Tox_Mean	*		NonTox_SD
18628	89.6	907.41	117.56	1450.82	395.72
7637	89.51	73.34	27.64	29.36	14.81
18630	89.5	43.93	7.32	28.84	19.07
20724	89.42	129.06	13.73	84.89	33.2
1391	89.36	137.56	11.95	97.71	30.33
9124	89.34	485.07	50.76	377	101.38
6653	89.28	830.4	93.61	600.19	144.19
14504	89.23	193.86	27.28	143.51	178.6
15340	89.06	69.9	15.13	41.14	10.49
13480	88.97	943.91	57.53	727.01	183.71
31	88.97	491.78	51.48	336.52	102.2
6912	88.91	287.28	41.05	192.94	64.6
1877	88.91	915.58	61.13	695.34	186.18
18957	88.67	669.41	87.85	370.05	148.77
1728	88.65	319.76	41.83	250.03	114.42
15462	88.65	688.54	39.2	544.83	120.31
17290	88.61	342.44	109.85	176.04	95.2
2830	88.53	480.81	74.77	302.61	68.84
15980	88.51	87.93	7.82	63.44	23.3
1542	88.51	333.53	54.06	227.68	86.93
25644	88.49	526.27	60.01	339.06	180.51
853	88.41			454.81	
17787	88.36	826.1	151.31		238.58
17284		635.52	51.97	1566.79	1003.66
107	88.2 88.19	252.62 326.08	24.41	184.06	54.85
17237	88.19	384.32	81.64 80.65	129.2 229.17	72 60.98
9929	88.06	844.74	76.52	671.49	
21424	88.04	660.38	72.95	492.38	182.55 123.46
14953	87.98	488.75	46.12	387.24	80.16
3549	87.93	275.64	34.39	201.23	82.02
15621	87.76	566.49	83.33	369.32	89.2
14881	87.75	1044.64	138.55	1704.91	636.28
40	87.69	510.83	67.57	362.72	186.44
16780	87.47	505.81	68.58	309.18	111.74
17571	87.37	292.38	39.42	228.41	
25468	87.35	801.88	493.93		57.78 1100.94
2480	87.32	312.02	28.4	2330.1 234.99	74.25
20714	87.29	834.07	204.49	567.74	703.63
4449	87.24	331.63	39.44	238.4	93.3
20776	87.24 87.24	44.07	5.91	29.47	12.54
20481	87.23	175.64			
20057	87.18	268.06	48.93 63.12	96.78 139.68	34.85 54.54
14882					
64	87.08 87.07	849.4 241.43	143.25	1301.88	416.62
23203	87.05	185.72	61.1 51.14	134.1 102.53	43.68 42.82
9125	87.05	672.86	23.21		138.72
2831	86.94	406.28	112.72	636.51 249.86	81.54
25469		623.21			
317	86.84 86.71		308.3 3.51	1632.67	752.14
4573		30.87 991.46		1270 19	20.66
1695	86.63		117.12	1270.18	234.31
1090	86.5	20.99	9.06	58.33	36.53

TABLE 5XX: VALPROATE Afformay Docket 44921-5133-91-4XO Timepoint(s): 24, 96 hrs Document No. 1935323.1							
CCCC Identifier	LDA Score	Tox Meen	Tem Ca	Monlox Moan			
	<u> </u>	Ļ — — — — — — — — — — — — — — — — — — —	TOXLSD				
24707	86.39	858.13	96.24	1262.15	456.36		
12118	86.39	128.64	30.31	270.14	191.82		
16227	86.37	92.61	7.47	124.84	65.08		
20133	86.34	58.33	2.78	53.93	35.7		
1058	86.31	293.74	39.68	231.15	142.22		
16895	86.29	981.29	178.8	1714.67	560.79		
17161	86.21	921.52	109.1	787.54	372.15		
670	86.21	912.89	115.96	1208.83	267.82		
11353	86.2	139.69	41.19	92.3	33.81		
9841	86.18	1573.12	179.4	2171.05	563.5		
4360	86.05	126.15	41.6	264.82	128.89		
21078	86.02	893.7	55.83	737.66	215.48		
12496	85.92	108.37	13.93	76.33	29.99		
17187	85.91	59.95	13.03	31.54	17.07		
4392	85.86	1356.7	232.83	2202.58	661.19		
1359	85.85	194.12	42.29	122.69	33.72		
746	85.84	31.64	12.59	125.53	81.76		

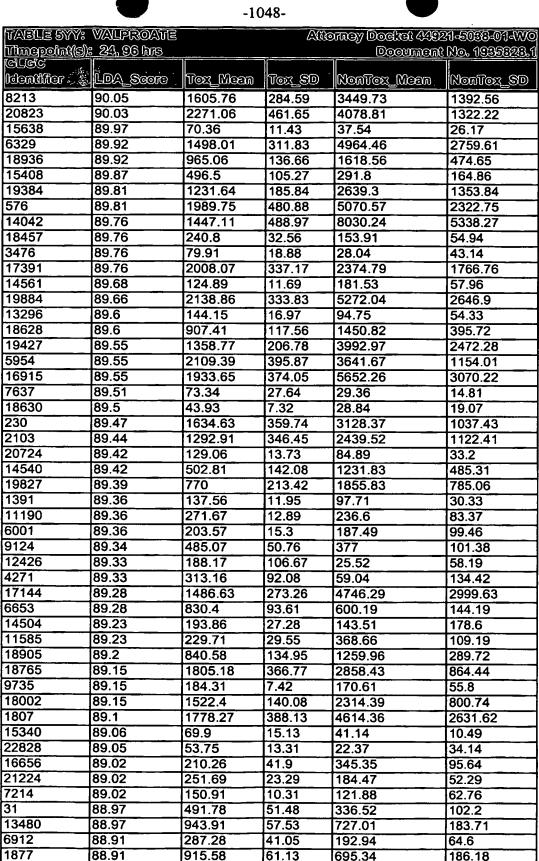


88.91

55.51

5.67

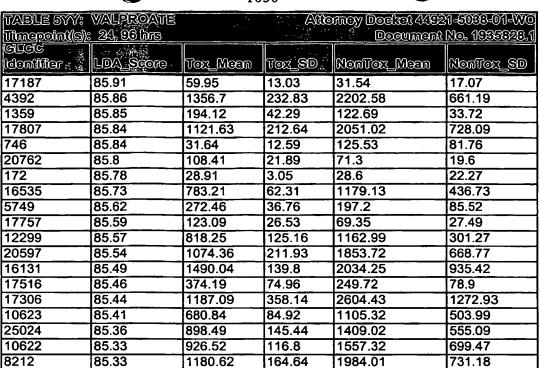
32.79

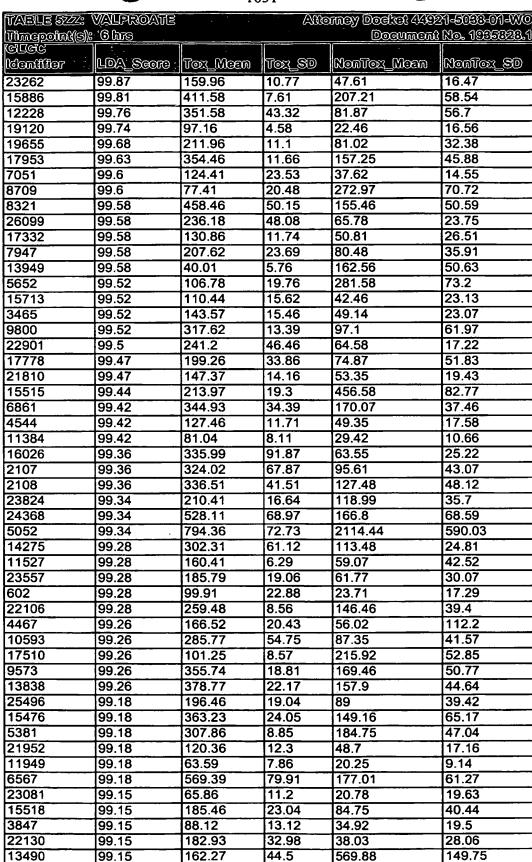




		-10	49-		
Timepoint(S)			Affe	may Docket 4492 Document	1-5033-01-WO No. 1935323.1
CLCC Conditor	LDA_Scoro	Tox_Meen	Tox_SD	NooTox_Noon	NonTox_SD
18957	88.67	669.41	87.85	370.05	148.77
1728	88.65	319.76	41.83	250.03	114.42
15462	88.65	688.54	39.2	544.83	120.31
17290	88.61	342.44	109.85	176.04	95.2
2830	88.53	480.81	74.77	302.61	68.84
15980	88.51	87.93	7.82	63.44	23.3
1542	88.51	333.53	54.06	227.68	86.93
25644	88.49	526.27	60.01	339.06	180.51
853	88.41	826.1	151.31	454.81	238.58
17787	88.36	635.52	51.97	1566.79	1003.66
17284	88.2	252.62	24.41	184.06	54.85
107	88.19	326.08	81.64	129.2	72
17237	88.19	384.32	80.65	229.17	60.98
9929	88.06	844.74	76.52	671.49	182.55
21424	88.04	660.38	72.95	492.38	123.46
14953	87.98	488.75	46.12	387.24	80.16
3549	87.93	275.64	34.39	201.23	82.02
15621	87.76	566.49	83.33	369.32	89.2
14881	87.75	1044.64	138.55	1704.91	636.28
40	87.69	510.83	67.57	362.72	186.44
16780	87.47	505.81	68.58	309.18	111.74
17571	87.37	292.38	39.42	228.41	57.78
25468	87.35	801.88	493.93	2330.1	1100.94
2480	87.32	312.02	28.4	234.99	74.25
20714	87.29	834.07	204.49	567.74	703.63
4449	87.24	331.63	39.44	238.4	93.3
20776	87.24	44.07	5.91	29.47	12.54
20481	87.23	175.64	48.93	96.78	34.85
20057	87.18	268.06	63.12	139.68	54.54
14882	87.08	849.4	143.25	1301.88	416.62
64	87.07	241.43	61.1	134.1	43.68
23203	87.05	185.72	51.14	102.53	42.82
9125	87	672.86	23.21	636.51	138.72
2831	86.94	406.28	112.72	249.86	81.54
25469	86.84	623.21	308.3	1632.67	752.14
317	86.71	30.87	3.51	44	20.66
4573	86.63	991.46	117.12	1270.18	234.31
1695	86.5	20.99	9.06	58.33	36.53
24707	86.39	858.13	96.24	1262.15	456.36
12118	86.39	128.64	30.31	270.14	191.82
16227	86.37	92.61	7.47	124.84	65.08
20133	86.34	58.33	2.78	53.93	35.7
1058	86.31	293.74	39.68	231.15	142.22
16895	86.29	981.29	178.8	1714.67	560.79
17161	86.21	921.52	109.1	787.54	372.15
670	86.21	912.89	115.96	1208.83	267.82
11353	86.2	139.69	41.19	92.3	33.81
9841	86.18	1573.12	179.4	2171.05	563.5
4360	86.05	126.15	41.6	264.82	128.89
21078	86.02	893.7	55.83	737.66	215.48
12496	85.92	108.37	13.93	76.33	29.99







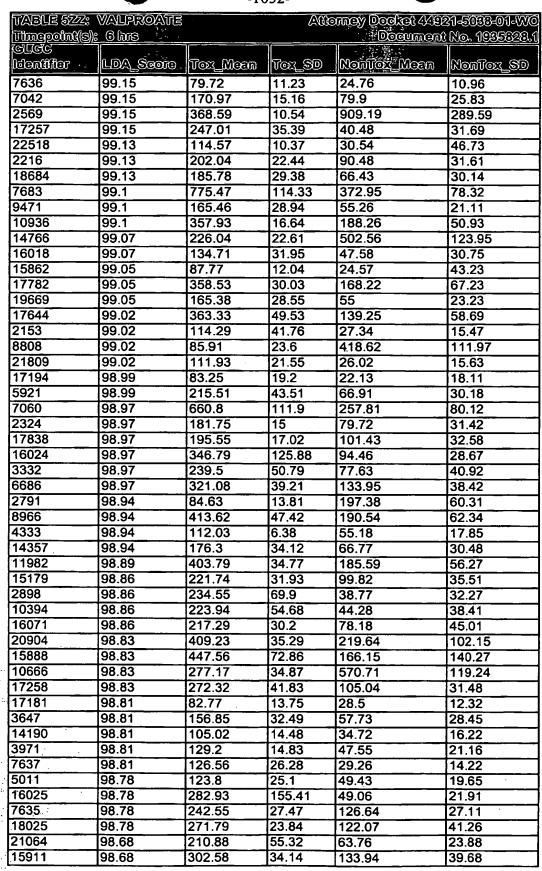
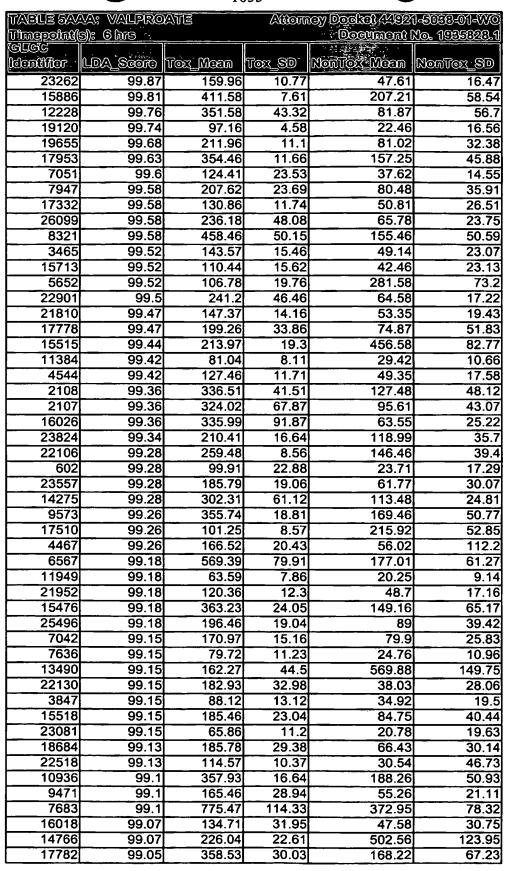




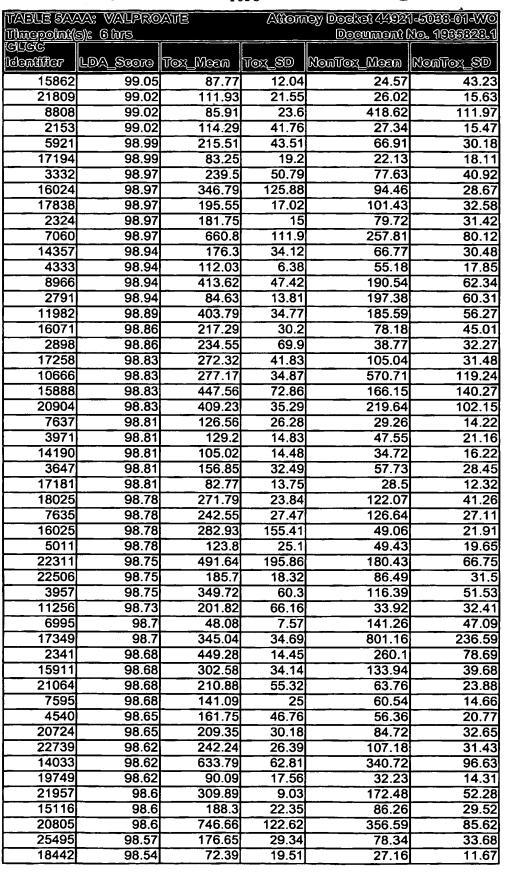
TABLE STACE	WAILPROATE		om∆' :	may Docket 4492	X1-5028-01-XXO
Mingpoin((S):					No. 1935023.1
SDUS Tentifoness	LDA_Scor	Tox_Meen ;	TON SOF	MeeM_xoluon	KonTox_SD :
7595	98.68	141.09	25	60.54	14.66
20724	98.65	209.35	30.18	84.72	32.65
4540	98.65	161.75	46.76	56.36	20.77
22739	98.62	242.24	26.39	107.18	31.43
19749	98.62	90.09	17.56	32.23	14.31
21957	98.6	309.89	9.03	172.48	52.28
15116	98.6	188.3	22.35	86.26	29.52
25495	98.57	176.65	29.34	78.34	33.68
18442	98.54	72.39	19.51	27.16	11.67
17687	98.44	104.25	12.74	39.5	15.52
4414	98.38	139.81	12.39	66.99	22.52
16725	98.38	66.78	10.34	162.23	46.07
20090	98.36	358.17	112.71	108.92	40.16
23220	98.3	197.68	24.82	84.5	29.72
21801	98.3	191.41	25.44	96.64	22.78
21407	98.28	188.48	55.27	50.85	27.48
8597	98.28	175.63	10.05	102.84	33.09
23250	98.28	209.87	12.1	124.75	29.06
1401	98.28	87.71	8.93	43.36	12.81
1843	98.25	98.62	41.23	29.41	16.15
3035	98.25	88.17	44.87	26.67	11.75
3787	98.22	54.75	1.97	28.81	11.11
15857	98.22	179.17	37.78	77.35	19.5
21905	98.17	91.1	11.38	45.92	12.83
15489	98.17	134.19	6.54	76.32	23.64
1481	98.15	129.77	8.15	58.27	29.62
16524	98.15	75.52	19.53	28.02	10.68
21580	98.12	101.77	21.17	40.13	16.38
18400	98.12	146.5	32.63	49.68	24.09
15359	98.09	121.87	15.4	54.81	22.3
15829	98.09	159	59.56	24.75	53.2
11843	98.09	60.93	9.99	30.73	9.99
3865	98.09	111.86	18.72	46.23	19.25
22039	98.09	76.96	4.02	40.3	19.16
19226	98.07	357.6	47.65	186.16	54.68
14295	98.04	93.13	17.27	30.13	23.6
1844	98.01	368.98	81.85	114.47	62.97
4832	97.99	85.2	20.78	35.16	15.85
3253	97.96	286.87	14.72	171.53	52.61
22396	97.96	229.43	65.13	98.81	27.9
22150	97.96	167.27	20.26	82.56	27.96
12028	97.96	66.8	18.03	22.08	10.28
15662	97.93	82.56	9.91	36.56	49.45
19053	97.93	72.78	13.91	28.14	54.44
17688	97.93	145.07	20.59	55.81	29.42
11314	97.93	237.45	55.64	98.69	30
21951	97.93	227	30.63	104.69	33.99
3788	97.93	72.12	6.02	35.71	12.63
1580	97.91	88.88	14.84	24.77	25.2
2192	97.91	140.85	60.48	38.85	20.13
8664	97.85	77.55	10.77	46.67	200.12



TABLE 5727: Timepoin((s)):		· · · · · · · · · · · · · · · · · · ·	Altorney Docket 44921-5033-01-WO Document No. 1985328.1		
CLCC ldentifer	LDA_Score	Tox_Meen	Tox_SD .	Moem zenden	NonTox_SD
21491	97.8	170.35	23.28	79.46	23.14
10544	97.8	420.34	40.99	179.2	70.52
17590	97.8	279.39	39.93	105.9	45.96
20899	97.8	181.9	39.69	69.04	23.76
24235	97.77	672.88	64.31	328.94	168.73
20702	97.77	134.07	14.12	49.97	39.93
4495	97.72	140.91	10.51	68.26	26.43

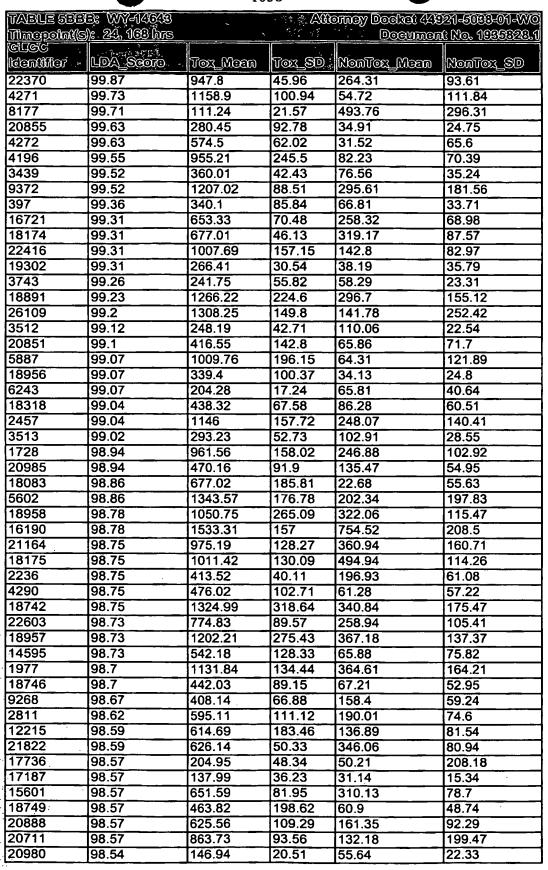






	va: Walpro	ATE	Altom	rey Docket 44921	1-5033-01-000
Timepoint(<u>s): 6 ins</u>	,		Document (No. 1985323.1
refree Identifier	LDA_Score	Tox_Mean	Tox_SD	MOONTOX_MOON	NonTox_SD
17687	98.44	104.25	12.74	39.5	15.52
4414	98.38	139.81	12.39	66.99	22.52
16725	98.38	66.78	10.34	162.23	46.07
23220	98.3	197.68	24.82	84.5	29.72
21801	98.3	191.41	25.44	96.64	22.78
21407	98.28	188.48	55.27	50.85	27.48
8597	98.28	175.63	10.05	102.84	33.09
23250	98.28	209.87	12.1	124.75	29.06
1401	98.28	87.71	8.93	43.36	12.81
1843	98.25	98.62	41.23	29.41	16.15
3035	98.25	88.17	44.87	26.67	11.75
3787	98.22	54.75	1.97	28.81	11.11
15857	98.22	179.17	37.78	77.35	19.5
21905	98.17	91.1	11.38	45.92	12.83
15489	98.17	134.19	6.54	76.32	23.64
1481	98.15	129.77	8.15	58.27	29.62
16524	98.15	75.52	19.53	28.02	10.68
21580	98.12	101.77	21.17	40.13	16.38
18400	98.12	146.5	32.63	49.68	24.09
15359	98.09	121.87	15.4	54.81	22.3
15829	98.09	159	59.56	24.75	53.2
11843	98.09	60.93	9.99	30.73	9.99
3865	98.09	111.86	18.72	46.23	19.25
22039	98.09	76.96	4.02	40.3	19.16
19226	98.07	357.6	47.65 17.27	186.16	54.68
14295 1844	98.04 98.01	93.13 368.98	81.85	30.13 114.47	23.6 62.97
4832	97.99	85.2	20.78	35.16	
3253	97.99	286.87	14.72	171.53	15.85 52.61
22396	97.96	229.43	65.13	98.81	27.9
22150	97.96	167.27	20.26	82.56	27.96
12028	97.96	66.8	18.03	22.08	10.28
15662	97.93	82.56	9.91	36.56	49.45
19053	97.93	72.78	13.91	28.14	54.44
17688			20.59	55.81	29.42
11314	97.93		55.64	98.69	30
21951	97.93		30.63	104.69	33.99
3788	97.93		6.02	35.71	12.63
1580	97.91	88.88	14.84	24.77	25.2
2192	97.91	140.85	60.48	38.85	20.13
8664	97.85		10.77	46.67	200.12
21491	97.8		23.28	79.46	23.14
10544	97.8		40.99	179.2	70.52
17590	97.8		39.93	105.9	45.96
20899	97.8		39.69	69.04	23.76
24235	97.77	672.88	64.31	328.94	168.73
20702	97.77	134.07	14.12	49.97	39.93
4495	97.72	140.91	10.51	68.26	26.43
24284	97.69		25.85	30.52	15.92
21802	97.62	87.66	40.89	27.01	15.05





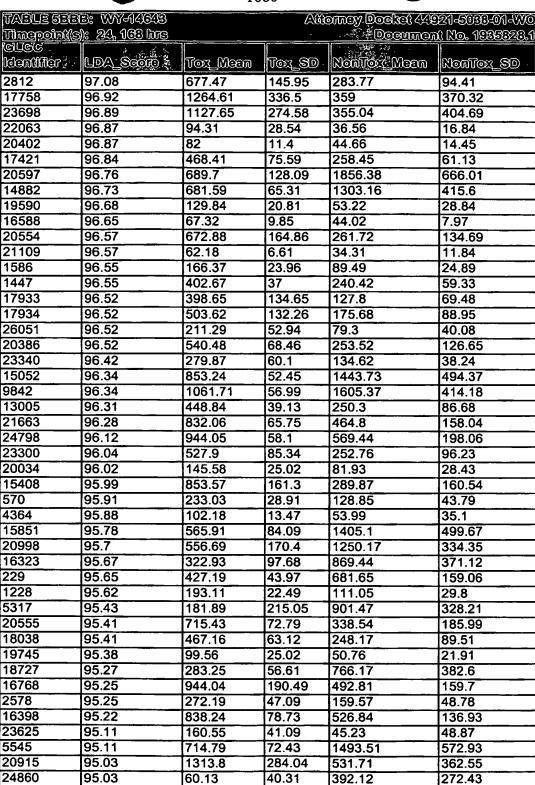
	3. 1000 4 4000				
	3: WY-14643		Alic	omey Docket 44e	
): 24, 163 hrs	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	·	Dogumen	<u>l No. 1995328.1</u>
lcondilor GLCC	LDV. Score	Tox_Mean	TOXESD	MEEM_KOTMOK	NonTox_SD
18315	98.51	243.52	47.29	45.75	35.72
18890	98.49	1969.92	295.27	744.33	347.05
18316	98.49	405.88	66.36	72.7	56.05
18747	98.46	897.75	179.11	152.25	112.71
14621	98.43	325.62	38.07	141.88	44.5
19591	98.43	555.75	45.73	252.68	92.76
4940	98.38	618.48	125.38	1612.91	443.53
15175	98.38	521.95	60.64	230.61	64.52
22737	98.38	677.82	194.98	164.81	92.55
18125	98.38	1071.07	78.78	574.13	156.75
22139	98.35	1036.01	79.75	625.02	133.81
14264	98.35	329.47	59.89	89.69	69.09
13507	98.35	218	8.11	364.51	90.06
9373	98.35	402.28	45.23	128.48	69.57
9757	98.33	552.69	80.49	281.51	67.37
16546	98.27	568.23	89.41	190.1	83.52
21354	98.17	2275.68	351.86	416.77	385.66
3860	98.17	1003.64	154	391.78	156.35
1421	98.11	261.75	50.24	138.27	22.59
20859	98.06	107.85	18.05	41.73	20.06
2768	98.06	1259.86	62.68	2066.78	442.44
17353	98.06	375.3	160.54	38.1	49.13
22847	98.01	1801.36	146.24	1147.13	233.04
18319	98.01	245.39	79.76	36.06	32.94
22602	97.98	484.33	93.76	120.28	84.04
22224	97.98	475.42	82.24	145.78	87
3842	97.96	243.92	76.28	67.28	27.92
23336	97.96	143.78	59.25	23.95	22.91
21341	97.85	1857.47	238.55	851.87	295.96
22079	97.8	1865.96	269.83	4856.82	1476.77
19044	97.77	810.85	29.22	524.48	182.33
21010	97.74	1749.82	238.11	671.62	288.26
3260	97.69	495.15	161.17	174.24	83.07
16945	97.66	1109.78	95.07	718.77	139.18
9240	97.64	580.79	53.02	337.17	81.11
7517	97.61	177.3	16.8	90.17	32.22
16836	97.58	132.53	27.9	63.15	16.36
9106	97.58	573.57	48.69	324.11	84.68
17999	97.58	894.56	49.7	1579.27	335.08
16769	97.53	401.78	106.2	124.45	58.94
20388	97.5	332.86	41.62	771.09	281.25
16434	97.5	529.32	68.06	285.72	69.62
20038	97.5	291.17	52.31	67.58	53.18
15015	97.5	367.93	62.14	191.75	51.02
10533	97.48	1061.54	144	511.32	195.08
23427	97.48	746.46	133.49	312.88	111.58
3460	97.4	78.31	12.72	222.99	99.67
17027	97.4	368.6	65.63	1152.81	406.42
20986	97.37	869.32	111.47	335.98	168.01
15833	97.29	481.16	50.39	277.27	67.17
22823	97.19	727.09	57.76	425.33	110.64

95.03

326.26

33.47

187.97



16434

20388

23427

17027

97.53

97.5

97.5

97.4

97.48

401.78

529.32

332.86

746.46

368.6

106.2

68.06

41.62

65.63

133.49

124.45

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771.09

312.88

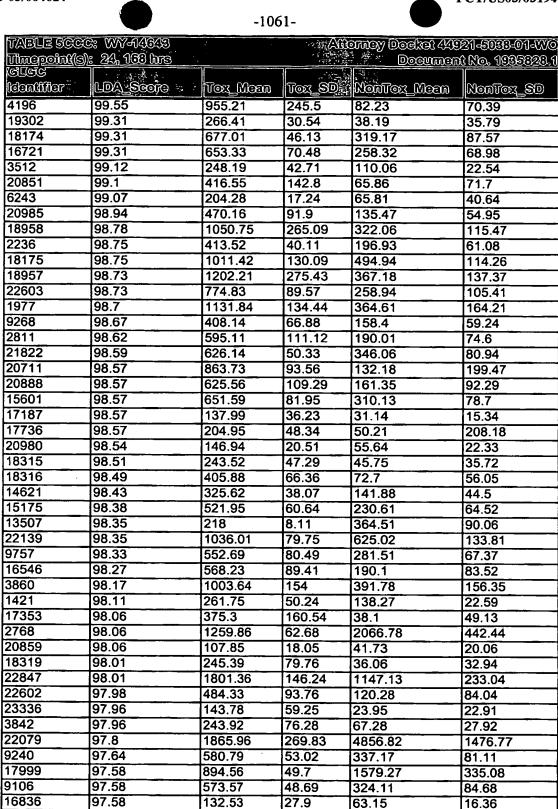
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58.94

69.62

281.25

111.58





24798

23300

96.28

96.12

96.04

832.06

944.05

527.9

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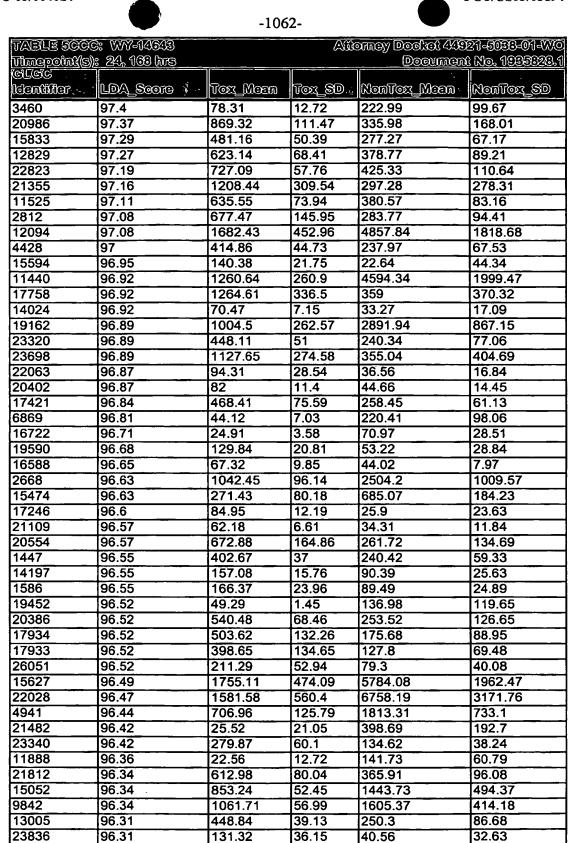
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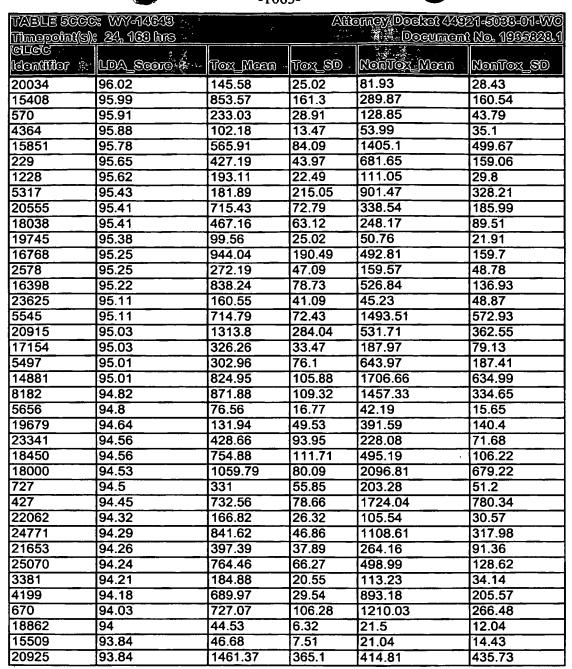
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252.76

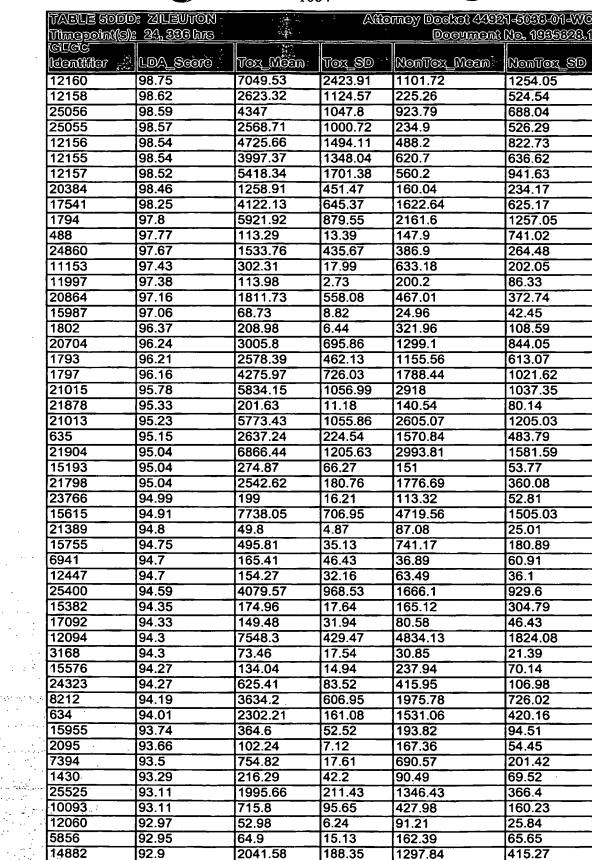
158.04

198.06









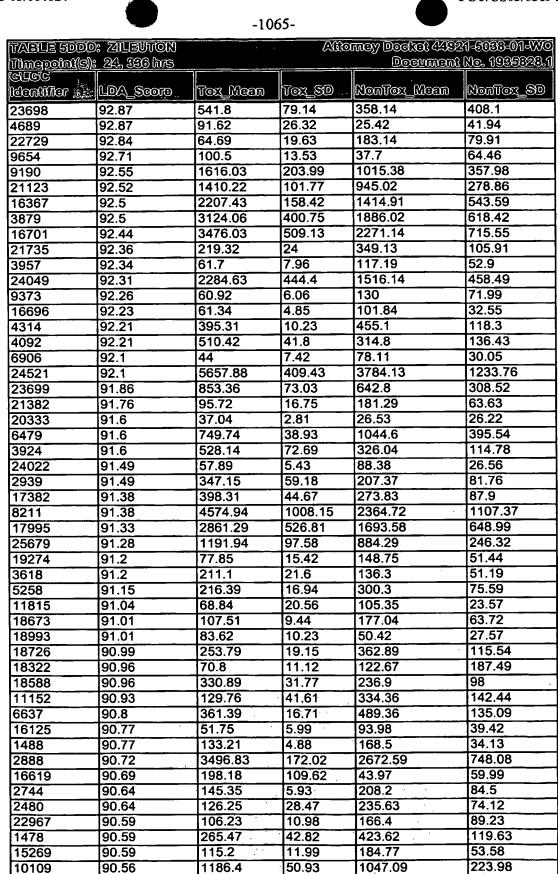


90.51

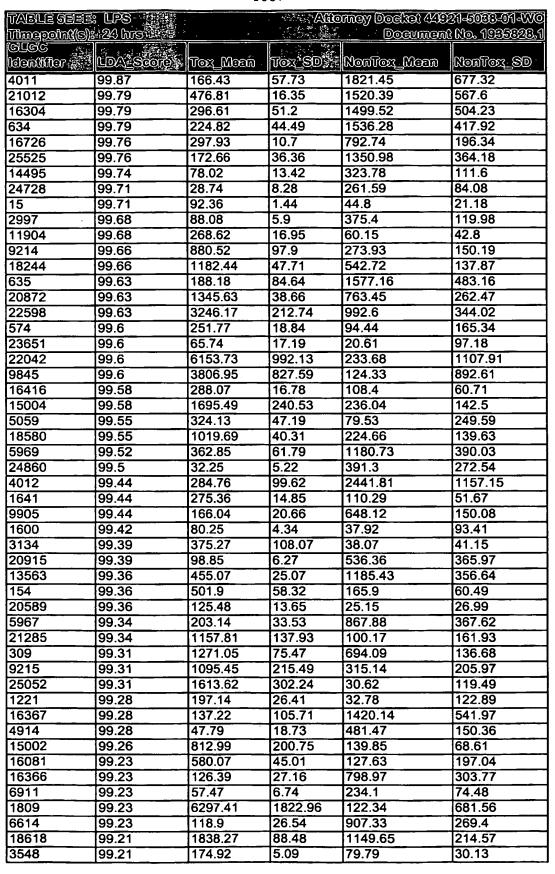
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TABLE SEE Vinegoin((s):				may Docket 442/ Document	
GCGG GCGGG		Tox_Meen	Tox_SD &	Nontrozz Mean	NonTox_SD ·
14964	99.18	161.42	102.69	1006.2	317.11
22512	99.18	354.47	227.36	30.39	59.45
1602	99.18	170.64	16.69	467.13	108.67
10109	99.18	1938.46	117.34	1045.64	220.17
8584	99.15	144.43	32.68	1400.37	635.95
10071	99.13	90.84	33.37	30.7	24.06
22522	99.13	112.21	12.19	248.85	63.35
15741	99.13	317.97	109.01	1252.69	388.68
17541	99.13	316.82	124.41	1633.35	638.47
21522	99.13	765.82	52.59	164.35	209.31
11416	99.13	283.22	20.98	115.75	35.97
25802	99.13	516.44	15.56	257.7	80.46
15872	99.13	73.07	25.46	499.66	169.35
4636	99.13	457.49	50.41	74.1	125.75
21660	99.13	5230.59	324.32	1744.04	720.76
20529	99.13	1181.01	95.34	129.82	185.65
6615	99.1	89.58	20.45	438.68	128.87
20448	99.07	159	29.63	42.64	73.93
6263	99.07	77.77	18.31	292.55	100.65
1561	99.07	1985.06	196.05	870.62	217.06
14767	99.07	69.48	6.08	310.71	115.85
11849	99.07	1291.53	27.15	746.01	163.9
14384	99.07	542.05	32.59	247.13	63.39
2855	99.07	794.02	58.03	420.6	87.21
20249	99.05	78.03	10.56	24.83	20.92
15185	99.05	263.18	54.68	60.65	100.78
24469	99.05	1244.67	166.79	620.92	197.95
17333	99.05	148.37	21.45	51.16	34.11
12779	99.05	451.8	238.57	67.96	54.36
8273	99.05	219.01	79.36	43.6	33.76
20810	99.05	2037.68	83.17	1154.93	263.95
18385	99.05	178.44	102.58	21.57	29.85
22515	99.05	4183.61	1044.52	121.12	348.28
20864	99.02	55.18	25.79	472.15	380.76
5920	99.02	67.33	29.28	461.44	217.92
17324	99.02	81.82	19.34	378.9	117.26
24589	99.02	395.8	197.61	55.53	53.19
19411	99.02	111.17	7.01	33.82	21.69
25313	99.02	312.92	23.51	99.39	60.94
6823	99.02	814.26	140	251.11	106.22
8215	99.02	873.46	52.7	386.99	135.82
23005	98.99	270.87	18	124.39	86.19
20055	98.99	304.31	43.15	67.96	73.87
10984	98.99	79.7	65.47	1058.22	304.87
20944	98.99	1456.36	145.65	619.91	160.17
6532	98.99	317.77	23.11	140.71	43.19
5175	98.97	344.51	77.31	40.15	62.99
4969	98.97	2466.07	420.51	259.82	239.47
1678	98.94	22.06	13.4	124.71	41.32
2744	98.94	510.03	36.96	207.36	83.36
15503	98.91	181.26	37.44	64.23	59.72
L			<u> </u>	·	• — — — — — — — — — — — — — — — — — — —

TABLE SEE				may Docket 449	
Mmcgoin((S))	24 hrs			Doguman	
CLCC Identifier :	LDA_Scoro	Tox_Moen	Tox_SD	Now ox Mean	NonTox_SD
18001	98.91	196.94	39.51	718.21	179.34
682	98.91	664.18	326.43	109.18	95.85
17284	98.89	66.24	7.09	184.56	54.71
20462	98.89	1386.9	54.08	832.62	161.68
22513	98.89	6801.87	2063.44	24.21	724.48
24228	98.89	1963.56	170.96	977.17	260.22
23825	98.89	98.15	18.36	38.05	25.86
7427	98.86	242.61	40.71	32.31	29.32
18611	98.86	2091.17	198.59	1139.38	540.19
16080	98.83	333.96	51.66	71.05	142.79
20354	98.83	352.09	24.78	51.73	57.92
155	98.83	242.82	80.27	41.45	24.98
5667	98.83	1364.04	112.29	816.08	305.28
18750	98.81	372.57	8.69	246.42	71.72
22321	98.73	445.71	89.53	76.62	108.24
4178	98.73	79.54	11.94	39.39	54.77
10949	98.73	390.51	153.27	1874.53	687.28
18250	98.73	1694.19	100.64	952.01	198.91
12606	98.7	161.97	57.03	741.43	238.52
1893	98.7	164.59	74.91	31.84	31.29
5496	98.68	113.96	19.27	493.5	154.89
20701	98.68	2698.56	266.1	879.33	385.5
1572	98.65	172.32	13.47	73.12	32.33
19469	98.62	124.43	69.52	477.5	113.18
25675	98.62	1145.98	19.45	741.67	207.51
25687	98.62	2034.6	159.67	1275.29	658.59
21643	98.6	1666.53	167.12	891.15	220.23
24771	98.57	119.53	97.47	1109.43	314.81
20523	98.57	316.37	52.14	48.66	67.77
15626	98.57	2208.57	185.27	1329.28	250.81
18989	98.54	247.79	152.33	1480.44	689.51
20716	98.54	776.01	61.15	1643.73	473.59
15652	98.54	2214.91	91.58	1501.41	366.17
20698	98.54	3387.66	619.21	894.32	433.33
2667	98.52	317.82	43.77	809.25	200.01
1550	98.49	50.78	24.28	431.87	211.34

		-10				
The Unionality)): Various				Docket 44921-5633-61-WO Document No. 1935323.1	
Identifier.	LDV ZOOGO	Tox_Mean	Tox_SD	NonTox_Meen	MonTox_SD	
20983	80.16	699.35	155.97	1005.91	291.23	
4259	78.68	872.19	120.42	688.78	128.81	
11576	78.68	42.97	21.82	82.03	29.1	
23068	78.34	337.97	152.95	602.09	216.21	
40	78.21	174.77	72.5	368.49	185.84	
15372	78.11	235.86	46.01	181.71	55.03	
4440	77.92	521.11	171.56	811.07	198.73	
20741	77.72	56.74	26.65	21.22	29.83	
7903	77.72	30.87	24.61	91.85	73.86	
13055	77.69	314.8	83.29	481.93	173.91	
3823	77.52	793.93	216.14	520.48	172.77	
1246	77.46	42.88	20	79.11	30.1	
19728	77.4	309.99	139.76	517.14	159.37	
8143	77.15	86.21	47.18	35.73	105.66	
5634	76.97	101.03	53.66	35.79	60.92	
17729	76.83	1144.04	188.18	916.66	210.39	
15029	76.76	1153.7	316.29	1594.83	523.1	
20757	76.61	628.44	378.55	265.1	101.02	
20984	76.6	907.16	202	1189.53	300.46	
6015	76.5	1014.49	395.11	1519.13	389.63	
15365	76.49	911.59	179.51	707.12	353.7	
22554	76.42	936.55	345.68	1508.43	434.36	
2435	76.31	238.98	44.37	187.81	45.95	
9191	76.3	381.39	188.57	700.04	284.22	
633	76.23	1035.25	269.13	1345.13	284.78	
6471	76.01	335.96	97.67	509.97	190.25	
729	75.97	133.33	51.18	226.84	81.36	
16329	75.94	476.38	256.14	255.42	104.07	
10611	75.93	140.38	141.73	21.78	29.86	
3916	75.89	1137.68	315.72	1549.62	408.07	
2569	75.84	696.92	495.63	913.6	280.73	
7918	75.77	85.91	26.54	62.72	31.29	
15382	75.74	293.92	222.54	161.59	305.54	
255	75.59	341.21	92.99	464.88	124.43	
22722	75.52	395.48	556.93	22.55	41.68	
11635	75.5	194.77	69.22	294.23	87.63	
16847	75.47	894.72	145.41	712.69	169.88	
1867	75.38	823.2	173.19	625.16	162.19	
20839	75.35	1382.24	215.11	1128.38	213.94	
547	75.32	483.82	102.27	371.33	89.89	
17549	75.25	841.2	147	651.48	144.29	
25702	75.25	634.55	124.24	491.54	177.05	
22559	75.24	683.97	197.13	979.9	319.54	
23285	75.12	504.92	120.97	356.86	132.69	
11403	75.05	397.6	225.11	179.74	198.49	
9067	75.03	1013.09	266.39	708.46	235.21	
15393	75.01	313.66	64.63	429.1	98.24	
13056	74.95	205.08	53.55	289.43	92.14	
10109	74.95	1225.48	174.73	1042.6	223.01	
24771	74.88	813.83	245.68	1115.47	315.73	
5934	74.83	232.5	105.47	371.97	166.12	

TABLE SFFF	: Cercinogen=	ම්කරුලාගම	A	omoy Docket 449	21-5033-01-WO
Timpeint(s):				Document	No. 1935323.1
refer Identifier	LDY 2000	Tox_Meen	Tox_SD	NonTox_Moin!	NonTox_SD :
5464	74.82	573.92	273.07	322.1	134.97
22931	74.76	58.34	37.34	140.64	97.53
24615	74.73	1024.85	188.08	829.18	195.6
6473	74.72	100.21	36.16	159.86	60.45
18525	74.71	192.5	144.81	203.43	77.82
15900	74.64	241.59	54.79	184	77.26
7888	74.62	367.74	111.47	262.4	139.88
1846	74.56	442.88	87.61	553.88	111.48
18713	74.56	467.98	136.85	329.64	109.36
18795	74.42	805.43	297.81	534.59	197.41
4441	74.41	1020.22	174.79	846.69	217.89
11830	74.31	988.21	424.5	615.36	243.9
22370	74.21	181.13	49.71	269.95	104.72
17533	74.18	198.65	90.33	308.74	124.97
11644	74.18	570.25	242.53	861.41	219.77
9012	74.15	447.75	242.26	707.87	273.4
23299	74.11	364.84	199.84	198.53	145.93
17175	74.09	866.87	216.39	606.64	164.99
12030	74.06	130.76	41.74	88.56	26.4
3367	74.04	765.01	229.59	526.96	195.19
20879	73.95	339.87	222.19	630.85	268.79
20986	73.94	200.11	64.05	342.36	172.2
4914	73.93	336.27	135.21	484.55	150.01
3411	73.88	1506.3	275.64	1799.96	454.13
15842	73.84	225.78	49.2	179.93	50.04
21458	73.78	558.82	240.46	395.15	291.91
15684	73.77	535.32	171.5	357.54	133.92
20939	73.73	254.05	59.42	205.48	70.48
6190	73.65	111.15	26.5	138.78	31.34
20712	73.56	827.09	243.59	1121.96	381.01
15135	73.56	982.15	194.11	784.61	186.24
25705	73.48	1130.61	452.71	732.69	175.44
17394	73.44	484.24	156.91	338.77	141.41
16005	73.42	497.67	98.02	402.72	80.72
23854	73.42	605.72	142.51	448.39	148.54
20427	73.37	957.46	132.45	788.39	160.54
7074	73.36	95.53	88.43	90.31	47.48
13966	73.35	242.42	97.55	173	40.64
15700	73.35	321.6	97.74	452.04	123.03
9475	73.35	562.32	280.75	867.4	305.84
22930	73.32	247.44	200.56	546.96	351.23
4091	73.25	471.63	134.48	340.62	93.48
2150	73.17	645.2	130.14	786.17	162.88
22929	73.15	542.45	417.96	1259.22	787.08
3266	73.15	205.41	44.72	156.16	36.08
2901	73.15	79.07	22.22	104.35	30.98
11404	73.08	362.81	158.8	217.06	125.26
22928	73.07	126.54	87.09	288.07	184.84
10540	73.05	53.88	42.58	23.14	16.86
18715	72.97	257.87	78.53	194.8	76.01
11136	72.96	449.61	137.53	312.81	116.46

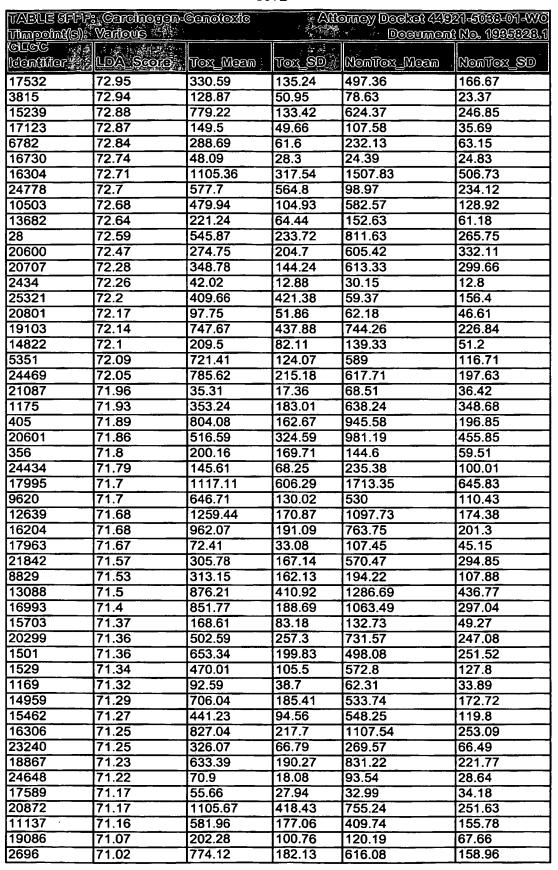




TABLE SFFF: Cardinogen-Cenotoxic Timpoint(s): Various			Afformay Docket 4/4921-5053-01-WC Document No. 1935522.1			
	LDA_Score	Tox_Meen	Tox_SD	Moontox_Meen	COS_XOTAON	
17758	70.99	152.5	72.7	369.15	378.61	
17104	70.96	714.4	187.94	538.37	138.23	
17101	70.85	245.79	88.54	181.78	63.4	
10545	70.77	334.5	136.91	215.02	84.92	
13282	70.54	182.55	50.18	226.06	78.52	
6911	70.53	170.87	69.42	235.47	74.25	
794	70.5	625.94	167.38	806.91	228.44	
17086	70.49	162.73	43.06	120.13	46.89	
20807	70.44	1084.34	174.14	905.22	211.25	

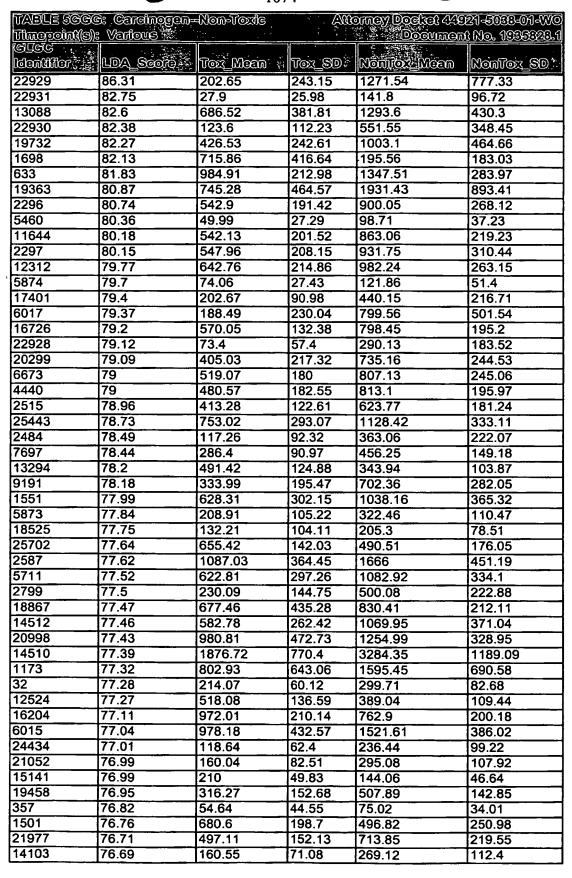


TABLE SCCC	s: Cardinogen=	-Non-Texte	A	Dinay Docket 449	21-5033-01-WO
Timepoint(S):	: Vartous		· · · · · · · · · · · · · · · · · · ·	Dogument	
identifier.		Tox_Mean	Tox_SD_	Monitox Wosu	NonTox_SD;
3411	76.59	1332.3	361.54	1806.07	447.92
23417	76.56	337.52	112.64	226.74	68.65
3823	76.48	696.96	185.24	522.69	176.92
13563	76.46	1272.5	1063.56	1181.18	312.74
9016	76.41	1605.31	1194.36	2662.59	971.34
6007	76.37	426.96	77.88	554.92	111.97
10503	76.36	455.68	101.8	583.59	128.28
9336	76.17	114.48	64.74	276.17	169.66
17850	75.94	504.84	132.42	376.73	95.85
4091	75.94	470.39	101.29	340.3	94.39
20707	75.81	453.29	493.23	610.87	290.64
17849	75.78	1570.36	493.86	1069.97	305.55
19470	75.75	334.94	132.9	513.28	149.42
14738	75.65	940.09	234.19	1342.28	357.93
4093	75.62	725.12	144.3	565.89	161.11
2569	75.55	677.8	411.57	914.77	283.28
23390	75.5	673.73	232.49	440.42	149.99
2299	75.49	214.32	101.04	359.78	126.42
1478	75.46	289.8	109.15	427.18	117.78
20872	75.26	958.3	204.21	758.78	262.97
6406	75.26	125.54	80.07	56.2	78.4
17887	75.22	822.69	360.31	1166.09	312.15
4090	75.2	790.43	147.59	601.11 -	150.05
19993	75.17	523.53	141.7	394.77	187.13
26123	75.12	484.05	206.18	286.56	147.67
5943	75.07	328.64	183.9	655.3	309.44
23362	75.03	367.93	155.31	210.62	68.03
23070	75.01	138.72	31.01	104.6	28.91
15654	74.95	474.6	162.84	320.1	145.23
20430	74.9	480.93	246.6	834.64	378.27
17179	74.89	123.13	43.67	83.31	41.87
20862	74.83	170.81	66.32	275.48	96.48
11404	74.77	346.74	157.49	217.16	125.51
17049	74.76	229.42	98.95	340.73	98.41
3995	74.75	1188.34	436.49	1635.65	371.62
24811	74.72	981.08	431.27	1520.23	449.47
22558	74.7	2457.9	548.19	3224.82	776.48
794	74.65	580.03	190.24	808.8	226.58
1561	74.64	608.51	210.01	881.05	218.39
7888	74.59	350.2	109.39	262.65	140.26
22820	74.59	503.78	208.71	306.29	127.03
6824	74.52	766.23	366.65	405.29	201.16
6390	74.47	113.7	53.01	59.45	38.3
23448	74.44	2363.27	1438.39	1051.79	811.05
14962	74.38	493.78	167.48	409.25	114.02
1867	74.34	829.89	194.73	624.42	160.84
14007	74.26	151.2	37.63	206.51	64.51
4441	74.25	1007.74	178.02	846.6	218.02
15955	74.24	144.38	137.03	195.89	92.94
10109	74.11	1278.13	244.78	1040.49	219.4
20466	74.06	293	99.2	431.14	148.29

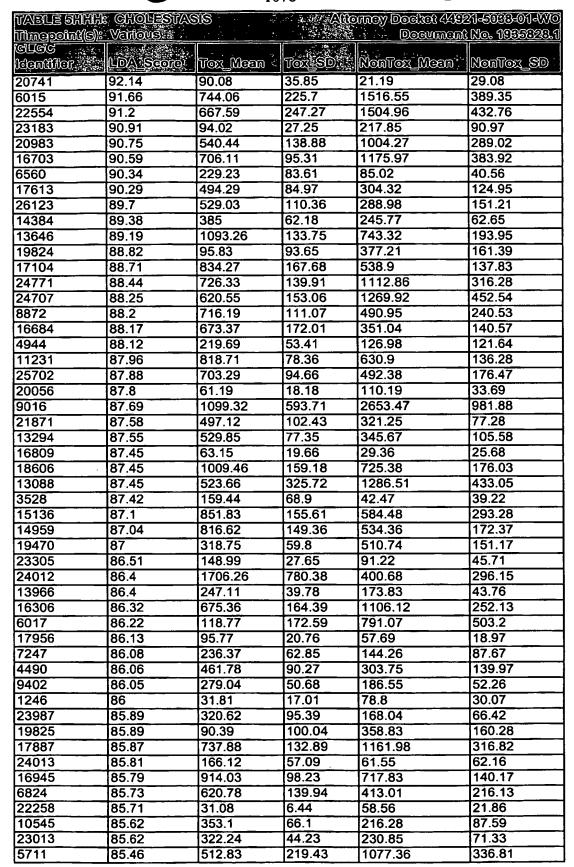
TABLE SEEC: Cereinogen-Non-Toxic Timepoint(s): Various GUGG			Affermay Docket 4/1921-5033-01-WO Document No. 1935328.1		
	LDA_Secte	Tox_Mean	Tox_SD !	NonTox_Moon;	NonTox_SD
23854	74.05	625.85	175.43	447.35	146.56
2149	73.99	737.52	211.62	978.87	219.16
24771	73.92	782.11	295.53	1117.26	313.23
16684	73.89	557.07	248.27	349.5	137.39
356	73.83	112.43	92.51	147.13	64.24
8984	73.79	259.82	81.37	178.26	56.75
13646	73.69	981.81	229.01	741.19	192.24
1550	73.66	224.43	157.87	437.37	210.13
17292	73.65	513.55	224.67	758.44	246.74
1479	73.54	209.56	82.63	298.91	94.51
1447	73.54	297.12	61.7	239.48	59.43
17324	73.53	266.43	79.83	381.68	117.25
25747	73.47	582.23	229.47	421.39	232.45
24810	73.37	236.63	127.1	422.34	148.72
20741	73.34	59.11	43.76	21.05	29.08
1529	73.27	449.84	139.42	573.7	126.21
8182	73.2	1114.17	340.22	1464.93	330.86
15535	73.14	665.35	137.93	516.19	134.91
8317	73.14	376.97	158.53	643.26	219.6
15335	73.07	508.46	165.1	359.73	151.62
17473	73.04	353.48	142.47	227.44	93.48
20864	73.03	1059.38	686.68	453.34	352.78
24228	73.02	772.77	127.78	985.56	264.52
11635	72.98	198.14	66.56	294.4	87.69
10509	72.96	95.38	35.94	139.78	54.12
18606	72.92	948.1	210.63	722.76	173.7
14959	72.83	749.08	210.81	531.96	170.07
20429	72.81	390.99	171.02	631.51	260.07
23321	72.68	255.86	108.44	237.45	63.41
2150	72.65	638.05	142.4	786.77	162.3
9134	72.46	588.63	132.56	469.81	104.59
25480	72.46	421.15	151.83	611.36	191.9
2505	72.44	552.09	200.64	759.15	189.26
22582	72.41	297.74	125.32	441.85	141.39
5749	72.4	265.17	70.18	195.41	85.11
3815	72.39	104.79	28.13	79.23	25.37
16205	72.34	1370.36	314.88	1090.44	256.99
24645	72.3	292.1	102.19	400.77	171.29
6405	72.26	61.65	28.48	39.31	34.42
4748	72.22	870.64	350.08	1197.05	350.11
3254	72.21	362.51	115.54	253.72	87.89
21054	72.19	305.12	160.26	522.03	206.99
17123	72.18	144.86	42.38	107.6	36.01
2578	72.12	218.28	69.5	158.33	47.55
17175	72.11	854.18	223.44	606.32	164.58
25686	72.08	904.7	224.67	716.42	183.96
293	72	146.02	67.63	238.27	84.09
9136	72	441.84	113.66	335.26	86.94
16507	72	123.55	29.96	93.01	34.31
17549	71.96	794.93	142.99	652.37	145.68
3987	71.94	342.64	83.07	267.98	77

TABLE SCC: Cardinogen—Non-Toxic Timepoint(s): Various			Altomay Dockat 44921-5033-01-WO Document No. 1935323.1		
ldeniijer. GTGC	LDA_Seoro,	Tox_Meen	Tox_SD	Menio Meni	KonTox_SD :
18906	71.94	57.48	49.51	82.24	35.68
20056	71.94	77.77	27.94	110.46	33.73
11153	71.89	459.58	195.06	637.39	200.55
4259	71.88	828	158.81	689.63	128.92
15700	71.84	328.33	95.82	452.19	123.16
10545	71.84	320.5	112.94	215.12	86.12

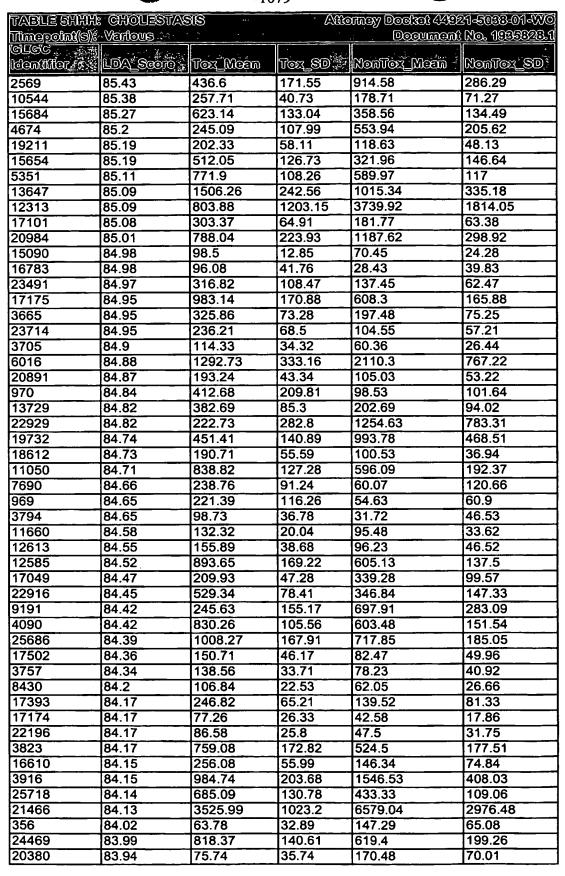
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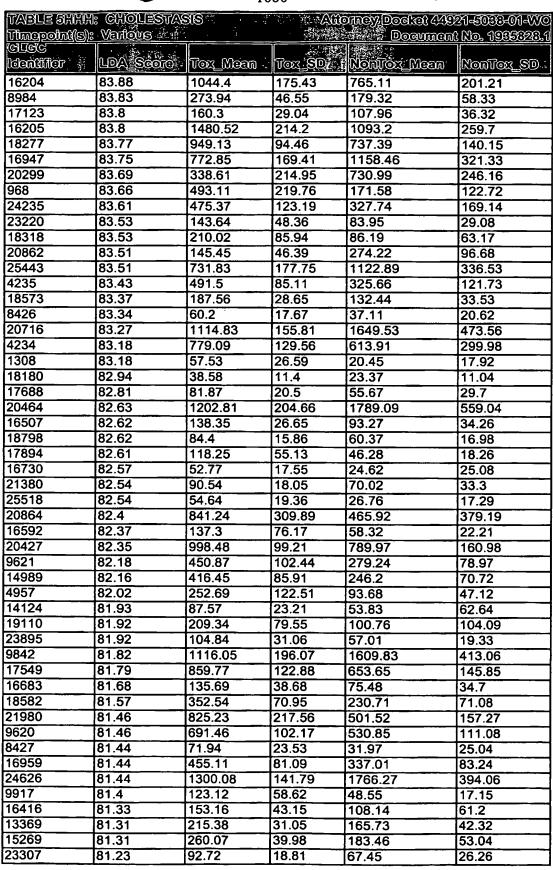




TABLE SHIH: CHOLESTASIS			Afformery Decket 44921-5083-01-WO			
vinepoin((s):	imereini(s): Various			Document	No. 1935323.1	
CECC Constitution LDA_Score Tox_Meen		Tox_SD 🎉	MOONTOX_MOON	NonTox_SD .		
18492	81.17	254.19	55.76	173.22	62	
19949	81.14	213.35	57.75	145.42	41.98	
3987	81.04	376.65	54.58	268.65	77.43	

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				may Docker 440	
				<u>Dodumen</u>	
	LDA_Scoro.			Monitor: Monitor	NonTox_SD ,
6532	85.19	223.44	59.41	138.34	40.54
20529	84.65	685.88	500.38	113.59	138.52
13353	82.6	171.98	81.96	288.76	56.48
20354	82.57	223.1	148.24	46.67	43.96
21740	81.59	1448.49	618.99	715.13	252.93
4969	81.5	904.09	601.25	243.18	209.99
22515	80.96	1196	1162.05	94.19	281.83
19769	80.58	1257.27	435.1	740.27	235.92
960	80.5	131.11	51.24	218.3	64.52
2161	80.33	1075.21	600.78	346.34	227.87
20698	80.3	1903.78	966.73	866.13	377.41
3773	80.19	205.25	126.8	63.46	51.98
17709	80.19	102.6	51.82	35.96	40.49
12587	80.14	48.63	39.86	111.33	47.26
3121	80.11	443.89	231.43	830.94	241.08
13167	79.98	76.27	20.48	115.28	31.01
21025	79.98	32.06	41.16	90.49	50.94
19411	79.92	93.71	56	32	16.5
20701	79.89	1739.07	815.35	854.66	336.97
22619	79.87	518.38	182.48	293.49	105.78
12577	79.78	547.97	398.82	145.74	108.54
21125	79.62	94.31	73.69	222.98	91.57
4244	79.6	93.61	33.17	155.43	48.67
21281	79.54	208.78	63.76	310.16	78.18
24200	79.37	955.52	460.95	423.15	223.45
26133	79.35	453.37	246.61	184.07	211.62
17664	79.26	619.55	303.89	269.89	142.81
8215	79.18	640.26	221.32	379.61	125.48
16809	79.13	94.45	67.95	27.69	19.96
11536	79.08	300.55	93.01	508.41	193.96
14491	79.07	250.4	82.02	155.54	63.55
17591	78.99	222.63	90.4	126.46	38.38
15170	78.91	110.06	56.54	199.04	54.54
18389	78.86	53.99	32.24	20.78	29.03
22017	78.75	280.47	150.04	120.99	87.23
21209	78.74	273.68	209.93	77.74	69.54
10532	78.64	431.38	138.95	274.62	87.95
8522	78.61	356.62	203.78	143.76	58.49
1221	78.58	393.01	336	21.14	86.43
9053	78.56	31.52	31.1	75.91	32.25
14208	78.56	82.48	35.65	142.67	50.27
22018	78.55	300.65	112.77	170.83	85.85
18159	78.37	136.04	53.91	74.52	74.28
7451	78.28	1775.99	568.64	1119.65	275.04
19410	78.28	143.96	40.96	86.38	28.24
1223	78.28	235.78	82.05	134.5	79.38
2430	78.25	66.49	41.52	22.48	26.71
15426	78.1	192.78	42.26	268.57	62.27
24225	78.04	291.99	74.98	386.24	86.65
2557	78.03	66.88	28.9	34.66	15.3
11205	77.99	664.5	183	929.43	242.75
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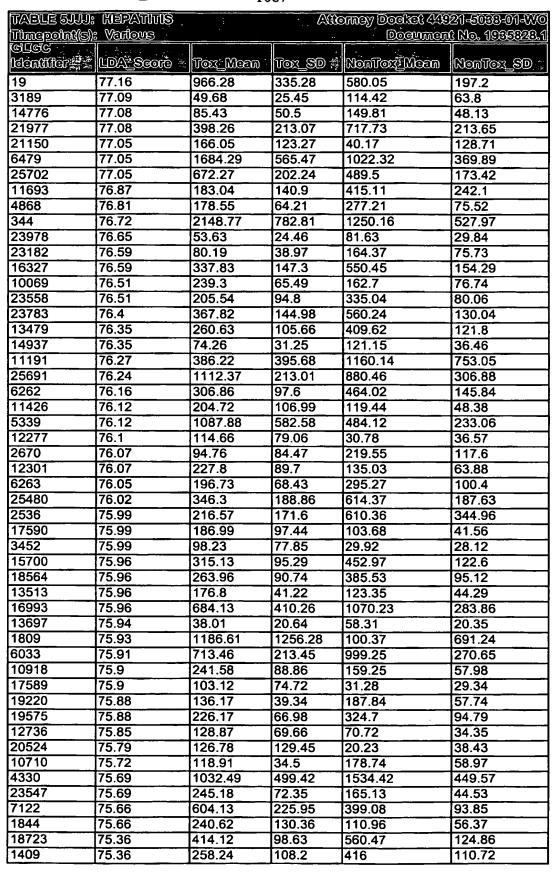
TABLE SII: (I	(EVOIDUS:		Allo Sallo	mey Docket 449 Documen	21-5099-01-W0 } No. 1935929.1
GTGC .	LDV. Segio	Tox_Moen	Toxesd 4	MonTox_Mean	NonTox_SD
6720	77.98	140.71	111.52	28.02	95.66
22569	77.96	88.79	42.82	150.58	55.53
11202	77.95	86.3	29.93	54.75	17.96
21073	77.6	373.06	105.13	248.97	69.63
14502	77.6	233.68	61.43	165.14	45.27
13332	77.58	121.59	76.28	232.63	81.86
23583	77.38	136.19	75.07	55.12	36.14
5622	77.38	2247.02	593.25	1573.74	347.68
8917	77.38	102.79	62.89	40.81	40.57
19729	77.28	213.35	151.18	565.29	328.65
15004	77.27	357.34	139.02	235.19	156.73
1841	77.21	153.51	107.56	44	45.85
21078	77.19	488.43	145.36	746.56	212.27
19	77.16	966.28	335.28	580.05	197.2
15961	77.16	114.38	66.55	46.93	42.39
3189	77.09	49.68	25.45	114.42	63.8
19412	77.08	641.91	207.2	379.3	104.76
21977	77.08	398.26	213.07	717.73	213.65
14776	77.08	85.43	50.5	149.81	48.13
25702	77.05	672.27	202.24	489.5	173.42
6479	77.05	1684.29	565.47	1022.32	369.89
21150	77.05	166.05	123.27	40.17	128.71
5384	76.91	107.89	92.63	24.83	58.5
11693	76.87	183.04	140.9	415.11	242.1
4868	76.81	178.55	64.21	277.21	75.52
344	76.72	2148.77	782.81	1250.16	527.97
23978	76.65	53.63	24.46	81.63	29.84
6825	76.62	292.14	112.44	431.5	114.14
16327	76.59	337.83	147.3	550.45	154.29
23182	76.59	80.19	38.97	164.37	75.73
23558	76.51	205.54	94.8	335.04	80.06
10069	76.51	239.3	65.49	162.7	76.74
23783	76.4	367.82	144.98	560.24	130.04
14937	76.35	74.26	31.25	121.15	36.46
13479	76.35	260.63	105.66	409.62	121.8
11423	76.31	59.15	30.69	33.16	14.65
15606	76.29	439.18	116.76	616.36	137.2
11191	76.27	386.22	395.68	1160.14	753.05
25691	76.24	1112.37	213.01	880.46	306.88
6262	76.16	306.86	97.6	464.02	145.84
5339	76.12	1087.88	582.58	484.12	233.06
11426	76.12	204.72	106.99	119.44	48.38
12277	76.12	114.66	79.06	30.78	36.57
12301	76.07	227.8	89.7	135.03	63.88
2670	76.07	94.76	84.47	219.55	117.6
6263	76.05	196.73	68.43	295.27	100.4
25480	76.02	346.3	188.86	614.37	187.63
17590	75.99	186.99	97.44	103.68	41.56
9712	75.99 75.99	48.43	38.82	87.6	37.71
2536	75.99 75.99	216.57	171.6	610.36	344.96
15700	75.99 75.96	315.13	95.29	452.97	122.6
.0.00	7 0.00	010.10	33.23	702.31	122.0

TABLE 5III: :1	139ATIMS: ==	St. Ty	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	mey Docket 449	21-5033-01-770
Timeroint(s):					} No. 1985823.1
CTCC CTCC	LDA_Score.	Tox_Meen ~	Tox_SD:	NGON KOTÜÜÖN	NonTox_SD:
16993	75.96	684.13	410.26	1070.23	283.86
18564	75.96	263.96	90.74	385.53	95.12
1809	75.93	1186.61	1256.28	100.37	691.24
17589	75.9	103.12	74.72	31.28	29.34
1844	75.66	240.62	130.36	110.96	56.37
18723	75.36	414.12	98.63	560.47	124.86
1409	75.36	258.24	108.2	416	110.72
21707	75.17	129.5	88.96	38.35	48.56
9905	75.17	448.73	140.85	653.71	147.4
16134	75.12	50.24	33.8	107.77	54.16
43	75.04	275.18	107.99	440.5	129.15
1127	75.01	54.77	35.42	132.68	106.49
14997	74.97	727.29	466.27	274.5	256.4
19952	74.87	73.16	36.85	129.15	51.29
20523	74.86	213.55	195.22	43.75	52.13
25370	74.85	73.05	47.97	159.16	91.66
1850	74.76	3940.44	2490.47	2421.78	994.13
12312	74.73	633.19	253	983.49	261.14
17567	74.73	1374.9	222.13	1176.07	213.88
15410	74.71	261.99	54.95	355.34	84.5
794	74.65	494.55	292.28	812.28	219.24
11959	74.6	62.74	24.79	98.12	31.21
22867	74.6	181.38	56.74	253.14	66.42
20248	74.57	36.29	11.89	23.9	15.77
11904	74.51	120.95	65.02	58.58	41.48
17883	74.49	32.83	10.85	22.09	15.53
851	74.32	325.42	112.25	440.25	103.99
23321	74.27	157.42	87.01	240.68	62.64
1578	74.22	24.28	13.7	44.84	17.94
19103	74.21	515.02	246.96	752	230.58
811	74.1	487.49	178.05	682.5	143.93
10109	74.07	1328.91	368.41	1038.15	211.11
4590	74	31.31	22.8	52.03	26.82
3292	73.94	4673.65	3021.02	2495.2	1241.78
15002	73.94	218.02	94.89	138.71	73.56
1561	73.91	1227.46	383.54	861.17	205.43
699	73.85	905.09	272.9	601.96	143.39
15378	73.78	75.68	28.98	120.31	37.39
4198	73.77	1367.98	283.56	1081.44	224.98
19443	73.73	930.76	318.25	1381.35	432.79
11203	73.69	72.98	35.89	41.44	16.27
13480	73.67	492.44	158.54	735.66	179.45
24219	73.66	598.86	272.69	373.62	181.18
18695	73.62	73.29	25.91	117.33	47.28
3131	73.62	281.05	109.32	441.09	153.75
17894	73.45	71.39	25.91	46.5	20.4
15652	73.45	1849.73	323.35	1491.36	363.06
25317	73.39	1991.17	610.79	1364.85	451.42
23044	73.34	224.47	70.74	150.77	54.5
12606	73.34	505.74	307.66	748.02	233.25
1843	73.31	49.54	24.82	28.93	15.86

TABLE 311: HEPATITIS · Attorney Docket 44921-5133-91-WO							
Threpoint(s): Verlous Document No. 1985							
(C) LC(C	र स्कॉश्र‡्			5. 整 鑫			
identifier 🦟	LDV Scolo?	Tox_Mean	Tox SD 💈	NonTox_Mean	NonTox_SD _		
16726	73.29	545.56	188.44	799.89	192.44		
18453	73.26	326.42	276.99	652.91	259.76		
134	73.26	65.63	53.79	119.84	51.3		
412	73.25	2812.13	1414.38	1604.48	771.99		
21709	73.23	234.87	45.04	192.24	46.77		
20	73.12	543.32	225.55	340.68	128.61		
14139	73.12	34.81	15.11	53.35	18.1		
11635	73.07	201.89	80.06	294.54	87.37		
1694	73.06	1340.6	291.11	1067	228.73		
15191	73.04	3258.78	2347.81	1154.02	1229.65		
14933	72.93	35.74	28.33	51.32	21.05		
1753	72.91	268.73	115	446.66	170.87		
23445	72.88	109.37	89.84	239.79	130.02		
1583	72.87	49.4	24.94	27.97	13.12		
9826	72.85	28.76	25.99	51.99	20.68		

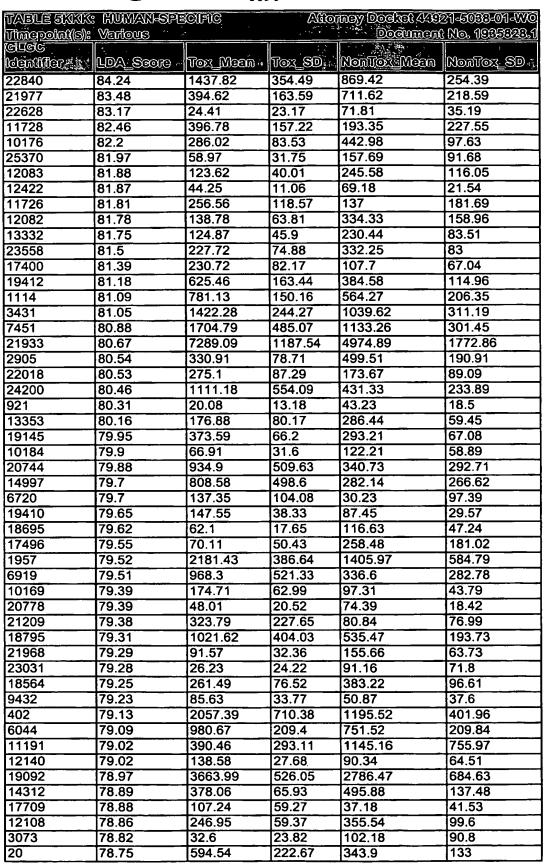
TABLE SW:				mey Docket 449	
Tingpoint(S): GLEC	Various		70.23	Dogriway	1935323.1 No. 1935323.1
ldentifier	LDA Sono:	Tox_Moon	Tox_SD	Meenlest Meen	E CE EXOTINGLY
20529	84.65	685.88	500.38	113.59	138.52
13353	82.6	171.98	81.96	288.76	56.48
4969	81.5	904.09	601.25	243.18	209.99
22515	80.96	1196	1162.05	94.19	281.83
19769	80.58	1257.27	435.1	740.27	235.92
960	80.5	131.11	51.24	218.3	64.52
2161	80.33	1075.21	600.78	346.34	227.87
20698	80.3	1903.78	966.73	866.13	377.41
17709	80.19	102.6	51.82	35.96	40.49
3773	80.19	205.25	126.8	63.46	51.98
12587	80.14	48.63	39.86	111.33	47.26
21025	79.98	32.06	41.16	90.49	50.94
13167	79.98	76.27	20.48	115.28	31.01
19411	79.92	93.71	56	32	16.5
12577	79.78	547.97	398.82	145.74	108.54
21125	79.62	94.31	73.69	222.98	91.57
4244	79.6	93.61	33.17	155.43	48.67
24200	79.37	955.52	460.95	423.15	223.45
26133	79.35	453.37	246.61	184.07	211.62
8215	79.18	640.26	221.32	379.61	125.48
11536	79.08	300.55	93.01	508.41	193.96
14491	79.07	250.4	82.02	155.54	63.55
17591	78.99	222.63	90.4	126.46	38.38
15170	78.91	110.06	56.54	199.04	54.54
22017	78.75	280.47	150.04	120.99	87.23
21209	78.74	273.68	209.93	77.74	69.54
10532	78.64	431.38	138.95	274.62	87.95
8522	78.61	356.62	203.78	143.76	58.49
9053	78.56	31.52	31.1	75.91	32.25
22018	78.55	300.65	112.77	170.83	85.85
18159	78.37	136.04	53.91	74.52	74.28
1223	78.28	235.78	82.05	134.5	79.38
7451	78.28	1775.99	568.64	1119.65	275.04
2430	78.25	66.49	41.52	22.48	26.71
15426	78.1	192.78	42.26	268.57	62.27
24225	78.04	291.99	74.98	386.24	86.65
2557	78.03	66.88	28.9	34.66	15.3
11205	77.99	664.5	183	929.43	242.75
6720	77.98	140.71	111.52	28.02	95.66
22569	77.96	88.79	42.82	150.58	55.53
11202	77.95	86.3	29.93	54.75	17.96
14502	77.6	233.68	61.43	165.14	45.27
21073	77.6	373.06	105.13	248.97	69.63
8917	77.38	102.79	62.89	40.81	40.57
5622	77.38	2247.02	593.25	1573.74	347.68
23583	77.38	136.19	75.07	55.12	36.14
19729	77.28	213.35	151.18	565.29	328.65
15004	77.27	357.34	139.02	235.19	156.73
			107.56	44	45.85
1841	77.21	153.51	145.36		212.27
21078	77.19	488.43		746.56	
15961	77.16	114.38	66.55	46.93	42.39





Timepointle): HEPATITIS)): Various :			omey Docket 44921-5033-01-WC		
CELES SELEN	LDA_Score :	Tox_Media	Tox_SD:	New Town	KonTox SD	
21707	75.17	129.5	88.96	38.35	48.56	
9905	75.17	448.73	140.85	653.71	147.4	
16134	75.12	50.24	33.8	107.77	54.16	
43	75.04	275.18	107.99	440.5	129.15	
1127	75.01	54.77	35.42	132.68	106.49	
14997	74.97	727.29	466.27	274.5	256.4	
19952	74.87	73.16	36.85	129.15	51.29	
20523	74.86	213.55	195.22	43.75	52.13	
1850	74.76	3940.44	2490.47	2421.78	994.13	
12312	74.73	633.19	253	983.49	261.14	
17567	74.73	1374.9	222.13	1176.07	213.88	
15410	74.71	261.99	54.95	355.34	84.5	
794	74.65	494.55	292.28	812.28	219.24	
11959	74.6	62.74	24.79	98.12	31.21	
22867	74.6	181.38	56.74	253.14	66.42	
20248	74.57	36.29	11.89	23.9	15.77	
17883	74.49	32.83	10.85	22.09	15.53	
851	74.32	325.42	112.25	440.25	103.99	
23321	74.27	157.42	87.01	240.68	62.64	
1578	74.22	24.28	13.7	44.84	17.94	
	74.21	515.02	246.96	752	230.58	
19103			178.05	682.5		
811	74.1	487.49			143.93	
10109	74.07	1328.91	368.41	1038.15	211.11	
4590	74	31.31	22.8	52.03	26.82	
3292	73.94	4673.65	3021.02	2495.2	1241.78	
15002	73.94	218.02	94.89	138.71	73.56	
1561	73.91	1227.46	383.54	861.17	205.43	
699	73.85	905.09	272.9	601.96	143.39	
15378	73.78	75.68	28.98	120.31	37.39	
4198	73.77	1367.98	283.56	1081.44	224.98	
19443	73.73	930.76	318.25	1381.35	432.79	
11203	73.69	72.98	35.89	41.44	16.27	
13480	73.67	492.44	158.54	735.66	179.45	
24219	73.66	598.86	272.69	373.62	181.18	
18695	73.62	73.29	25.91	117.33	47.28	
3131	73.62	281.05	109.32	441.09	153.75	
17894	73.45	71.39	25.91	46.5	20.4	
15652	73.45	1849.73	323.35	1491.36	363.06	
25317	73.39	1991.17	610.79	1364.85	451.42	
23044	73.34	224.47	70.74	150.77	54.5	
12606	73.34	505.74	307.66	748.02	233.25	
1843	73.31	49.54	24.82	28.93	15.86	
16726	73.29	545.56	188.44	799.89	192.44	
18453	73.26	326.42	276.99	652.91	259.76	
134	73.26	65.63	53.79	119.84	51.3	
412	73.25	2812.13	1414.38	1604.48	771.99	
21709	73.23	234.87	45.04	192.24	46.77	
20	73.12	543.32	225.55	340.68	128.61	
14139	73.12	34.81	15.11	53.35	18.1	
11635	73.07	201.89	80.06	294.54	87.37	
1694	73.06	1340.6	291.11	1067	228.73	
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TABLE SUU:			Awa	erney Docket 44E	21-5053-01-440			
Timepoint(s): Vafious Decument No. 1995323.1								
Conditor.	LDV Score	Tox_Mosm	Tox_SD	NonTox_Mean	NonTox_SD			
15191	73.04	3258.78	2347.81	1154.02	1229.65			
14933	72.93	35.74	28.33	51.32	21.05			
1753	72.91	268.73	115	446.66	170.87			
23445	72.88	109.37	89.84	239.79	130.02			
1583	72.87	49.4	24.94	27.97	13.12			
9826	72.85	28.76	25.99	51.99	20.68			
16472	72.8	22.42	11.5	47.24	28.65			
25052_	72.79	283.57	334.72	25.65	120.49			
1572	72.79	111.28	42.96	72.06	31.45			
20090	72.76	180.42	102.74	107.22	36.61			
19244	72.74	1396.24	317.12	1097.32	242.02			
15612	72.72	188.45	134.19	453.11	329.12			
10248	72.66	44.57	22.72	25.35	25.09			
1558	72.66	49.45	32.85	93.19	39.59			
107	72.64	77.74	35.72	131.66	73.29			
15387	72.6	665.35	155.05	516.09	117.06			
15313	72.52	58.54	44.05	26.75	36.48			





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	HUMAN-SPE			may Docket 449	
Threpoint(s):				Doguman	: 1. 19
ldentijer GEGG	LDA_Score	Tox_Mom	GOS_xoI	New Training of the contract o	COS_XOTAON
20042	78.73	1003.07	216.55	645.21	257.9
21707	78.73	162.01	111.15	39.68	49.73
22452	78.7	960.47	557.34	392.16	328.5
7583	78.68	228.76	126.78	49.16	123.23
2514	78.64	993.58	369.54	543.64	280.42
2161	78.49	1045.81	594.64	360.79	261.88
12306	78.46	2478.81	1208.77	1128.61	492.12
11727	78.4	292.65	143.54	183.04	242.97
22906	78.33	1389.24	754.41	551.23	409.34
2242	78.29	3622.99	1276.38	2414.77	867.53
19575	78.25	218.29	50.87	322.91	95.32
13389	78.13	22.03	24.27	52.75	25.56
21125	78.06	102.32	88.94	220.39	92.92
4017	77.98	52.57	15.23	76.26	29.77
15191	77.95	3619.23	2031.67	1189.78	1291.95
23029	77.95	309.4	199.62	774.42	457.96
5523	77.87	832.64	284.21	457.1	305.15
1221	77.83	321.74	281.91	29.27	114.79
18397	77.8	59.44	18.44	39.4	28.71
14425	77.8	1489.83	906.78	442.39	416.21
20354	77.75	217.48	158.68	50.15	53.78
3773	77.72	169.93	103.2	66.67	59.37
8600	77.69	25.88	38.63	81.46	56.67
23569	77.63	185.99	54.76	261.79	59.35
6986	77.63	222.4	51.16	150.37	58.74
18660	77.63	78.49	24.98	130.16	52.58
4002	77.63	88.99	20.17	127.35	41.79
13479	77.62	273.15	118.63	406.58	123.27
22340	77.6	337.31	92.44	529.36	183.71
21940	77.56	272.48	81.53	394.79	112.01
1639	77.55	135.8	40.16	197.55	45.66
17768	77.54	606.75	115.77	772.57	144.1
1805	77.49	2206.4	549.17	1444.53	630.29
5339	77.48	1249.53	696.92	493.6	248.82
11504	77.45	449.62	157.25	708.33	224.61
17132	77.43	4521.4	997.41	3453.96	1046.97
15189	77.41	4278.64	2464.35	1627.27	1623.23
19	77.37	1037.61	366.95	586.54	205.06
16680	77.32	230.94	115.18	400.82	135.74
23608	77.29	827.62	365.14	393.95	179.15
3722	77.27	598.89	155.66	394.17	143.77
21679	77.27	34.85	16.31	61.91	24.06
10710	77.24	115.76	28.9	177.63	59.17
20542	77.24	149.29	26.62	116.42	42
4703	77.2	743.74	280.28	419.12	237.06
11536	77.2	310.62	85.6	504.27	194.81
514	77.13	364.25	86.27	254.71	91.51
15700	77.11	317.02	76.81	450.28	123.79
12210	77.1	558.33	178.98	316.33	178.22
2010	76.89	3919.07	1538.49	2669.01	1250.02
12423	76.82	111.83	26.15	169.3	72.58

TABLE BXXXX		CFIC	Alto	may Docket 449	21-5033-01-WO
Timepoint(S):	Various :		1000	Document	No. 1935323.1
Mewiller : :	LDA_Score	Tox_Moon	Tox_SD 🐉	Noviox Weew	NonTox_SD :
6477	76.61	3083.49	926.01	2253.54	859.82
15190	76.53	4664.62	2400.07	1803.1	1674.56
17693	76.5	113.84	37.59	211.77	128.43
1246	76.44	44.79	17.25	78.58	30.33
3131	76.2	267	103.71	438.19	154.44
20743	76.05	93.27	24.47	140.84	38.05
23368	76	36.91	21.97	76.65	35.22
19952	75.99	80.45	34.08	127.97	51.75
1973	75.98	283.34	69.05	392.8	106.86
1169	75.93	38.34	10.11	63.46	34.46
17324	75.9	247.92	83.06	380.02	117.37
21941	75.88	340.65	75.78	463.69	109.92
16449	75.86	184.98	103.27	332.27	190.55
25480	75.86	384.35	140.12	608.7	192.43
21090	75.85	82.45	43.47	147.1	55.77
26029	75.79	310.57	196.68	196.7	332.64
373	75.77	284.68	114.89	476.29	164.84
4244	75.72	102.54	49	154.12	49.13
24508	75.68	171.11	70.36	112.35	46.67
20735	75.64	285.82	128.7	188.63	132.06
14933	75.63	26.63	26.27	51.15	21.24
1409	75.57	267.04	98.98	412.84	113.05
13090	75.56	26.25	30.71	81.24	66.75
19411	75.53	70.68	27.45	33.5	21.46
17300	75.52	42.83	19.22	67.76	26.81
1731	75.52	54.61	24.66	84.25	30.69
1753	75.44	271.25	100.03	443.2	171.87
19085	75.39	146.43	58.83	86.02	45.82
851	75.35	339.64	108.01	437.84	105.59
10517	75.32	33.63	9.62	45.64	11.52
16871	75.16	39	8.86	57.34	23.73
6478	75.16	4878.91	2045.76	3213.89	1789.74
9053	75.07	28.69	28.29	75.09	32.78
20698	75.03	1766.99	880.06	887.97	428.52
15299	75.02	149.67	123.48	77.39	128.38
6013	75	2510.29	636.71	1896.39	624.56
7067	74.9	223.91	82.58	337.9	92.02
16809	74.84	79.79	55.92	29.18	24.62
13092	74.72	87.8	86.79	222.03	123.26
4234	74.63	759.33	181.76	614.35	299.69
4003	74.58	114.34	28.03	179.28	80.55
23837	74.55	33.28	9.97	55.19	26.61
1546	74.55	242.59	59.39	301.49	75.11
20701	74.52	1569.77	736.94	873.99	379.6
22515	74.45	1090.61	1299.95	116.84	354.19
11202	74.43	72.84	20.68	55.54	19.16
18727	74.41	1041.79	296.09	760.15	382.87
25064	74.4	1021.41	432.29	1190.34	355.96
1843	74.38	56.29	29.21	29.24	16.11
17468	74.35	448.74	80.13	563.38	116.21
1141	74.24	237.35	53.35	176.45	55.87

TABLE SXXX Timepoin(S):	: KUMAN-SPE Various	CIFIC	Afformey Docket 44221-5033-01-WO Document No. 1935323.1			
ldentifier .	LDA_Score	Tox_Mean	GEZTOI	Nonvez Meen	NonTox_SD:	
18402	74.19	48.27	14.82	69.85	21.07	
22867	74.15	182.26	51.51	251.75	67.04	
1792	74.02	194.59	59.08	303.36	111.8	
8640	73.98	217.48	94.58	125.61	91.84	
19710	73.97	335.06	92.06	238.53	107.23	
20699	73.96	2777.64	805.72	2126	824.57	
14004	73.9	37.61	15.31	76.03	62.83	
20601	73.81	567.23	233.73	974.04	458.89	
3292	73.72	4467.58	2433.76	2539.97	1352.98	
1876	73.7	559.04	194.56	776.44	201.8	
1170	73.68	70.66	21.59	110.77	55.21	
9826	73.64	25.81	24.52	51.58	21.01	
12010	73.59	69.42	18.66	106.46	37.49	

TABLE STILL: 10	ignear ang Fiva	r Enlargement	· Practical Company	may Docket 4x92	11-5033-01-WO
	avohas avohas			Dogumant	17.0° J8889:5597J
Identifier	LDV Score			NOONTOX_MOON	NonTox_SD
20915	81.71	1357.88	797.41	507.57	306.08
6673	80.12	569.69	134.49	806.36	247.49
12071	79.67	401.9	136.67	643.43	180.12
15146	79.64	113.08	46.74	226.46	110.55
17541	79.32	2743.59	1047.5	1592.85	586.82
15125	79.2	2842.86	1394.32	1608.65	535.95
4198	79.03	835.29	124.05	1099.33	230.51
14131	78.92	110.62	82.52	31.86	27.47
6479	78.51	610.47	262.11	1058.34	390.72
7022	78.41	102.69	55.02	35.25	36.09
9032	78.19	804.57	191.86	598.36	153.21
8438	77.99	45.32	29.77	95.82	44.95
4291	77.98	159.97	73.17	314.14	138.5
20724	77.92	47.7	29.7	86.32	32.64
14103	77.91	146.35	59.13	269.95	112.07
2544	77.65	147.84	46.91	224.99	67.65
17324	77.65	263.78	66.86	382.15	117.35
17401	77.32	204.21	88.35	440.87	216.67
16067	77.08	357.79	157.08	164.36	110.94
6672	77.03	50.65	17.13	78.82	25.22
12386	77.02	135.03	51.86	227.77	84.85
7223	76.99	367.26	91.11	246.51	70.47
15755	76.95	500.12	167.48	748.54	175.96
17601	76.83	57.78	25.38	103.87	39.5
17766	76.82	612.13	93.59	484.14	91.21
8820	76.67	71.07	30.02	41.75	33.08
11827	76.6	23.35	6.73	39.11	17.22
8212	76.56	2844.24	967.49	1951.8	704.21
3581	76.55	428.5	101.19	306.63	72.34
23445	76.55	100.16	72.37	240.17	130.04
17470	76.27	288.91	122.93	150.05	76.41
5497	76.2	434.15	183.08	649.4	184.65
18989	75.89	2841.79	1727.07	1431.62	573.74
1795	75.75	1189.63	728.56	510.99	334.94
21657	75.61	462.08	165.28	762.09	292.8
16703	75.55	1812.5	580.21	1147.47	357.53
15120	75.49	158.84	36.08	238.23	94.67
9805	75.48	555.5	140.45	386.54	94.93
12155	75.45	2368.04	2360.22	572.57	410.44
15127	75.3	1257.57	486.54	674.31	302.62
23917	75.26	1285.56	577.93	814.72	342
23296	75.25	495.81	137.77	330.23	95.8
4199	75.13	689.15	154.38	899.09	203.59
5496	75.08	323.55	139.72	498.43	153.01
22802	75.03	63.91	24.72	109.02	53.45
5026	75.02	32.08	39.61	122.05	86.86
3121	74.96	1226.38	402.34	804.64	231.33
1479	74.87	200.76	71.6	299.5	94.41
21056	74.79	191.7	54.91	257.01	72.37
9268	74.77		125.35	155.86	54.66
19992	74.76	269.61 881.24	236.92	614.26	213.08
10002	117.10	1001.27	1200.92	017.20	12.10.00

TABLE SLLL: D	ndveer and Live	inemental r	Allo	may Docket 4492	21-5033-01-WO
Timeroing(s): V	artous .				No. 1985323.1
CLCC CLCC	LDA_Score	Tox_Mean	Tox_SD	MonTox_Monh	COS_XOTAON
12156	74.73	2833.78	3074.47	422.63	506.52
17155	74.73	225.73	81.81	135	60.86
14208	74.71	89.89	38.85	142.45	50.46
20698	74.64	563.9	164.59	910.96	450.64
21917	74.62	30.66	14.51	76.73	66.47
15126	74.5	2113.36	872.47	1247.44	500.98
3925	74.45	1123.43	311.95	806.43	297.82
3860	74.44	715.73	289.22	383.81	143.83
14202	74.43	115.02	55.72	56.76	51.95
18295	74.4	72.77	35.66	118.51	48.1
24323	74.38	549.98	139.07	412.1	103.39
22707	74.35	29.28	15.96	53.4	24.1
18867	74.1	661.28	442.42	831.46	209.88
4093	74.06	733.35	154.45	565.09	160.3
9402	74.05	138.18	31.4	189.55	53.15
20914	74.04	1034.46	1047.32	209.39	203.19
11153	74.02	415.59	170.72	639.47	199.55
21382	74.01	124.5	34.9	182.93	63.6
4312	74	289.09	281.36	56.11	138.04
8213	73.98	5073.74	1865.14	3387.66	1342.21
14390	73.98	103.52	18.95	83.06	19.6
18749	73.96	208.45	163.58	57.88	42.14
15872	73.93	310.84	116.91	505.13	168.2
15124	73.81	2066.34	877.47	1326.87	404.07
18726	73.77	249.86	74.81	366.36	114.75
5549	73.71	93.55	51.18	42.99	65.36
15673	73.66	1183.22	314.09	911.4	183.31
3969	73.59	466.47	120.45	575.17	143.79
14586	73.57	552.83	105.46	446.44	96.58
1822	73.52	32.71	13.65	56.48	23.25
3256	73.5	1349.88	363.84	1003.68	275.51
5622	73.49	1210.26	325.65	1608.5	372.01
9296	73.45	927.31	201.31	711.93	160.38
3924	73.44	448.13	107.79	322.57	113.24
20701	73.44	580.85	171.68	893.42	395.57
8036	73.41	121.88	50.9	191.37	67.12
4250	73.41	100.43	28.79	137.62	37.73
1888	73.38	65.91	43.7	31.26	34.19
6941	73.34	109.34	62.47	34.85	59.77
7225	73.34	275.06	61.15	345.74	95.13
16320	73.31	66.47	21.72	100.68	32.33
1588	73.29	160.78	45.74	237.17	84.84
9595	73.29	128.37	36.86	182.28	57.95
21975	73.28	219.86	113.17	270.04	80.28
3963	73.26	340.36	77.76	434.04	
6824	73.25	621.85	260.83	409	111.09 211.56
18900	73.23	1057.41	207.22	797.52	
25056	73.17	2718.94			172.65
12157		3128.89	2431.7	874.2	469.5
11152	73.14 73.12	173.48	3251.72	489.1	646.35
			100.42	339.14	140.77
219//	73.12	579.7	113.74	711.76	222.37

TARIE GIII • In	ndvær end Live	ද පිත්වැගෙනුනෙන් :	<u> </u>	iney Docket 4492	21_570503_01_07767
	Svela Ence			Dogument	
	LDV Score			Nontox_Mean	015
24763	73.1	59.1	26.97	95.2	40.12
1478	73.03	313.56	101.5	426.83	118.62
25069	72.82	578.11	455.6	192.73	229.02
17752	72.78	333.01	91.76	476.24	141.38
20614	72.76	27.97	11.93	46.15	21.49
6911	72.67	177.76	39.76	235.63	75.02
4407	72.5	92.88	31.92	145.8	57.69
23321	72.48	298.34	62.2	235.95	64.35
17154	72.35	255.54	91.83	186.36	78.12
18747	72.28	424.39	283.26	146.69	103.58 ·
1973	72.22	308.28	69.83	394.17	107.1
25087	72.2	40.05	26.66	100.94	76.02
25453	72.19	251.78	62.76	326.09	79.65
1551	72.15	753.2	363.62	1035.27	366.89
5998	72.11	143.33	48.28	203.78	71.4
18725	71.88	128.49	57.46	217.6	84.51
6055	71.73	857.56	258.28	1096.97	228.01
25281	71.66	197.38	56.7	152.9	48.14
16366	71.6	1297.79	498.27	780.6	281.32
7872	71.57	221.32	64.73	296.29	81.79
20913	71.47	1079.76	1404	244.93	188.26
2505	71.46	599.25	149.26	758.23	191.97
12087	71.43	765.1	250.74	1036.17	312.63
20299	71.43	529.36	194.11	732.03	249.09
19679	71.35	246.33	115.64	395.24	139.47
18400	71.29	30.61	11.77	50.59	24.67
7927	71.13	172.46	77.9	289.86	115.85
20429	71.06	409.47	195.57	631.67	259.92
16725	71.06	117.86	29.74	163.47	46
21012	70.93	2131.54	841.59	1497.4	545.85
20354	70.87	21.56	10.92	53.41	60.18
4242	70.85	341.78	186.52	524.19	210.15
9136	70.84	440.83	115.89	334.95	86.57
15980	70.8	47.86	18.25	64.06	23.28
6653	70.66	471.14	123.46	605.45	143.35
19730	70.65	186.08	99.69	318.05	151.39
1312	70.61	742.32	138.77	634.05	136.17
4809	70.58	42.2	10.04	61.08	25.56
64	70.56	101.58	23.87	135.61	44.32
15028	70.47	1368.28	486.36	1761.2	513.47
16217	70.35	362.58	100.1	453.79	152.13
14545	70.27	24.21	8.86	35.48	16.42
16604	70.25	59.25	26.01	86.18	33.88
15996	70.25	29.48	23.7	111.23	139.07
1640	70.24	32.97	13.51	52.85	24.55
15391	70.21	1143.73	271.75	981.39	176.45
25055	70.19	1636.52	2110.72	195.07	298.82
19287	70.16	45.92	15.88	63.95	21.46
10886	70.11	758.51	202.33	984.08	414.2
15601	70.07	438.24	151.02	307.47	75.18
1794	70.05	4051.87	2705.1	2109.88	1144.21

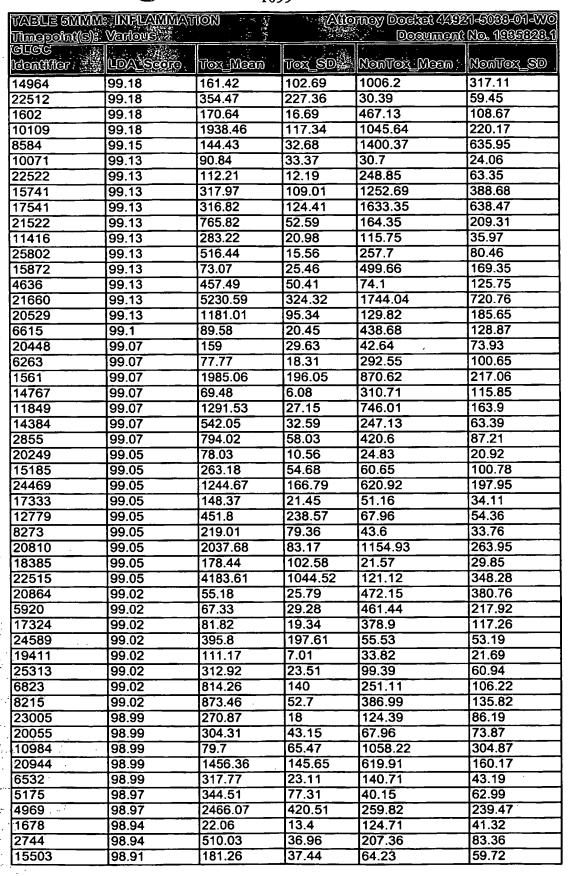
WO 03/064624

PCT/US03/03194

-1097-

TABLE SLUL: D	nducer and Liver	: finemegralai	Affor	may Docket 4482	N-5033-01-WO
Vingeoin((s)): V	arious -		8.4	Document	No. 1935323.1
@E@G	2-12-14-12-12		100000		
	Trany Regions	rox meen :	rox ap	MeeM_xoToox	Koulox 20
4527	70.04	23.15	7.24	33.88	14.38

TABLE SIMM			Alio	may Docket 4402	A-5033-01-WO
Timepoint(s):	Various	:	<u> </u>	Document	No. 1935323.1
CECC Ideniiier	LDA_Scorc	Tox_Meen	Tonger	Meen Tee Thom	NonTox_SD :
4011	99.87	166.43	57.73	1821.45	677.32
21012	99.79	476.81	16.35	1520.39	567.6
16304	99.79	296.61	51.2	1499.52	504.23
634	99.79	224.82	44.49	1536.28	417.92
16726	99.76	297.93	10.7	792.74	196.34
25525	99.76	172.66	36.36	1350.98	364.18
14495	99.74	78.02	13.42	323.78	111.6
24728	99.71	28.74	8.28	261.59	84.08
15	99.71	92.36	1.44	44.8	21,18
2997	99.68	88.08	5.9	375.4	119.98
11904	99.68	268.62	16.95	60.15	42.8
9214	99.66	880.52	97.9	273.93	150.19
18244	99.66	1182.44	47.71	542.72	137.87
635	99.63	188.18	84.64	1577.16	483.16
20872	99.63	1345.63	38.66	763.45	262.47
22598	99.63	3246.17	212.74	992.6	344.02
574	99.6	251.77	18.84	94.44	165.34
23651	99.6	65.74	17.19	20.61	97.18
22042	99.6	6153.73	992.13	233.68	1107.91
9845	99.6	3806.95	827.59	124.33	892.61
16416	99.58	288.07	16.78	108.4	60.71
15004	99.58	1695.49	240.53	236.04	142.5
5059	99.55	324.13	47.19	79.53	249.59
18580	99.55	1019.69	40.31	224.66	139.63
5969	99.52	362.85	61.79	1180.73	390.03
24860	99.5	32.25	5.22	391.3	272.54
4012	99.44	284.76	99.62	2441.81	1157.15
1641	99.44	275.36	14.85	110.29	51.67
9905	99.44	166.04	20.66	648.12	150.08
1600	99.42	80.25	4.34	37.92	93.41
3134	99.39	375.27	108.07	38.07	41.15
20915	99.39	98.85	6.27	536.36	365.97
13563	99.36	455.07	25.07	1185.43	356.64
154	99.36	501.9	58.32	165.9	60.49
20589	99.36	125.48	13.65	25.15	26.99
5967	99.34	203.14	33.53	867.88	367.62
21285	99.34	1157.81	137.93	100.17	161.93
309	99.31	1271.05	75.47	694.09	136.68
9215	99.31	1095.45	215.49	315.14	205.97
25052	99.31	1613.62	302.24	30.62	119.49
1221	99.28	197.14	26.41	32.78	122.89
16367	99.28	137.22	105.71	1420.14	541.97
4914	99.28	47.79	18.73	481.47	150.36
15002	99.26	812.99	200.75	139.85	68.61
16081	99.23	580.07	45.01	127.63	197.04
16366	99.23	126.39	27.16	798.97	303.77
6911	99.23	57.47	6.74	234.1	74.48
1809	99.23	6297.41	1822.96	122.34	681.56
6614	99.23	118.9	26.54	907.33	269.4
18618	99.21	1838.27	88.48	1149.65	214.57
3548	99.21	174.92	5.09	79.79	30.13



TO SUE SMMM	INFLAMMAT	MOI	$\Delta \Omega$	TON DOCKOR (VIEW	M-50683-0M-4WO
TABLE IMMM: Timogoin(S):	Vadors:	0000		mey Docket 4492 Document	No. 1935023.1
CCC CC	STATE .				
ldeniifer	LDA Score	Tox_Moon 🧦	TOX_SD .	MOONTOX_MOON	NonTox_SD.
18001	98.91	196.94	39.51	718.21	179.34
682	98.91	664.18	326.43	109.18	95.85
17284	98.89	66.24	7.09	184.56	54.71
20462	98.89	1386.9	54.08	832.62	161.68
22513	98.89	6801.87	2063.44	24.21	724.48
24228	98.89	1963.56	170.96	977.17	260.22
23825	98.89	98.15	18.36	38.05	25.86
7427	98.86	242.61	40.71	32.31	29.32
18611	98.86	2091.17	198.59	1139.38	540.19
16080	98.83	333.96	51.66	71.05	142.79
20354	98.83	352.09	24.78	51.73	57.92
155	98.83	242.82	80.27	41.45	24.98
5667	98.83	1364.04	112.29	816.08	305.28
18750	98.81	372.57	8.69	246.42	71.72
22321	98.73	445.71	89.53	76.62	108.24
4178	98.73	79.54	11.94	39.39	54.77
10949	98.73	390.51	153.27	1874.53	687.28
18250	98.73	1694.19	100.64	952.01	198.91
12606	98.7	161.97	57.03	741.43	238.52
1893	98.7	164.59	74.91	31.84	31.29
5496	98.68	113.96	19.27	493.5	154.89
20701	98.68	2698.56	266.1	879.33	385.5
1572	98.65	172.32	13.47	73.12	32.33
19469	98.62	124.43	69.52	477.5	113.18
25675	98.62	1145.98	19.45	741.67	207.51
25687	98.62	2034.6	159.67	1275.29	658.59
21643	98.6	1666.53	167.12	891.15	220.23
24771	98.57	119.53	97.47	1109.43	314.81
20523	98.57	316.37	52.14	48.66	67.77
15626	98.57	2208.57	185.27	1329.28	250.81
18989	98.54	247.79	152.33	1480.44	689.51
20716	98.54	776.01	61.15	1643.73	473.59
15652	98.54	2214.91	91.58	1501.41	366.17
20698	98.54	3387.66	619.21	894.32	433.33
2667	98.52	317.82	43.77	809.25	200.01
1550	98.49	50.78	24.28	431.87	211.34

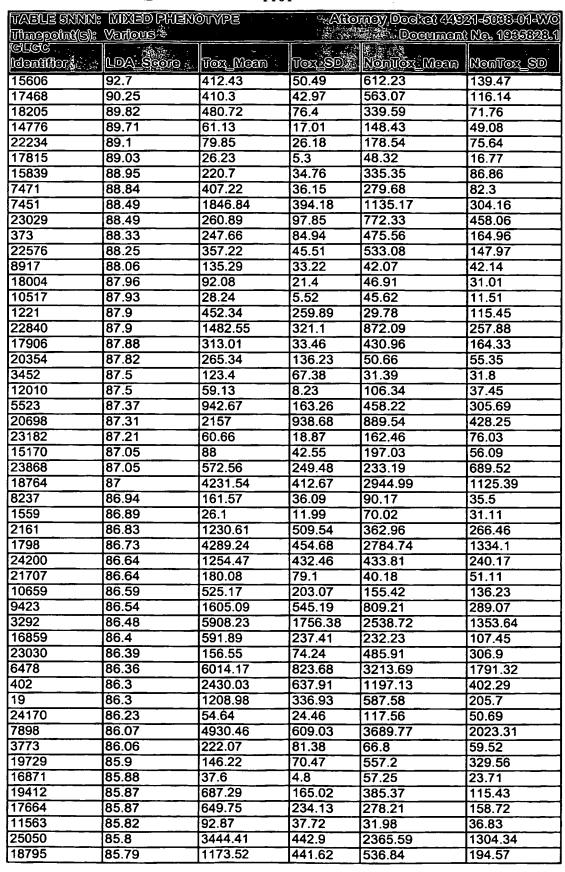


TABLE SXXXX:		DIYPE	Align	mey Docket 44921-5083-01-WO	
Timepoint(s):	Various :	<u>, </u>	2.75	Document	<u> </u>
CCCC	LDA_Score :=	Tox_Meem	Tox_SD.		NonTox_SD 3
3431	85.69	1544.2	194.5	1040.69	310.99
21977	85.61	321.88	154.91	710.51	218.66
13353	85.58	142.6	54.04	286.13	59.76
16446	85.53	33.14	8.85	62.62	20.55
20	85.52	677.77	212.99	344.57	133.55
11727	85.51	305.09	113.65	183.52	242.75
5384	85.5	122.1	52.78	26.76	61.13
11839	85.48	22.4	18.92	72.34	43.16
354	85.27	108.79	27.74	82.01	153.06
20524	85.2	183.57	186.08	22.39	43.23
7897	85.16	5026.51	553.34	3443.12	2129.75
8477	85.07	549.17	155.84	300.32	116.31
1264	85.06	7661.79	1097.37	4248.44	3333.92
22380	85.06	169.47	29.99	268.51	108.89
19012	85.05	770.22	223.05	438.26	162.83
12979	85.02	849.06	213.38	507.28	264.22
12301	84.97	221.22	64.45	137.36	66.49
1114	84.95	784.76	111.17	565.4	206.84
20161	84.89	93.65	43.4	28.67	55.35
18660	84.87	71.79	21.38	129.94	52.56
25237	84.84	27.81	8.21	46.96	14.07
23869	84.81	183.61	109.1	64.33	132.43
13910	84.75	595.17	256.02	334.68	144.63
6109	84.73	5062.67	612.62	3577.61	2270.94
21305	84.71	102.49	19.3	160.21	64.73
11720	84.7	1391.1	372.23	739.89	262.69
15191	84.7	4454.06	1670.95	1196.05	1298.31
16130	84.68	5489.79	1043.64	3516.83	2337.77
16132	84.65	5576.25	699.92	3387.56	2223.54
20778	84.54	42.88	20.91	74.29	18.46
3073	84.5	27.17	17.75	101.86	90.69
22266	84.47	1300.02	172.66	1708.32	355.56
14425	84.46	1582.38	902.47	447.23	425.39
3725	84.36	112.91	46.17	44.27	53.59
14997	84.35	904.57	456.19	284.18	270.05
1350	84.33	64.19	8.94	101.77	31.73
15538	84.28	422.49	51.3	318.33	100.25
17779	84.28	257.98	58.6	403.58	139.36
12083	84.26	116.98	43.39	244.98	116.05
4731	84.24	242.3	152.93	53.19	75.67
14534	84.23	6841.04	941.06	4581.71	3863.48
396	84.22	366.11	76.57	217	87.76
6479	84.17	1948.92	533.14	1036.43	385.69
21209	84.11	390.41	233.24	81.61	78.56
3216	84.1	59.47	12.28	85.97	24.13
19421	84.07	4234.7	478.19	2937.97	1757.49
4746	84.06	72.05	19.08	34.44	29.01
11728	84.04	414.23	112.95	194.29	227.78
25317	84.01	2439.58	494.72	1376.62	460.73
111	83.99	4804.2	499.29	3144.58	2037.61
15189	83.82	5084.12	1961.4	1634.96	1633.37

TABLE SINN: MIMED PHENOTYPE Three Mainte			Aftomay Docket 44221-5033-01-WO Document No. 1935323.1		
(G) _ (G) _ (C)		Tox Mean &	Tox_SD !	Meen Txollwoll	NonTex_SD:
25051	83.8	4432.49	459.55	2679.89	1549.16
16275	83.77	4799.21	631.58	3424.79	2264.62
21098	83.76	2466.39	679.48	1140.37	528.02
16809	83.74	96.71	50.6	29.31	24.93
2368	83.71	735.22	293.69	1084.68	198.83
12082	83.64	121.2	67.54	333.43	159.05
17829	83.64	3573.37	470.6	2364.78	1197.64
14591	83.61	37.32	12.53	70.26	24.38
20700	83.53	4924.3	672.7	2928.32	1593.46
21679	83.4	33.75	12.43	61.77	24.12
1805	83.4	2412.57	518.34	1446.94	630.27
15190	83.26	5503.52	1949.25	1811.64	1683.48
17039	83.24	72.05	12.32	109.04	32.05
19373	83.24	1718.02	400.78	1025.64	514.06
23349	83.1	84.4	16.95	132.91	33.71
21097	83.07	1695.3	601.55	918.24	384.35
25481	83.05	4569.06	559.89	3051.77	1745.38
11966	83.03	196.55	30.4	295.67	95.81
23569	83.02	178.01	61.2	261.45	59.45
4590	83	25.6	14.08	51.57	26.92
25370	82.95	54.43	32.48	157.2	91.71
4213	82.95	7673.5	1203.32	4441.5	3875.31
6477	82.92	3589.01	566.41	2253.93	859.56
23872	82.86	175.04	116.05	73.93	155.07
6013	82.73	2842.65	343.79	1897	624.63
19411	82.72	78.5	28.65	33.63	21.53
20896	82.71	25.99	6.26	51.88	36.56
15387	82.65	680.01	113.62	519.63	120.56
22910	82.63	201.8	41.58	284.3	62.67
15103	82.58	137.13	17.88	179.53	33.01
14139	82.55	33.97	7.23	52.9	18.29
15187	82.44	64.75	13.07	108.77	43.44
18644	82.44	3043.69	500.75	2170.22	809.8
16963	82.39	6828.55	1207.62	4270.05	3536.32
22909	82.36	40.05	10.54	62.52	20.77
9424	82.32	1934.87	554.59	1006.7	372.95
14533	82.31	7970.91	1413.59	5046.93	4888.24
21940	82.23	249.98	44.32	394.32	112.17
1246	82.2	42.58	17.23	78.42	30.36
25883	82.18	2820.03	289.81	2245.09	1055.18
24825	82.12	1465.13	481.46	893.2	387.12
4254	82.07	5999.1	691.12	3997.89	2553.49
1540	82.04	100.84	27.83	161.94	58.63
15017	82.02	5813.73	801.68	3964.02	2711.45
1639	82.01	116.75	34.19	197.38	45.66
2367	81.98	283.22	144.41	398.47	98.14
1558	81.94	43.61	21.04	92.17	40.02
17709	81.93	119.41	59.33	37.46	41.78

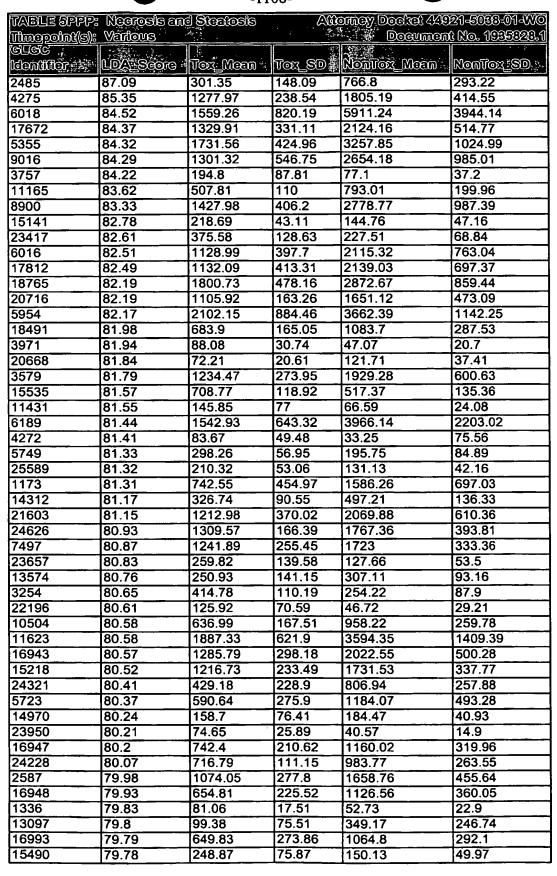
TABLE 5000 Timepoint(s):	D: NECROSIE : Vailous	3	Allon	ngy Docks: 4492 Document	1-5033-01-WO No. 1935323.1
(G.T.G.C.	LDA Score	Tox Mein	Tox SD:	Kontox Medi	
1246	80.45	39.39	19.36	80	29.62
11536	80.41	291.33	76.27	511.85	193.27
24321	79.54	447.79	210.79	817.55	252.02
1973	78.1	263.98	77.84	397.5	104.55
6033	77.89	654.45	220.35	1006.22	265.5
18564	77.81	274.17	84.41	386.79	94.93
4330	77.28	989.08	402.28	1543.74	446.87
22930	77.23	175.96	200.95	556.38	347.59
811	76.99	506.29	141.21	684.41	144.58
21173	76.96	110.85	51.97	199.21	74.6
3431	76.92	1356.96	256.43	1029.63	308.06
12946	76.85	259.09	92.83	353.08	98.59
21977	76.77	449.95	212.02	719.84	213.68
20778	76.44	51.26	16.69	75.14	18.07
15170	76.44	125.27	64.79	199.59	54.12
14767	76.43	188.25	78.17	316.07	114.56
24366	76.25	112.86	47.6	189.63	58.13
22929	76.21	433.57	606.13	1278.77	774.89
6263	75.91	206.22	64.26	296.23	100.65
4951	75.86	402.24	192.51	195.68	151.17
19103	75.83	497.14	189.78	756.27	230.2
9053	75.71	35.84	29.21	76.34	32.18
21025	75.54	37.93	38.95	91.05	50.97
7582	75.31	307.79	140.61	523.74	200.31
22870	75.25	628.86	193.01	903.08	269.18
11492	75.24	348.48	120.69	528.02	156.61
851	75.23	333.37	84.37	441.52	104.61
16465	75.25 75.1	302.33	69.82	412.35	104.75
19952	75.04	76.98	33.9	129.77	51.32
13167	75.04	83.28	25.63	115.5	30.99
3131	75.01	255.27	119.84	444.64	151.26
7344	74.88	117.22	54.42	190.68	59.36
8387	74.88	208.1	69.85	293.14	68.69
10184	74.79	63.35	48.59	124.29	57.96
7865	74.79	1138	246.56	857.72	202.94
1218	74.79	190.49	48.45	246.85	51.16
15755	74.68	581.08	130.93	748.07	179.7
11576	74.57	52.59	26.32	82.34	29.07
24161	74.5	335.75	75.75	466.01	123.48
17496	74.48	81.75	101.41	264.39	179.96
1314	74.45	240.55	55.21		
11635	74.45	203.44	79.24	187.28 295.8	44.13 86.86
9128					
7868	74.36 74.35	162.07	74.39 66.25	107.76 278.63	76 103.55
13757		166.73			
16982	74.33 74.32	138.92	44.46	197.52	51.43
		980.52	742.04	305.56	437.3
8549 22308	74.31	395.79	191.78	674.79	221.08
	74.2	1154.95	310.26	823.85	286.13
410	74.12	112.09	74.23	190.18	89.99
32	74.08	208.2	61.24	301.46	81.89
13749	74.07	26.12	19.62	47.66	23.7

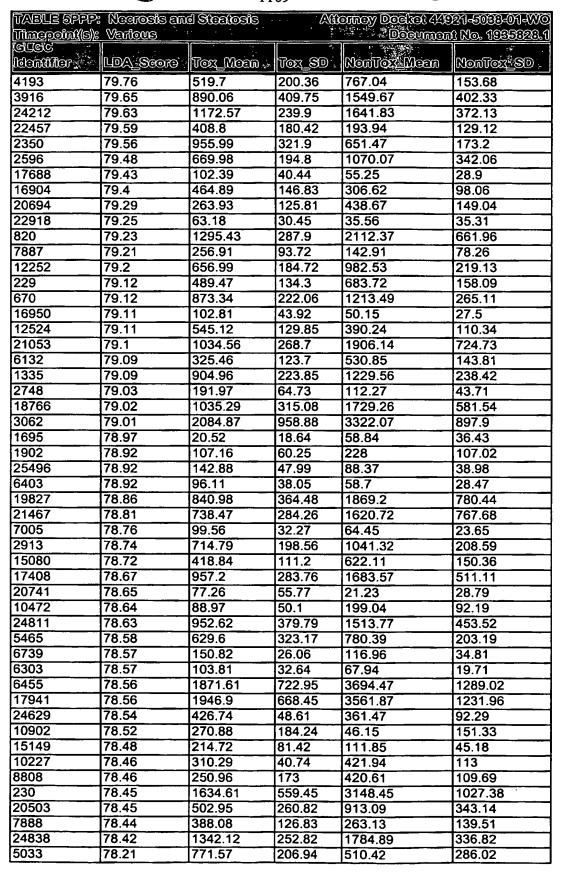
TABLE 5000			a Alloi	may Docket 4492	11-5033-01-WO
Timepoint(S):	: Verious	2 2 3	14.5°	Document	<u>No. 1935323.1</u>
Gentifier ::	LDA_Score	Tox_Mem.	<u>iox</u> ed	NonTox_Meen	NonTox_SD
1125	74.01	20.38	10.72	34.07	13.75
14933	73.98	28.51	16.98	51.9	21.1
16023	73.95	204.97	55.6	309.8	99.75
13670	73.94	72.32	26.53	110.24	33.08
5934	73.9	202.93	127.88	376.18	163.8
2150	73.82	631.27	135.79	789.66	161.38
2569	73.8	596.98	364.62	922.74	277.96
22027	73.72	7999.05	3868.53	8656.82	7794.21
9191	73.71	412.08	197.45	704.92	283.49
25480	73.68	397.65	180.78	615.76	188.42
22368	73.6	884.73	281.5	1207.52	308.66
3822	73.58	1983.36	611.51	1326.85	434.91
20601	73.54	514.03	311.33	990.58	453.58
9754	73.5	93.8	80.91	215.05	132.49
23368	73.49	41.74	20.99	77.78	35.07
11899	73.48	38.09	11.74	54.58	16.56
2897	73.46	64.58	28.75	43.73	24.77
6443	73.45	96.61	42.88	150.93	51.25
14970	73.45	129.9	46.69	186.65	39.82
6582	73.44	179.28	65.91	122.97	84.48
4914	73.44	313.12	147.35	488.63	147.01
7872	73.42	210.94	59.34	297.83	81.21
1409	73.3	297.42	98.63	416.39	111.92
14208	73.24	88.52	42.97	143.24	49.98
2536	73.23	280.92	185.23	612.93	346.5
4143	73.19	358.43	106.11	487.08	139.61
7003	73.19	253.93	118.2	403.22	125.34
14191	73.16	44.12	27.48	69.37	25.86
8520	73.11	287	90.04	384.3	94.24
7617	73.06	159.38	82.91	274.04	129.57
12616	73.05	34.08	21.18	57.16	28.05
25567	73.05	236.85	131.72	140.76	140.59
7069	72.96	228.53	60.85	307.62	74.43
21382	72.94	125.8	40.55	183.68	63.43
22612	72.88	262.18	98.53	353.43	93.14
15154	72.79	486.25	168.22	629.69	171.62
17339	72.7	469.13	284.04	873.43	471.58
13936	72.69	77.55	30.21	111.12	33.34
23124	72.68	147.31	38.13	188.04	38.79
3145	72.63	447.89	142.45	656.97	206.59
18854	72.58	98.61	35.17	145.94	45.17
2799	72.56	270.96	160.36	502.74	222.86
9012	72.56	446.74	225.37	713.11	272.1
18425	72.54	716.49	144.44	895.42	176.96
9423	72.52	1225.33	494.56	795.76	272.54
22197	72.52	274.53	126.51	151.03	80.01
15299	72.49	136.72	99.75	75.53	129.14
25370	72.47	80.14	69.8	160.06	91.19
28	72.45	515.39	249.36	818.4	261.35
22910	72.44	224.23	47.39	286.51	62.19
16327	72.24	393.85	134.63	550.82	156.05

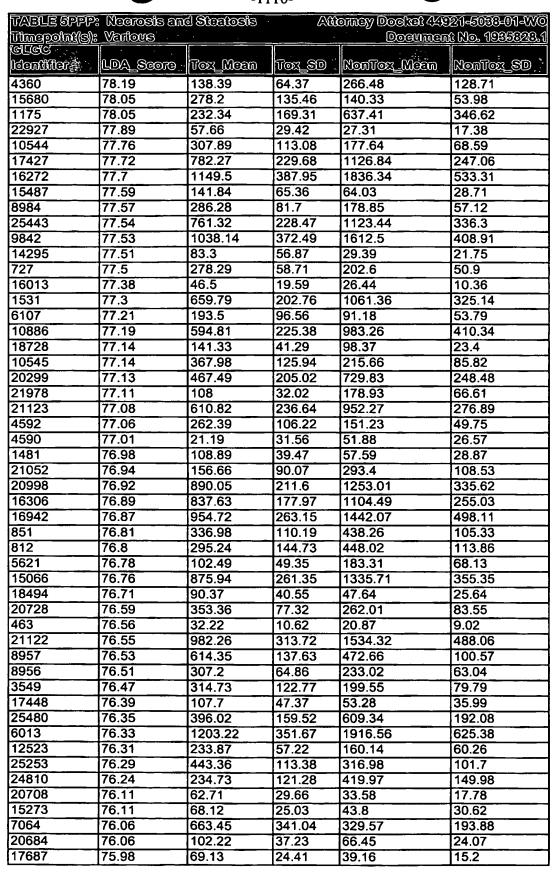
TABLE 5000	DE NEGROSIS			may Docket 4492	
Timegoin((s))	: Various			Document	No. 1935323.1
GEGG Gerijjer 🖫	LDA Score	Tox_Meen	Tox_SD	NonTox_Mean	NonTox_SD
16446	72.17	40.85	16.97	63.43	20.24
17401	72.07	247.03	105.9	442.09	217.8
1920	71.97	847.57	499.56	422.78	238.6
9254	71.86	134.75	39.82	186.06	47.53
24645	71.81	292.07	86.77	402.64	172.03
16450	71.73	155.04	82.99	253.23	90.21
3430	71.73	328.78	135.64	232.03	136.33
4133	71.71	258.76	93.66	380.44	110.36
15642	71.67	614.4	297.65	365.09	141.2
22862	71.58	292.41	156.22	462.12	162.35
22867	71.58	185.61	60.99	253.97	66.01
10509	71.56	86.96	50.74	140.94	53.12
15613	71.55	657.99	361.32	1205.53	818.49
19067	71.55	83.37	36.82	131.66	51.87
19085	71.49	138.9	61.3	84.31	44.17
1529	71.44	441.12	133.23	576.25	124.78
7066	71.4	265.46	71.19	337.12	76.8
18640	71.39	125.78	32.05	160.61	37.92
8438	71.39	58.17	43.6	95.9	44.8
15864	71.33	114.24	40.15	163.06	50.79
18727	71.27	1220.54	500.22	741.86	362.51
134	71.24	55.39	56.81	121.11	50.09
24657	71.19	41.61	24.82	71.32	34.89
16364	71.19	91.83	71.17	183.38	87.03
15700	71.14	334.61	115.23	454.01	121.99
4198	71.13	990.89	309.11	1095.49	227.27
12312	71.1	693.37	278.99	985.63	260.15
21396	71.05	339.39	107.99	474.01	135.61
22582	70.98	302.19	155.45	444.11	139.14
13332	70.92	151.77	67.73	232.77	82.91
21679	70.88	40.37	19.98	62.57	23.89
17468	70.83	462.08	94.5	566.67	115.34
4450	70.81	147.58	43.04	199.33	60.99
64	70.79	89.69	36.94	136.66	43.39
16730	70.78	52.05	33.75	23.72	23.98
1921	70.68	482.04	295.87	202.77	148.18
11966	70.67	209.37	63.32	299	95.26
15188	70.66	160.33	36.04	190	35.08
23524	70.66	102.6	55.19	69.88	66.6
4234	70.62	953.43	414.06	600.02	282.32
4843	70.56	382.91	91.27	493.63	116.68
25550	70.53	66.97	30.39	38.22	23.22
1791	70.5	59.89	15.32	88	34.32
573	70.49	596.83	329.62	907.15	340.47
812	70.47	328.96	109.26	451.05	113.45
15612	70.44	203.85	143.03	456.18	329.95
21980	70.39	435.55	235.06	509.54	157.8
20735	70.37	348.83	188.33	182.25	124.18
18453	70.27	395.8	247.38	654.27	261.72
16449	70.22	164.08	172.17	338.34	187.58
18810	70.2	674.27	122.51	780.88	129.73

-1107-

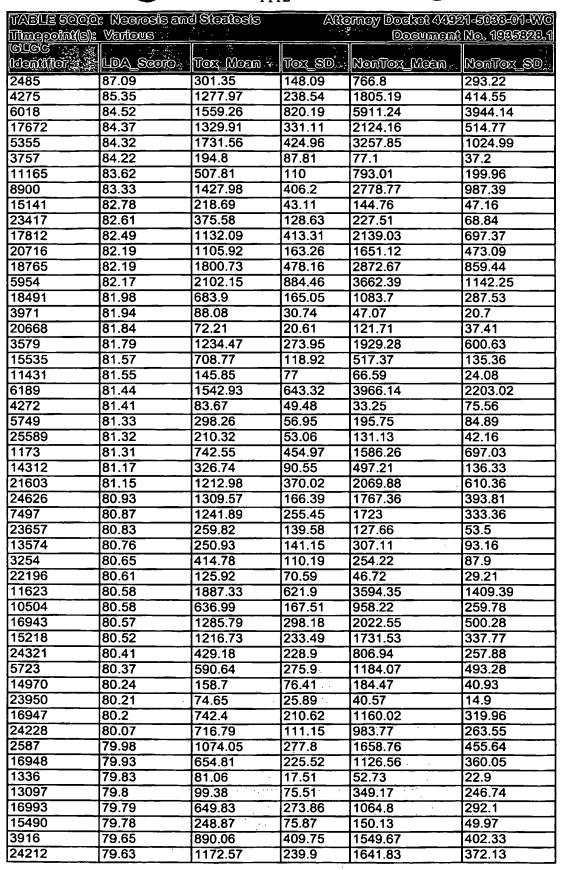
TABLE 5000		}	Vijoù	ney Docker 4492	
Timepoin((S))	Various	å ·	· · ·	Pocument Pocument	No. 1935323.1
(G) C GC	非国家 对。为:	47	ar new	25-1	
. refibinebl	FDW Scoile	Toxi_Woon	TOX_SD.	MEEM_NOTABLE	Noulox SD .
18128	70.14	85.99	30.56	121.64	31.04
3031	70.09	31.34	20.4	66.53	38.85
25701	70.05	105.45	30.26	142.53	47.12

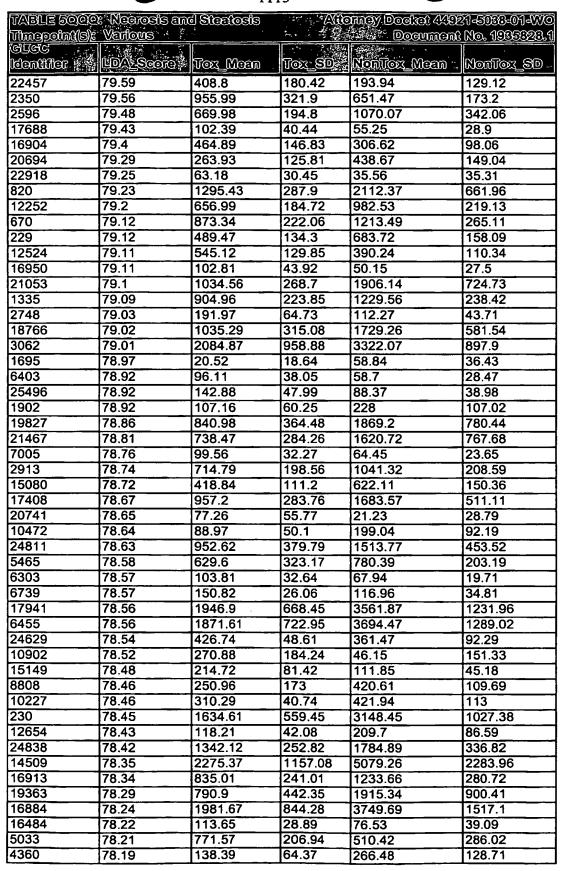






	00.	0.00			0.0000000000000000000000000000000000000
TABLE SPPP:] 2(63(63)2)	AVII (omey Docket 449	271-2020-01-01-0
Timepoint(S):	<u>Varioùs</u>	A 250	· *	<u>Documen</u>	1 No. 1935323.1
(C) C C	No.	j.			
(dentilier 🔭	LDA_Score -	Tox_Moon	Logi [®] Siol	Noulox Weeu	KionTox_SD 🥛
3831	75.95	76.21	49.71	33.73	23.37
24707	75.88	803.26	267.21	1268.52	454.81
1546	75.88	266.24	130.33	301.31	73.82
1447	75.86	299.06	55.12	240.19	59.89
588	75.83	549.32	261.23	944.83	266.61
20464	75.82	1158.23	293.14	1791.43	557.37
15087	75.82	116.15	39.85	80.28	31.73
11405	75.79	76.56	25.67	38.92	19.51
21977	75.78	457.76	166.47	711.73	219.29
32	75.77	240.43	118.96	298.15	82.32
17299	75.77	46.84	19.86	26.78	13.14
23961	75.77	762.83	315.82	1092.98	221.2
2016	75.75	186.11	45.37	130	33.98
21576	75.74	131.37	44.22	79.13	32.62





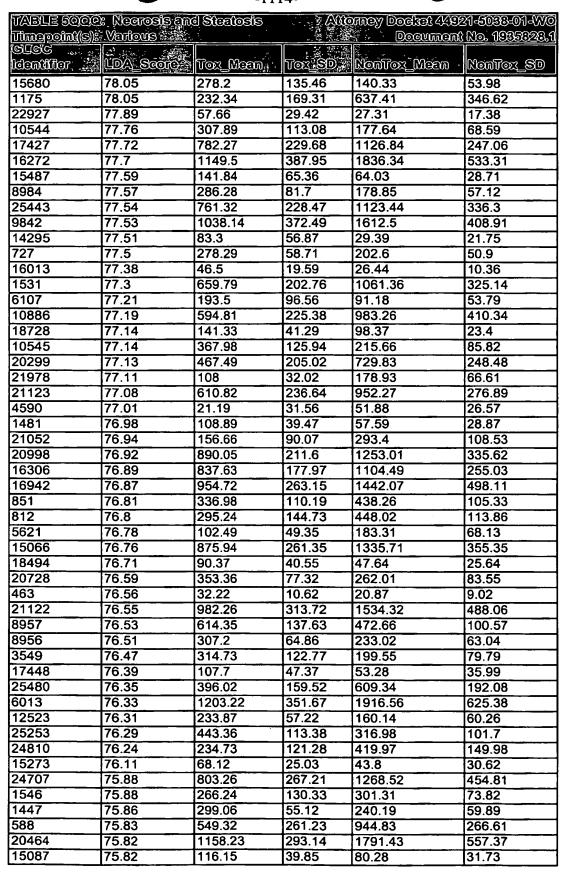
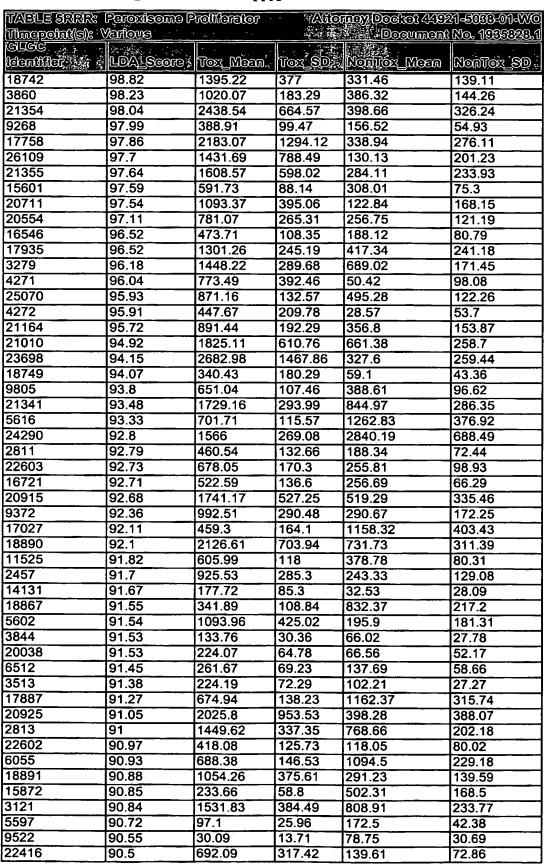
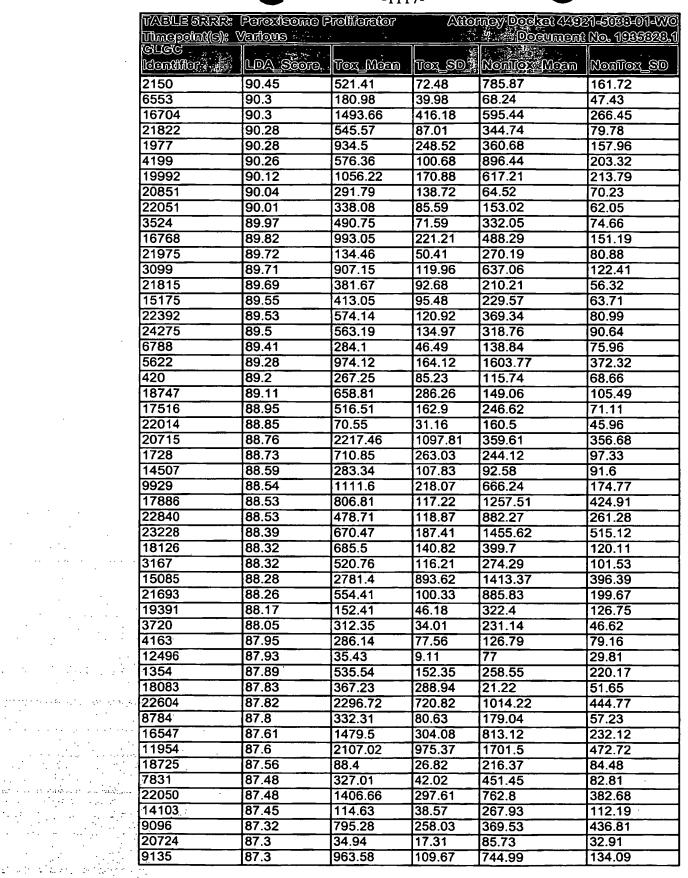
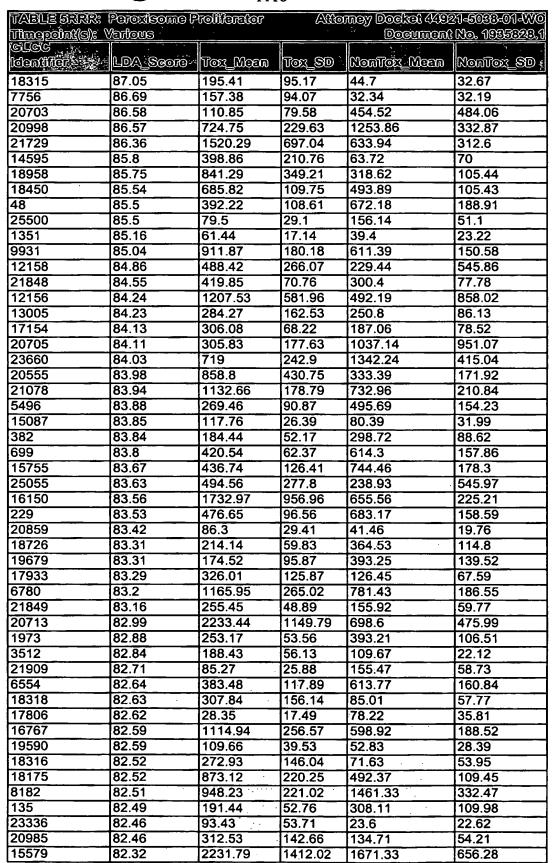


	TABLE 5000: Necrosis and Steriosis Attorney, Docket 44921-5093-01-WO							
Timegoint(s):	Vartious	<u> </u>	X.3	Poeument	NO. 1935323.1			
Conffig.	: OTOOS AU	Tox_Meen	Tox_SD	Meen Toxi	NonTox_SD			
11405	75.79	76.56	25.67	38.92	19.51			
21977	75.78	457.76	166.47	711.73	219.29			
32	75.77	240.43	118.96	298.15	82.32			
17299	75.77	46.84	19.86	26.78	13.14			
23961	75.77	762.83	315.82	1092.98	221.2			
2016	75.75	186.11	45.37	130	33.98			
21576	75.74	131.37	44.22	79.13	32.62			
20801	75.71	174.53	104.38	61.22	43.1			
20715	75.7	631.56	305.69	379.9	431.78			
811	75.64	498.38	186.42	679.27	146.6			
20734	75.63	406.23	226.62	193.81	122.13			
2098	75.63	197.62	62.14	131.89	39.14			
25078	75.6	257.77	72.5	360.32	102.61			









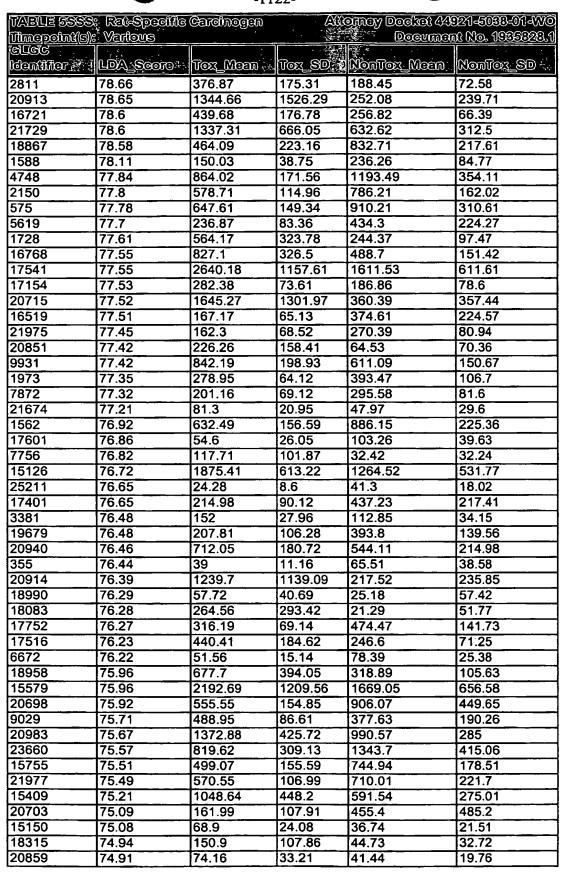
-1119-

TABLE SKRK: The point(s): \	Poroxisomo P Vailous	TOUTON		TOY Doctot 4492	11-5033-01-WC No. 1935323.1
GTGG.	海	FUNCTION FOR	Toz_SD &	NonTox_Mean	
22918	82.15	148.21	76.06	34.53	32.02
1421	82.14	206.14	55.75	137.96	22.3
18509	82.13	365.15	46.59	269.39	57.64
17203	82.09	1014.4	134.98	758.17	175.38
24	82.06	21.95	12.59	53.02	24.96

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TABLE 5888	: Red-Specific	Cardinogen	Atti	omey Docket 449	21-5033-01-WO
Timezoint(s):	. Various	<u> </u>		Documen	11 No. 1935323.1
powyyor * Garac	LDA Scoro ;	Tox_Meem	Tox_SD :	MonTox_Monn	NonTox_SD
20915	93.91	1805.09	604.22	511.5	314.52
16703	88.66	2138.04	506.86	1151	358.58
9268	88.25	336.95	120.8	156.25	54.84
16067	87.61	409.09	114.06	166.21	113.22
14131	87.2	150.18	85.27	32.26	27.88
4199	87.07	611.54	119.74	897.5	203.17
9805	86.93	601.47	126.8	388.13	96.51
24290	86.56	1754.24	422.93	2843.5	688.37
15872	86.1	265.64	82.22	503.15	168.47
9032	85.89	833	120.24	600.82	156.37
7022	85.56	108.49	40.67	36.13	37.46
1354	85.48	489.01	150.84	257.93	220.57
16704	85.15	1320.9	456.21	593.86	265.98
3860	85.1	863.45	299.89	385.85	144.31
18742	83.72	1099.78	570.72	331.3	139.42
20724	83.54	41.06	19.44	85.88	32.9
5496	83.52	283.08	84.44	496.65	154.04
18749	83.4	276.07	184.17	58.8	43.21
23445	83.38	82.35	59.13	238.47	130.21
5497	83.33	389.95	134.98	647.1	186.12
17758	83.32	1635.9	1397.51	339.32	276.79
5622	83.08	1056.24	205.4	1605.61	372.33
4272	83.02	326.33	262.98	28.6	53.81
21355	82.81	1197.89	828.88	284.72	234.39
26109	82.78	1047.85	906.25	130.36	201.6
21354	82.78	1824.88	1133.25	399.24	326.93
3969	82.63	427.9	66.47	574.31	144.07
3279	82.51	1233.57	424.63	688.98	171.78
25281	82.44	206.56	29.85	153.38	48.83
6824	82.41	608.07	167.81	412.35	215.83
20711	82.35	792.82	585.45	123.27	168.49
23698	82.27	2027.31	1621.74	327.27	260
3302	82.2	161.88	45.78	263.17	89.59
7926	82.17	145.03	33.86	94.57	52.51
14202	82.14	125.33	53.49	57.41	52.28
420	82.08	244.09	86.72	115.36	68.51
4291	82.06	143.23	61.43	312.22	138.74
20554	82.03	636.3	323.16	256.65	121.44
4271	81.78				
16547	81.62	550.39	486.67	50.73	98.25
6512		1328.12	373.64	812.39	231.92
21917	81.49 81.42	232.08 27.61	79.58	137.58	58.69 66.21
21341	81.38		11.21	76.12	
22050	81.3	1470.98	486.82	845.07	286.97
16701		1307.01	364.7	761.21	382.02
	81.25	3576.94	1006.26	2250.42	688.67
18747	81.14	540.21	308.81	148.55	105.43
3121	81.14	1370.17	421.73	808.06	233.87
15601	81.14	508.7	154	308.05	75.45
28	81.01	455.22 776.25	163.25	811.05	265.6
25070	80.95	776.25	192.1	495.05	122.45
5046	80.88	40.05	15.39	78.3	42.16

		-11.			
Vinepoint(s):	Ret-Specific Various:		?A00	omey Docket 449 Documen	121-5053-01-WO 11 No. 1995323.1
identijata i ja GTGG	LDA Score i	Tox_Meen	Ton SD	NonTox_Mean	NonToz_SD :
15673	80.85	1200.23	162.33	915.03	191.72
9372	80.84	783.92	415.34	290.82	172.65
8899	80.82	695.06	122.26	910.11	199.42
15146	80.8	124.94	35.52	224.58	111.01
15125	80.79	2526.33	930.66	1632.56	604.59
15127	80.74	1046.44	242.52	686.77	324.88
8315	80.63	205.65	79.92	75.33	61.5
21010	80.54	1512.33	722.25	661	259.12
15033	80.53	483.41	57.93	397.1	82.8
16546	80.52	384.87	171.05	188.26	80.91
8036	80.5	107.25	42.63	190.64	67.22
17935	80.44	1027.75	489.09	417.74	241.61
9595	80.34	116.46	25.48	181.72	57.94
21164	80.27	720.73	321.7	357.14	154.07
20925	80.25	1545.55	1118.98	398.57	388.7
3256	80.2	1363.2	223.24	1008.47	282.45
22602	80.11	346.86	156.71	117.77	80.11
14103	80.1	130.83	53.52	268.45	112.17
6281	80.09	428.91	67.82	322.98	57.65
6055	80.06	755.74	171.13	1095.41	229.36
19992	80.03	961.81	217.4	616.62	214.06
16944	79.95	653.89	186.47	493.26	118.6
17653	79.94	33.67	9.69	61.84	28.94
3963	79.93	305.58	62.1	433.33	110.78
22603	79.9	551.03	249.59	255.93	99.16
3844	79.84	115.57	40.04	66	27.82
3524	79.74	466.11	84.63	331.66	74.43
22416	79.71	533.31	369.04	139.63	73.03
24313	79.63	470.74	59.57	385.82	60.61
18900	79.6	1105.69	187.66	800.38	174.92
4198	79.56	808.6	112	1096	231
4163	79.55	248.62	94.31	126.64	79.23
11827	79.51	24.08	5.69	38.86	17.24
3720	79.5	294.46	48.31	231.04	46.59
21693	79.5	634.8	176.62	886.1	199.83
3513	79.49	186.87	85.46	102.25	27.33
9475	79.48	507.64	185.43	865.8	307.15
2544	79.42	142.29	38.28	223.97	68
12766	79.4	535.24	155.92	819.07	248.03
21676	79.39	56.27	22.06	23.05	23.13
5597	79.39	113.41	35.69	172.6	42.44
4312	79.22	300.11	231.72	59.29	145.18
1977	79.22	751.49	363.3	361.04	158.19
15175	79.14	351.74	129.02	229.74	63.77
1561	79.05	678.96	104.86	876.64	222.96
11525	78.98	543.41	145.13	378.73	80.39
16217	78.91	331.03	49.07	453.05	151.94
9929	78.88	984.42	275.55	666.24	175.2
5616	78.86	798.91	213.64	1264.02	377.29_
12087	78.83	721.43	172.31	1033.05	313.71
25500	78.72	92.72	36.52	156.3	51.14



Timepoint(s):	Rat-Specific Various	<u> </u>		omey Docket 449 	
Gentifier : .	LDV Score:	Tox_Mean	Tox_SD:	Nontroza Meañ	NonToiz_SD
25453	74.79	241.97	69.06	325.2	79.65
17886	74.76	902.13	187.48	1258.14	425.92
17933	74.67	272.09	138.91	126.39	67.68
24	74.6	30.14	19.68	53.04	24.99
8438	74.58	53.2	34.64	94.94	45.26

Timepoint(s):		A	Aïo	may Doctor 449	21-5033-01-WO No. 1935328.1
COMMON :	LDA Section	Tox_Mean	Toxi_SD	Noticia Mean	NonTox_SD ::
23710	99.44	426.99	158.47	39.74	127.2
23711	99.12	1638.85	605.56	175.11	252.99
18383	98.96	1708.97	388.87	745.76	148.48
24799	98.96	1195.6	333.09	301.34	104.38
22204	98.88	738.56	369.62	102.92	76.96
24800	98.78	461.64	85.12	137.87	62.98
21043	98.54	464.68	225.48	71.55	45.75
5339	98.22	1793.4	478.09	496.04	253.26
25805	98.01	132.61	31.16	50.71	18.07
25567	97.66	545.53	171.91	142.84	138.08
20744	96.92	1141.12	158.4	343.95	298.59
11136	96.17	631.45	96.47	314.65	116.78
6044	96.07	1316.46	200.37	751.26	207.08
4355	95.51	133.56	78.66	408.05	114.28
17461	95.43	2844.1	440.98	1402.43	543.42
3917	95.43	2920.63	643.23	1576.49	500
15080	95.37	316.04	55.21	620.44	150.65
7426	95.24	477.73	89.2	292.87	74.23
3944	95.22	198.86	23.52	380.78	282.11
23260	95.06	125.82	46.12	20.66	49.17
23709	94.76	1101.41	241.84	172.11	240.14
7416	94.74	819.53	98.21	1176.85	224.36
24251	94.34	1038.37	755.99	86.17	107.9
24798	94.31	1518.71	252.85	565.68	185.28
22311	94.28	511.57	285.28	179.32	61.1
3498	94.07	300.42	102.94	73.75	48.71
24797	94.07	515.62	308.75	64.38	43.43
957	93.97	264.22	94.11	94.59	44.99
21042	93.91	305.23	110.33	53.99	33.18
15841	93.83	199.05	70.49	58.42	27.28
4155	93.81	249.66	152.06	27.55	32.84
24803	93.81	3007.25	749.04	955.38	309.22
2789	93.78	317.62	114.62	74.43	42.55
3145	93.67	297.63	84.46	649.4	207.49
24801	93.57	1207.19	290.56	446.91	135.33
7642	93.54	67.34	17.76	122.77	35.28
11314	93.51	257.97	67.63	98.13	28.06
2342	93.41	401.37	137.42	134.67	55.66
4154	93.41	555.97	278.15	84.83	71.73
956	93.38	720.99	156.39	298.87	124.24
4725	93.3	579.8	359.59	21.53	107.74
2486	93.22	249.93	52.97	520.51	164.41
6988	93.2	2406.98	1034.92	410.58	325.25
21709	93.17	357.59	73.41	192.65	45.44
357	93.12	231.23	115.1	73.5	31.36
1597	93.12	609.69	268.54	115.4	119.12
6697	93.06	178.7	37.6	75.11	28.96
355	93.06	212.6	98.49	64.16	36.13
4731	93.04	254.16	159.28	53.52	76.17
6295	92.96	2644.86	728.83	1083.65	420
3435	92.93	184.96	25.05	287.41	58.82
0.100	102.00	1.04.00	120.00	1237.71	100.02

Thmerodat(s):	STEATOSIS Various		AMO	may Docket 449 Document	21-5033-01-WO No. 1985323.1
GEGG GEGG	LDA_Score	Tox_Moon	Tox_SD	NonToxi_Mean;	NonTox_SD :
12825	92.88	413.85	151.26	143.86	52.1
21951	92.85	235.98	51.62	104.25	32.95
13686	92.85	103.07	42.55	43.59	16.51
13785	92.85	91.31	36.25	28.32	17.53
21063	92.85	136.54	43.55	45.61	21.99
14997	92.82	813.66	304.23	286.03	274.33
17908	92.8	341.3	138.37	71.19	114.56
20943	92.77	504.3	179.19	266.22	58.79
11992	92.77	67.46	16.69	29.71	12.57
2040	92.74	774.24	317.67	220.97	113.13
4789	92.74	254.77	78.25	69.47	41
5953	92.74	1015.17	452.24	182.21	219.21
17380	92.72	501.31	97.98	259.51	56.66
15642	92.64	808.95	240.2	374.02	156.59
4879	92.5	43.62	17.28	129.37	58.19
12306	92.5	2687.68	503.28	1137.44	517.33
13838	92.5	305.8	60.31	157.62	44.52
3418	92.42	529.23	125.97	288.59	78
18783	92.34	799.23	207.78	388.28	110.02
7745	92.32	303.03	102.02	126.97	55.6
	92.26	557.57	199.34	208.63	88.95
	92.26	208.46	62.82	83.42	35.75
	92.24	233.6	72.24	90.59	42.72
	92.24	1786.46	657.16	555.14	414.33
	92.21	1059.35	415.5	106.33	248.96
13446	92.19	143.37	61.44	33.71	35.39
	92.16	165.73	44.72	72.18	26.43
12119	92.08	360.14	104.12	138.92	67.02
10018	92.08	446.94	151.08	201.19	91.27
	91.97	609.53	157.46	241.55	110.06
8634	91.97	294.7	88.11	115.8	60.8
11997	91.95	481.41	141.93	198.28	83.2
4670	91.95	1831.85	620.15	481.05	417.75
	91.81	785.73	283.53	350.8	158.06
22187	91.79	489.34	68.52	924.01	380.14
	91.79	137.48	48.83	48.4	30.03
25682	91.73	71.76	23.47	31.87	18.4
	91.71	60.23	28.77	167.14	63.23
11533	91.55	146.33	72.7	22.77	54.12
	91.55	606.59	168.59	329.6	87.98
	91.49	139.6	29.05	57.08	32.39
) 	91.44	307.02	105.81	121.33	68.32
	91.41	1422.51	224.04	760.02	380.58
	91.39	114.72	26.66	56.91	23.54
	91.39	163.31	40.52	65.42	44.71
	91.31	352.05	40.06	207.94	64.14
	91.28	318.47	66.17	178.84	58.86
	91.25	733.3	182.64	313.58	160.02
	91.2	264.41	107.68	78.93	76.74
	91.02	53.11	15.17	23.33	12.17
12 1007					36.79

-1126-



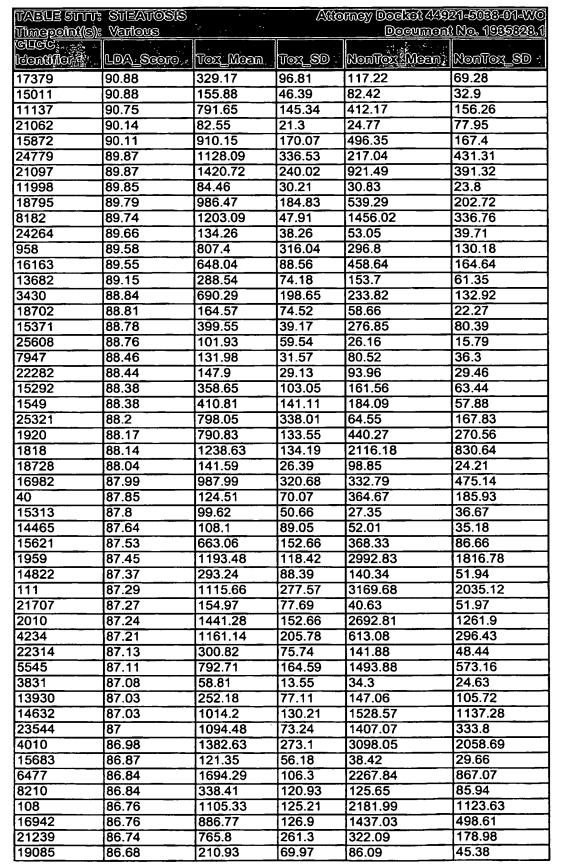
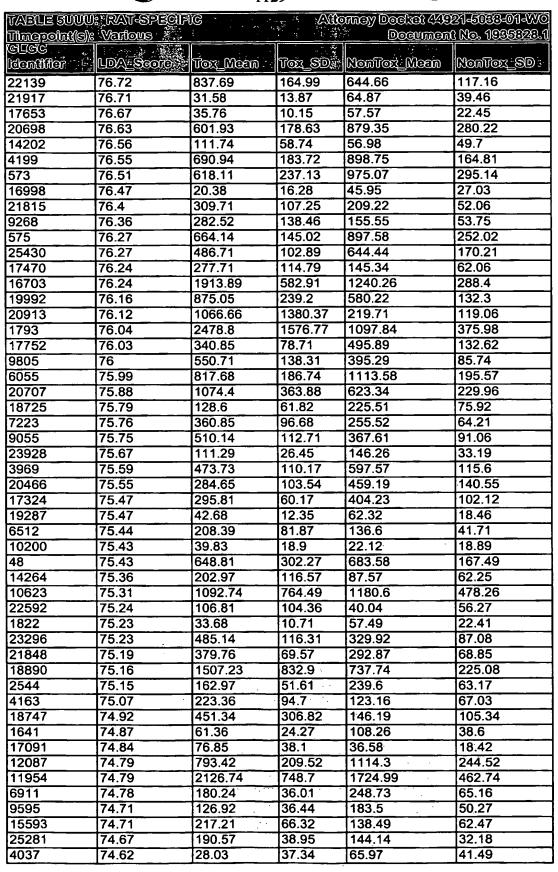
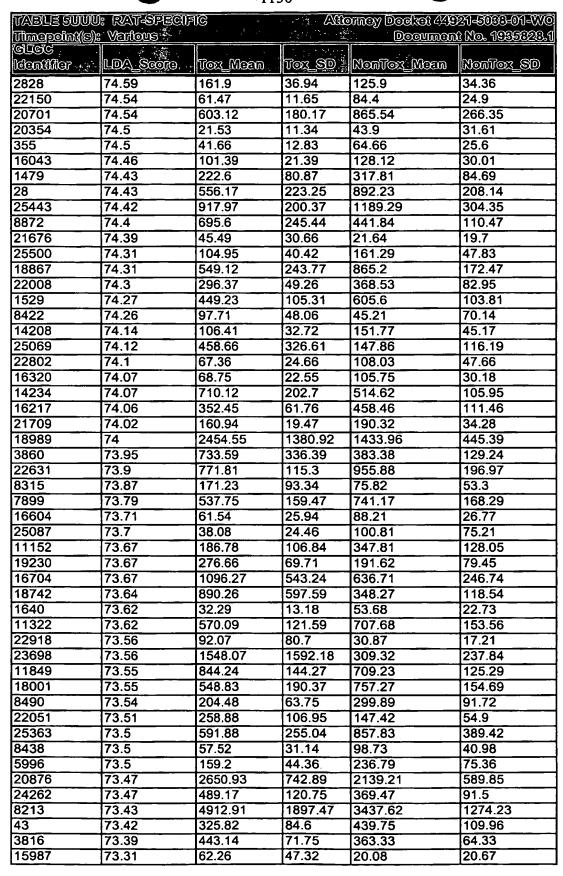


TABLE STU: Timepoing(s):			Affe	mey Docket 449 Document	21-5033-01-WO No. 1935323.1
രിവപ്പ	LDX Scoro	Tox_Mean	Tox_SD:	NonTox <u>#</u> Meen	KonTox_SD #
1798	86.68	1484.39	174.76	2804.34	1336.11
23491	86.66	67.14	20.87	140.44	66.74
22860	86.63	118.74	38.34	54.3	23.7
8211	86.52	1188.67	125.17	2378.65	1113.31
1853	86.52	1338.93	193.22	2982.14	1637.61
2968	86.44	1151.48	133.67	2449.68	1262.65
4012	86.44	1414	214.2	2443.23	1160.81
17306	86.36	1382.22	224.07	2606.3	1273.84
14981	86.34	1141.57	161.43	3446.36	2312.72

TABLE SUUU: RAT-SPECIFIC Timogoim((s): Verious GCGC			Afterney Docket 44921-5033-01-two Document No. 1935323.1		
	: : : : : : : : : : : : : : : : : : :	Tox_Meen	Tox_SD :	NonTox_Meen	NonTox_SD
15125	84.77	2623.95	842.22	1575.67	471.37
20915	84.21	1482.7	752.57	479.62	262.28
1354	84.01	450	153.08	233.59	190.41
6824	83.81	570.81	162.86	351.71	78.39
3256	83.57	1327.42	208.33	955.28	187.49
3121	83.13	1330.48	375.72	836.94	183.13
1795	81.97	1366.31	887.03	488.96	235.87
15127	81.68	1013.56	234.78	633.55	253.76
9475	81.6	554.87	188.47	926.41	276.42
15126	81.56	1930.63	559.32	1189.75	434.61
1794	81.53	5412.3	3108.18	2071.41	743.87
17541	80.76	2645.89	1005.53	1588.11	444.98
20914	80.53	1009.29	1047.24	178.67	134.52
17401	80.2	249.15	110.67	498.58	206.08
9032	80.16	777.18	139.95	567.86	106.91
6281	79.84	410.15	69.85	320.11	51.59
17155	79.8	215.12	68.73	120.66	39.81
5619	79.79	234.51	76.77	428.18	206.04
15872	79.72	316.51	151.16	505.15	145.68
5497	79.52	439.76	156.19	667.03	148.87
23445	79.44	107.93	72.7	261.76	108.44
12071	79.32	437.27	132.16	673.92	155.11
15673	79.32	1145.62	173.26	888.43	148.78
5496	79.04	324.6	106.16	510.54	122.43
3302	78.92	174.53	48.02	254.31	62.31
5622	78.92	1177.98	293.41	1609.15	289
15124	78.88	1906.64	608.89	1304.79	348.07
7926	78.72	145.13	39.34	91.73	48.52
16067	78.6	357.16	134.38	167.5	105.75
8036	78.55	118.43	46.42	195.61	61
18401	78.52	952.54	142.57	761.61	132.38
1551	78.39	726.73	197.84	1088.03	324.71
16519	78.27	172.13	64.03	364.2	199.28
21693	78.04	681.45	178.86	928.07	172.96
24290	77.96	2055.4	647.82	2979.79	584.6
14670	77.92	1672.79	437.76	1140.11	274.32
18749	77.76	223.32	181.08	58.27	43.29
6479	77.71	630.02	288.07	1032.96	330.38
15286	77.67	549.76	79.17	447.88	78.99
14103	77.43	176.73	118.86	297.35	100.28
15755	77.4	544.46	170.72	779.61	143.84
18900	77.28	1056.95	181.06	771.95	138.73
228	77.23	397.22	79.43	512.97	100.94
7022	77.16	86.36	52.28	29.16	25.94
2057	77.16	615.68	202.97	388.23	106.91
25211	76.91	24.5	9	43.05	18.48
5597	76.84	124.85	41.46	179.07	38.09
18726	76.83	251.29	75.38	375.83	101.91
14131	76.8	118.04	90.81	33.66	26.22
5140	76.79	44.4	21.02	74.83	28.36
4198	76.79	853.32	161.43	1091.61	171.92





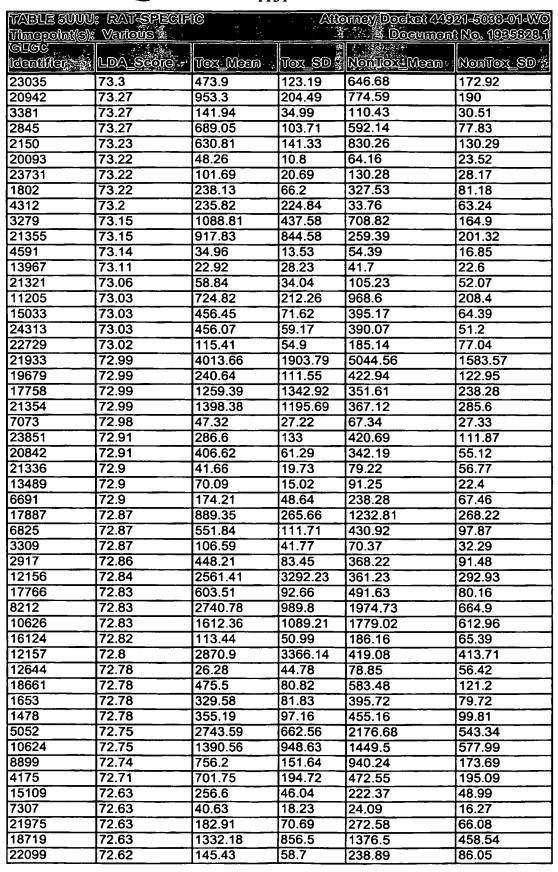
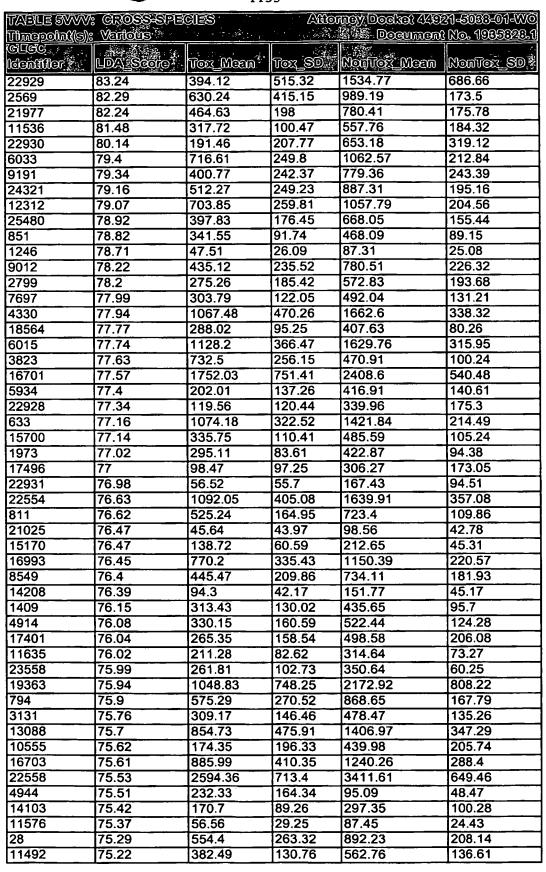
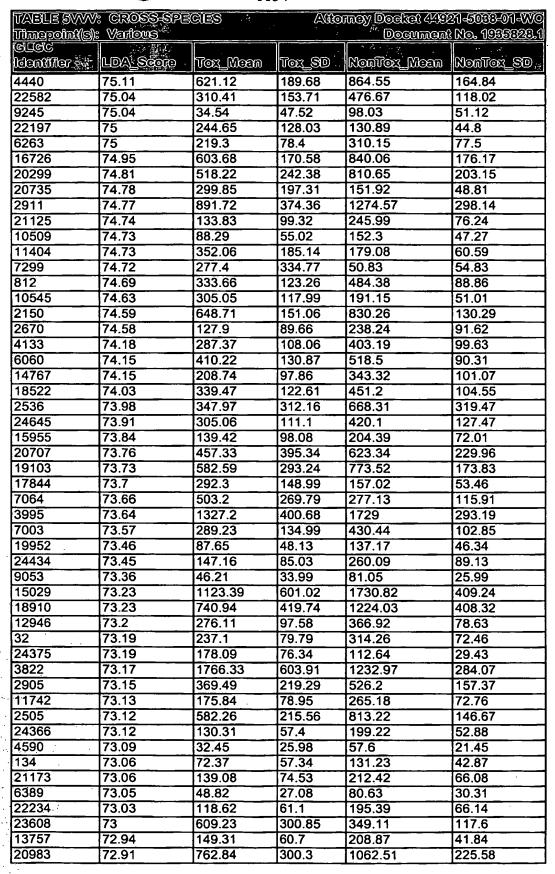
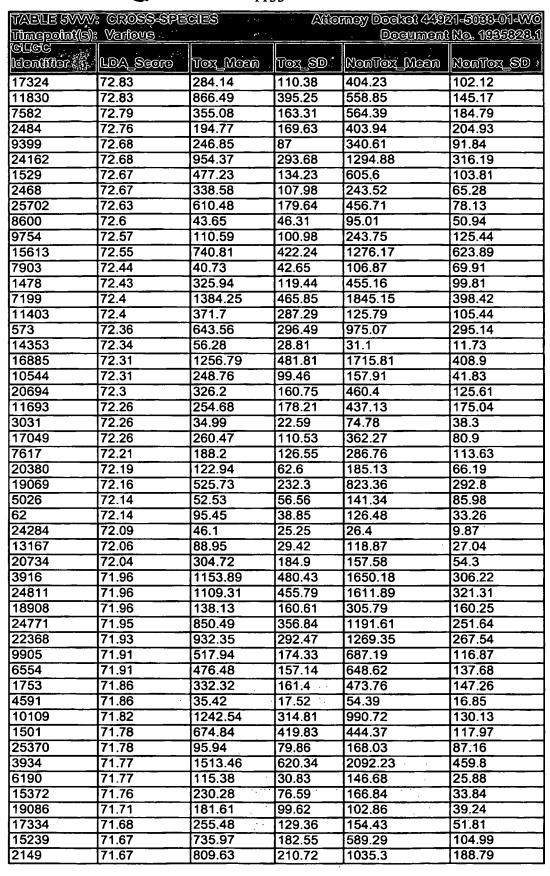


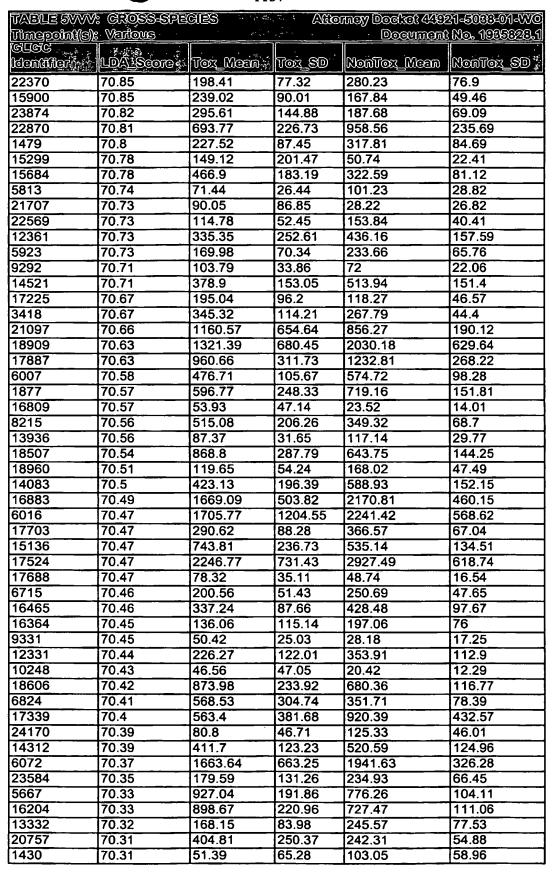
TABLE SUUU: RAT-SPECIFIC Aliomay Docket 44921-5083-01-WO					
Timepoint(s):	Various	<u> </u>		Document	: No. 1935323.1
GCGC :		4.1.3.			1.0
ldentifier :	LDA_Score -	ToxiMean	TOX_SD :	NonTox_Mean;	Moniox SD %
16701	72.59	3333.07	963.58	2408.6	540.48
6598	72.58	105.96	43.94	176.32	75.3
8880	72.58	176.61	92.7	348.91	169.26
14181	72.58	121.73	30.27	163.68	39.99
5877	72.55	257.38	60.52	195.77	52.29
3844	72.55	98	47.59	62.86	23.35
19298	72.55	483.75	222.96	289.1	72.69
18891	72.55	721.37	444.53	298.66	102.51
2588	72.51	163.3	60.42	88.17	53.39
6788	72.51	188.62	118.49	130.87	63.84
4272	72.51	240.67	265.09	23.84	51.73
15181	72.5	54.31	21.75	81.57	24.71







	: CROSS-SPE	GIES	Amo	may Doalet 449			
	goin((s): Various			<u>Doeument No. 1935323.1</u>			
ldowijjer 🔅 .	LDA_Score	Tox_Meen	Tox_SD	NonTox Mean	NonTox_SD		
4134	71.62	714.86	333.09	1003.63	288.21		
7893	71.62	933.46	426	1316.07	348.51		
2822	71.6	113.55	50.74	171.31	50.56		
23075	71.57	262.8	121.45	154.33	70.02		
7665	71.56	281.16	131.36	174.28	48.3		
19085	71.45	126.63	61.48	74.3	28.75		
13353	71.45	230.24	75.26	299.82	49.14		
3365	71.45	630.75	267.71	857.68	194.93		
14007	71.44	158.3	59.36	220.19	55.73		
21978	71.43	124.71	51.41	194.2	62.83		
18792	71.42	122.98	48.22	172.29	40.98		
4951	71.39	347.16	186.61	163.59	126.43		
16982	71.37	846.15	806.61	217.9	292.88		
23445	71.37	144.75	123.58	261.76	108.44		
22867	71.36	200.41	71.94	267.95	56.86		
15089	71.36	253.17	143.75	143.81	54.42		
2762	71.35	701.01	254.53	887.55	200.46		
3431	71.34	1330.63	434.05	979.49	230.62		
20503	71.31	668.44	359.37	995.08	297.94		
24225	71.31	321.66	88.44	397.66	74.06		
14512	71.27	791.91	361.34	1148.03	332.91		
6604	71.26	26.65	19.24	43.55	15.59		
19249	71.24	304.03	147.92	202.74	47.99		
10886	71.24	730.33	287.1	1046.2	292.18		
10984	71.24	802.42	375.97	1112.79	241.21		
13749	71.22	31.36	20.88	50.79	20.84		
14970	71.19	151.93	50.29	192.94	33.17		
16765	71.18	190.04	77.82	257.16	57.64		
24763	71.16	69.62	30.18	99.74	39.5		
3145	71.15	489	190.63	677.04	169.61		
16327	71.11	454.39	198.47	560.99	123.34		
12332	71.1	68.52	126.38	185.76	113.94		
5899	71.1	930.14	413.45	1287.79	254.28		
19729	71.08	303.79	232.82	616.99	311.69		
17591	71.05	175.12	74.27	119.36	24.95		
8829	71.04	286.02	172.15	167.16	55.3		
4670	71.03	901.92	702.31	370.87	215.27		
7243	71.02	78.71	35.67	46.14	16.9		
12958	71.02	838.44	339.37	1212.95	349.39		
2532	71	33.67	79.66	119.79	81.06		
8808	70.98	331.35	127.32	442.27	93.97		
9016	70.97	1847.63	936.34	2925.18	883.92		
7868	70.94	188.55	79.16	296.31	95.77		
5943	70.92	417.65	251.42	723.51	291.6		
10184	70.91	82.54	57.81	132.19	51.45		
8387	70.91	227.23	69.53	308.51	58.02		
12587	70.87	73.09	44.69	118.52	45.74		
1099	70.87	179.35	73.75	239.9	63.52		
14776	70.86	110.07	46.34	159.04	43.79		
11021	70.86	180.38	91.1	281.58	84.48		
7344	70.85	141.54	66.24	199.98	52.69		



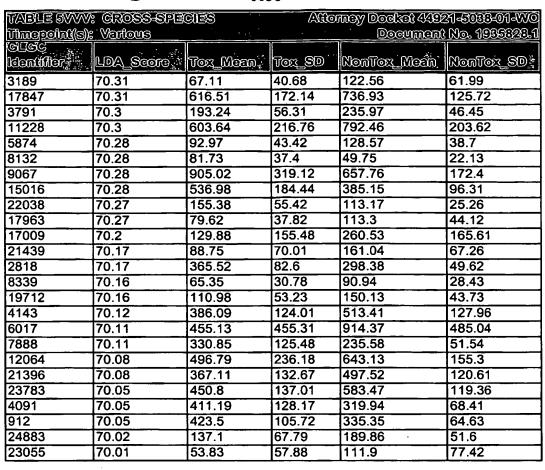
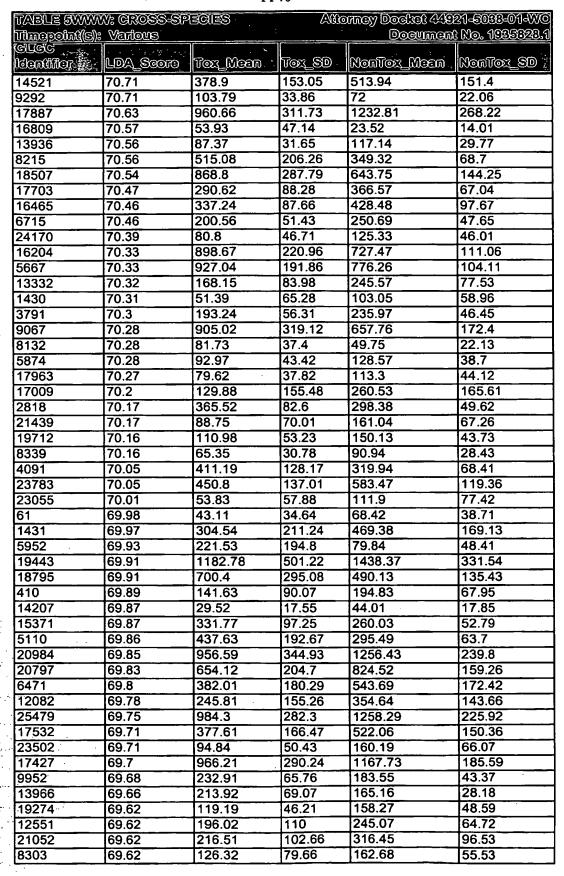


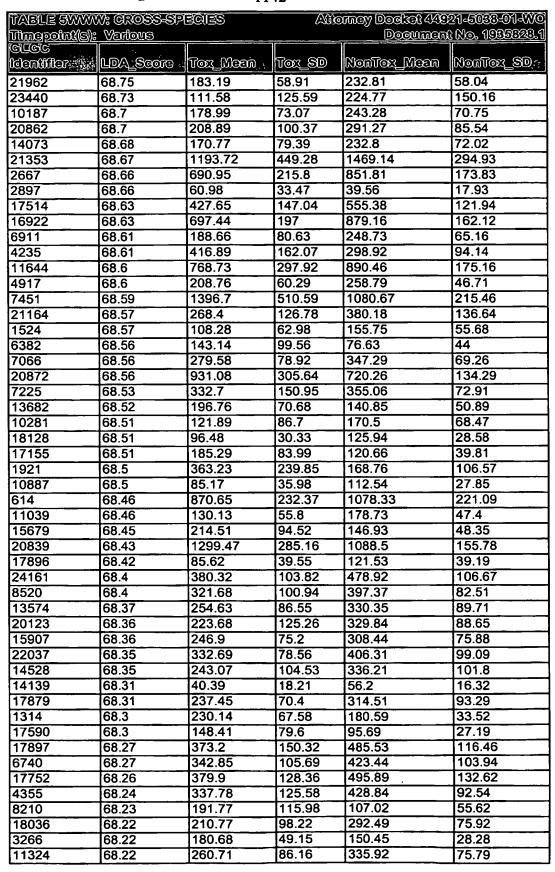
TABLE SWW			Affic	ringy Docket 449	31-5033-01-WO
Timopoint(s):	Various			: Document	No. 1935323.1
powyjoi fo Gree	LDA_Seore	Tox_Moon	Tox_SD	Montox: Mon	Noniox_SD :
18564	77.77	288.02	95.25	407.63	80.26
1973	77.02	295.11	83.61	422.87	94.38
10555	75.62	174.35	196.33	439.98	205.74
28	75.29	554.4	263.32	892.23	208.14
6263	75	219.3	78.4	310.15	77.5
2150	74.59	648.71	151.06	830.26	130.29
2670	74.58	127.9	89.66	238.24	91.62
4133	74.18	287.37	108.06	403.19	99.63
32	73.19	237.1	79.79	314.26	72.46
24366	73.12	130.31	57.4	199.22	52.88
4590	73.09	32.45	25.98	57.6	21.45
21173	73.06	139.08	74.53	212.42	66.08
6389	73.05	48.82	27.08	80.63	30.31
22234	73.03	118.62	61.1	195.39	66.14
23608	73	609.23	300.85	349.11	117.6
20983	72.91	762.84	300.3	1062.51	225.58
11830	72.83	866.49	395.25	558.85	145.17
2468	72.67	338.58	107.98	243.52	65.28
15613	72.55	740.81	422.24	1276.17	623.89
7199	72.4	1384.25	465.85	1845.15	398.42
3031	72.26	34.99	22.59	74.78	38.3
20380	72.19	122.94	62.6	185.13	66.19
62	72.14	95.45	38.85	126.48	33.26
5026	72.14	52.53	56.56	141.34	85.98
13167	72.06	88.95	29.42	118.87	27.04
24811	71.96	1109.31	455.79	1611.89	321.31
4591	71.86	35.42	17.52	54.39	16.85
25370	71.78	95.94	79.86	168.03	87.16
15372	71.76	230.28	76.59	166.84	33.84
2149	71.67	809.63	210.72	1035.3	188.79
4134	71.62	714.86	333.09	1003.63	288.21
2822	71.6	113.55	50.74	171.31	50.56
7665	71.56	281.16	131.36	174.28	48.3
13353	71.45	230.24	75.26	299.82	49.14
15089	71.36	253.17	143.75	143.81	54.42
22867	71.36	200.41	71.94	267.95	56.86
3431	71.34	1330.63	434.05	979.49	230.62
24225	71.31	321.66	88.44	397.66	74.06
10886	71.24	730.33	287.1	1046.2	292.18
19249	71.24	304.03	147.92	202.74	47.99
14970	71.19	151.93	50.29	192.94	33.17
24763	71.16	69.62	30.18	99.74	39.5
12958	71.02	838.44	339.37	1212.95	349.39
8808	70.98	331.35	127.32	442.27	93.97
10184	70.91	82.54	57.81	132.19	51.45
22370	70.85	198.41	77.32	280.23	76.9
7344	70.85	141.54	66.24	199.98	52.69
23874	70.82	295.61	144.88	187.68	69.09
22870	70.82	693.77	226.73	958.56	235.69
15684	70.78	466.9	183.19	322.59	81.12
12361	70.73	335.35	252.61		157.59
12301	10.13	000.00	1202.01	436.16	1107.08





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FARIE GWW	W. ଜନ୍ମରତ୍ର ହେଇ	<i>ર</i> હ્યા <u>ર</u> હ	Acc.	rney Docket 449	21_3022_01_00
Mingpoin((s): Magree 50000		RAIRO RAIRO			31-3185-31-00 3 No. 1935328.1
kandija: Landija:	LDA_Score	Tox_Meen	TOX_SD	MOONTOX_MORAN	NonTox_SD
7552	69.61	792.63	288.39	1042.29	230.88
3082	69.61	335.18	154.07	235.56	55.03
17104	69.6	667.73	196.44	505.08	94.35
7161	69.6	68.88	37.85	41.45	18.15
24290	69.6	2380.88	624.58	2979.79	584.6
23299	69.55	308.22	214.74	162.06	61.66
22060	69.52	157.67	57.22	214.67	62.93
2544	69.51	171.6	57.05	239.6	63.17
20778	69.49	61.34	20.43	77.02	17.03
20601	69.49	641.69	413.94	1060.41	403.83
5711	69.39	845.94	316.64	1151.27	304.37
8728	69.38	118	60.59	75.18	23.27
5608	69.38	147	55.51	103.48	25.47
8837	69.35	182.4	64.43	227.91	46.54
2140	69.29	64.21	59.65	97.81	49.35
23035	69.28	575.28	335.09	646.68	172.92
25701	69.28	110.34	41.63	149.74	44.71
20743	69.27	113.27	37.09	148.87	33.69
3032	69.27	92.49	64.8	165.88	78.14
2539		66.69	66.82	21.43	23.35
	69.26		600.72	1250.16	738.73
11191	69.24	623.1 415.77		549.44	138.08
2486	69.23		170.38		
10985	69.23	478.12	166.28	614.37	116.86 271.08
25039	69.22	762.14	293.16	1032.96	
4650	69.21	104.52	71.46	53.88	49.17
18434	69.21	639.89	257.21	839.13	216.35
16449	69.18	211.57	186.98	362.39	155.56
4588	69.09	33.17	14.98	43.74	11.79
23124	69.09	163.15	48.22	193.9	33.95
2242	69.09	2594.76	1333.11	2431.24	702.72
5465	69.08	649.21	200.8	814.17	179.49
7134	69.08	122.91	39.59	158.86	40.4
6629	69.03	352.77	98.64	436.59	94.79
10562	69.02	170.94	63.73	221.77	54.11
16450	69	185.48	93.27	265.68	79.3
22584	68.99	27.24	15.48	40.72	17.62
26123	68.98	403.94	224.97	248.33	85.97
4866	68.94	323.56	220.59	407.79	144.67
14520	68.92	718.89	287.37	929.15	271.99
3202	68.9	312.29	148.94	204.06	59.69
6638	68.9	62.37	36.79	86.23	25.38
5466	68.87	142.15	56.41	100.61	24.64
23626	68.86	201.12	116.89	120.63	56.66
23192	68.81	277.27	117.81	196.73	57.65
4205	68.8	291.77	147.91	182.61	54.27
11561	68.8	222.61	82.98	161.97	43.32
8715	68.78	1933.02	1288.57	1534.57	369.02
22196	68.78	74.28	48.92	39.71	17.41
12639	68.77	1220.95	226.32	1066.08	134.55
15398	68.76	120.19	79.21	64.19	37.26
1846	68.76	489.04	119.47	574.7	96.78
1.070	190.70	1,00.04	11.10.71	1-,	1909



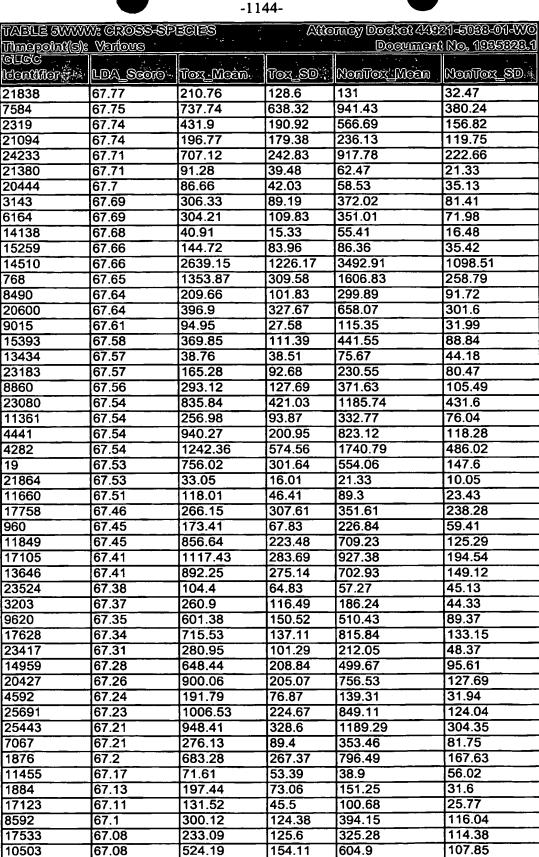


-	-112	, , , , , , , , , , , , , , , , , , ,		
V: CROSS-SP	EG(ES		may Docket 4492	21-5033-01-00
Various				No. 1935323.1
		. The		
	Tox_Moon -	Tox_SD 🕻	NonTox_Mean	Kovilox 20 4
68.19	135.62	62.17	177.96	51.29
68.19	371.95	133.14	281.27	62.96
68.19	79.42	28.99	105.75	30.18
68.18	168.56	77.4	225.51	75.92
68.17	1100.95	327.81	1091.61	171.92
68.17	134.98	49.93	165.98	43.79
68.14	269.91	98.59	196.18	57.35
68.14	207.15	63.56	156.69	36.59
68.14	385.05	87.95	476.29	94
68.12	186.7	104.72	274.46	97.23
68.1	631.68	410.82	352.05	127.82
68.1	243.93	91.51	169.17	69.36
68.1	122.48	84.05	183.46	74.07
68.09	157.75	80.37	104.74	48.03
68.09	421.66	118.6	517.97	107.18
68.05	100.57	53.04	139.26	48.14
68.05	401.43	109.81	326.56	59.27
68.03	886.8	306.99	1156.6	282.66
68.02	710.49	249.13	560.27	145.63
68.01	516.14	177.77	395.17	73.1
68.01	131.87	66.18	182.42	58.29
68.01	891.2	333.93	645.16	125.31
67.97	292.82	150.13	456.25	128.79
67.97	260.2	118.71	181.9	54.89
67.96	387.64	145.8	480.23	103.61
67.96	135.08	93.35	84.96	51.74
67.95	764.29	177.53	623.69	117.53
67.93	149.32	111.95	147.29	46.36
67.93	124.59	57.39	79	24.79
67.93	634.23	157.53	521.34	86.23
67.93	409.47	130.12	311.61	84.62
67.92	416.69	253.9	243.35	93.43
67.91	556.84	225.64	400.85	111.76
	119.69	68.66	181.52	65.2
67.89	128.84	144.38	36.23	30.29
67.89	688.28	367.64	1176.91	592.79
67.89	864.85	232.74	1019.13	201.64
	27.56	21.39	39.68	16.88
67.88	69.13	23.41	50.93	18.64
67.86	663.36	386.93	367.41	181.89
	110.77	40.71	80.47	24.88
	654.52	529	312.94	161.72
	404.48	194.32	254.8	98.77
67.82	224.45	103.51	153.06	51.22
67.82	85.24	34.32	115.46	30.25
67.82	70.89	64	26.57	37.27
67.81	426.5	191.71	281.27	81.11
67.81	151.79	182.36	402.11	309.52
67.81	102.58	60.82	62.89	27.41
67.78	915.55	270.61	1159.37	250.96
67.77	59.12	28.57	39.52	15.32
	Various 68.19 68.19 68.19 68.17 68.17 68.17 68.14 68.14 68.14 68.12 68.1 68.1 68.09 68.09 68.09 68.05 68.05 68.01 68.01 67.97 67.97 67.97 67.97 67.96 67.93	Various Var	Name	CROSS-SPECIES

20755

67.06

108.77



40.79

121.18

20.85



TABLE SWW	V: CROSS-SP		Allo	may Dockot 4492	X1-5033-01-WO
Timepoint(s):		4,41%	The State of the s	<u>Document</u>	No. 1935323.1
Maniffer I	LDV._S0010 ::	meeld_xoT	Tox_SD.	HoonTox_Moon	KonTox_SD :
1801	67.05	80.93	38	58.49	13.68
17684	67.05	277.13	115.19	335.97	75.04
228	67.04	430.29	134.04	512.97	100.94
4450	67.02	158.06	59.2	205.63	53.79
13282	67.02	177.9	79.38	243.36	70.87
11966	67.02	242.44	73.67	303.73	74.19
15291	67.01	96.86	53.21	62.38	19.96
1546	67.01	261.52	83.92	312.59	65.76
16306	66.99	962.35	308.44	1149.73	219.02
1867	66.99	752.96	205.36	598.57	131.93
22927	66.99	40.88	25.81	23.29	11.74
23166	66.99	232.45	97.58	162.7	51.7
4451	66.98	210.67	85.74	279.48	77.2
2079	66.98	195.85	68.11	229.68	54.62
18349	66.97	91.09	56.53	57	16.75
9423	66.9	1057.08	514.83	774.04	189.98
19824	66.89	289.5	177.58	408.58	150.59
7872	66.89	249.18	74.82	309.91	69.56
20466	66.88	351.24	138.81	459.19	140.55
21693	66.87	753.8	200.49	928.07	172.96
1548	66.87	557.12	146.84	674.13	116.09
12606	66.79	621.18	287.04	774.78	201.18
4449	66.79	182.55	79.34	251.5	78.17
1928	66.79	236.45	106.82	304.98	83.91
20464	66.77	1529.62	469.75	1893.1	544.17
25078	66.73	298.95	95.41	381.76	95.92
15292	66.7	213.86	99.54	146.93	34.99
16947	66.69	935.36	340.75	1225.46	279.74
17894	66.68	63.47	35.12	44.27	12.96
17739	66.62	327.62	158.91	473.82	169.89
21950	66.54	591.42	162.54	722.6	133.4
64	66.53	106.64	45.7	142.61	39.25
797	66.48	33.59	18.66	21.12	10.22
4234	66.47	811.89	366.43	568.15	259.91
17394	66.45	430.68	162.8	313.15	83.46
20716	66.45	1369.01	385.55	1726.3	418.55
6108	66.42	138.02	56.31	101.93	28.25
19825	66.41	266.04	171.17	390.25	148.94
18038	66.41	197.25	91.33	261.09	81.35
20430	66.39	605.69	381.32	883.43	355.77
3244	66.39	59.66	21	73.82	18.62
355	66.39	70.96	66.99	64.66	25.6
20056	66.35	90.58	34.47	114.44	29.89
1562	66.34	747.81	250.42	929.74	181.21
23854	66.34	553.01	193.42	421.19	115.14
18299	66.32	121.08	27.91	100.58	18.9
16610	66.28	198.74	109.91	131.99	52.47
23202	66.28	104.82	47.11	128.44	35.84
24885	66.23	1023.96	260.94	855.24	149.18
2192	66.23	52.33	26.61	34.72	15.08
10185	66.23	61.21	41.3	90.19	37.18



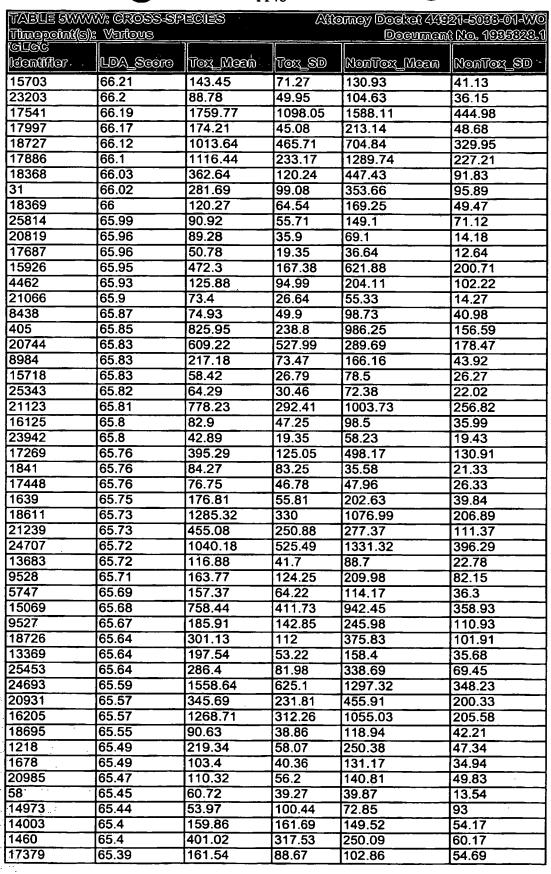


TABLE 500000: GROSS-SPECIES Altorney Docket 44921-5093-01-00				21-5033-01-WO	
Timepoint(s): Various			Document No. 1935323.1		
(G) CGC					
ldendifier	LDA_Score .	Tox_Meen	TOX_SD	MOONTOX_MOON	NonTox_SD :
20986	65.38	233.32	122.44	359.92	161.6
24019	65.35	42.24	35.05	20.47	16.32
22321	65.33	163.77	229.38	56.29	25.91
20	65.32	436.74	195.19	326.74	105.14
70	65.31	401.51	167.75	499.1	122.27
21975	65.27	258.36	101.5	272.58	66.08
15378	65.26	99.27	39.13	124.82	35.27
8267	65.24	703.24	383.23	973.99	404.92
15175	65.23	195.72	64.31	238.77	56.67
494	65.22	24.44	32.56	46.1	33.38
1694	65.19	1206.41	266.14	1040.67	177.4
19543	65.18	57.88	22.48	44.67	24.04
20844	65.18	809.4	218.34	681.31	144.38
17962	65.16	60.01	23.14	76.18	26.95
24657	65.16	53.84	32.67	75.25	31.19
22862	65.16	373.99	171.99	470.34	124.66
19745	65.16	63.45	27.98	46.34	14.67
3071	65.12	71.42	31.53	51.03	17.31
15654	65.1	378.32	147.51	303.37	91.13
17531	65.1	635.42	193.54	804.08	204.83
12083	65.09	189.53	108.48	258.03	109.22
17512	65.06	382.5	92.9	437.7	86.56
1521	65.05	202.1	111.43	137.4	51.17
25687	65.05	1428.29	309.52	1220.32	198.1
5496	65.04	427.7	199.98	510.54	122.43
13480	65.04	618.09	187.25	751.59	169.92
16257	65.02	404.02	145.61	520.25	157.53
11170	65.01	724.71	233.25	596.8	121.58

WE CLAIM:

- 1. A method of predicting at least one toxic effect of a compound, comprising:
- (a) preparing a gene expression profile of a tissue or cell sample exposed to the compound; and
- (b) comparing the gene expression profile to a database comprising at least part of the data or information of Tables 1-5.
- 2. A method of claim 1, wherein the gene expression profile prepared from the tissue or cell sample comprises the level of expression for at least one gene.
- 3. A method of claim 2, wherein the level of expression is compared to a Tox Mean and/or Non-Tox Mean value in Tables 1-5.
- 4. A method of claim 3, wherein the level of expression is normalized prior to comparison.
- 5. A method of claim 4, wherein the database comprises substantially all of the data or information in Tables 1-5.
- 6. A method of claim 1, wherein the tissue or cell sample is a liver tissue or liver cell sample.
- 7. A method of predicting at least one toxic effect of a compound, comprising:
- (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW; wherein differential expression of the genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW is indicative of at least one toxic effect.
- 8. A method of predicting the progression of a toxic effect of a compound, comprising:

- (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW, wherein differential expression of the genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW is indicative of toxicity progression.
- 9. A method of predicting the hepatotoxicity of a compound, comprising:
- (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW, wherein differential expression of the genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW is indicative of hepatotoxicity.
- 10. A method of identifying an agent that modulates the onset or progression of a toxic response, comprising:
 - (a) exposing a cell to the agent and a known toxin; and
- (b) detecting the expression level of two or more genes from Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW; wherein differential expression of the genes in Tables 1-3 is indicative of toxicity.
- 11. A method of predicting the cellular pathways that a compound modulates in a cell, comprising:
- (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW, wherein differential expression of the genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW is associated the modulation of at least one cellular pathway.
- 12. The method of any one of claims 7-11, wherein the expression levels of at least 3 genes are detected.

- 13. The method of any one of claims 7-11, wherein the expression levels of at least 4 genes are detected.
- 14. The method of any one of claims 7-11, wherein the expression levels of at least 5 genes are detected.
- 15. The method of any one of claims 7-11, wherein the expression levels of at least 6 genes are detected.
- 16. The method of any one of claims 7-11, wherein the expression levels of at least 7 genes are detected.
- 17. The method of any one of claims 7-11, wherein the expression levels of at least 8 genes are detected.
- 18. The method of any one of claims 1-3, wherein the expression levels of at least 9 genes are detected.
- 19. The method of any one of claims 1-3, wherein the expression levels of at least 10 genes are detected.
- 20. A method of claim 7 or 8, wherein the effect is selected from the group consisting of carcinogenesis, cholestasis, hepatitis, liver enlargement, inflammation, liver necrosis, liver steatosis and peroxisome proliferation.
- 21. A method of claim 9, wherein the hepatotoxicity is associated with at least one liver disease pathology selected from the group consisting of carcinogenesis, cholestasis, hepatitis, liver enlargement, inflammation, liver necrosis, liver steatosis and peroxisome proliferation.
- 22. A method of claim 11, wherein the cellular pathway is modulated by a toxin selected from the group consisting of acetominophen, 2-acetylaminofluorene (2-AAF),

acyclovir, ANIT, AY-25329, BI liver toxin, chloroform, bicalutamide, carbon tetrachloride, chloroform, CI-1000, clofibrate, colchicine, CPA, diclofenac, diflunisal, dimethylnitrosamine (DMN), dioxin, 17α-ethinylestradiol, gemfibrozil, hydrazine, indomethacin, LPS, menadione, phenobarbital, tacrine, thioacetamide, valproate, Wy-14643 and zileuton.

- 23. A set of at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW.
- 24. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 3 genes.
- 25. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 5 genes.
- 26. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 7 genes.
- 27. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 10 genes.
- 28. A set of probes according to any one of claims 23-27, wherein the probes are attached to a solid support.
- 29. A set of probes according to claim 28, wherein the solid support is selected from the group consisting of a membrane, a glass support and a silicon support.
- 30. A solid support comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW.

- 31. A solid support of claim 30, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.
- 32. A solid support of claim 31, wherein the array comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.
- 33. A solid support of claim 31, wherein the array comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.
- 34. A solid support of claim 31, wherein the array comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.
- 35. A computer system comprising:
- (a) a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW; and
 - (b) a user interface to view the information.
- 36. A computer system of claim 35, wherein the database further comprises sequence information for the genes.
- 37. A computer system of claim 35, wherein the database further comprises information identifying the expression level for the set of genes in the tissue or cell sample before exposure to a hepatotoxin.
- 38. A computer system of claim 35, wherein the database further comprises information identifying the expression level of the set of genes in a tissue or cell sample exposed to at least a second hepatotoxin.
- 39. A computer system of any of claims 35-38, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

- 40. A computer system of claim 39, wherein the external database is GenBank.
- A method of using a computer system of any one of claims 35-38 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW, comprising:
- (a) comparing the expression level of at least one gene in Tables 1-3 in a tissue or cell exposed to a test agent to the level of expression of the gene in the database.
- 42. A method of claim 41, wherein the expression levels of at least two genes are compared.
- 43. A method of claim 41, wherein the expression levels of at least five genes are compared.
- 44. A method of claim 41, wherein the expression levels of at least ten genes are compared.
- 45. A method of claim 41, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level when exposed to a toxin.
- 46. A method of claim 10, wherein the known toxin is a hepatotoxin.
- 47. A method of claim 43, wherein the hepatotoxin is selected from the group consisting of acetominophen, 2-acetylaminofluorene (2-AAF), acyclovir, ANIT, AY-25329, BI liver toxin, chloroform, bicalutamide, carbon tetrachloride, chloroform, CI-1000, clofibrate, colchicine, CPA, diclofenac, diflunisal, dimethylnitrosamine (DMN), dioxin, 17α-ethinylestradiol, gemfibrozil, hydrazine, indomethacin, LPS, menadione, phenobarbital,

tacrine, thioacetamide, valproate, Wy-14643 and zileuton.

- 48. A method of any one of claims 7-11, wherein nearly all of the genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW are detected.
- 49. A method of claim 48, wherein all of the genes in at least one of Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW are detected.
- 50. A kit comprising at least one solid support of any one of claims 30-34 packaged with gene expression information for said genes.
- 51. A kit of claim 50, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a hepatotoxin.
- 52. A kit of claim 51, wherein the gene expression information is in an electronic format.
- 53. A method of any one of claims 7-11, wherein the compound exposure is in vivo or in vitro.
- 54. A method of any one of claims 7-11, wherein the level of expression is detected by an amplification or hybridization assay.
- 55. A method of claim 54, wherein the amplification assay is quantitative or semiquantitative PCR.
- 56. A method of claim 54, wherein the hybridization assay is selected from the group consisting of Northern blot, dot or slot blot, nuclease protection and microarray assays.
- 57. A method of identifying an agent that modulates at least one activity of a protein encoded by a gene in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW comprising:
 - (a) exposing the protein to the agent; and

- (b) assaying at least one activity of said protein.
- 58. A method of claim 57, wherein the agent is exposed to a cell expressing the protein.
- 59. A method of claim 58, wherein the cell is exposed to a known toxin.
- 60. A method of claim 59, wherein the toxin modulates the expression of the protein.
- 61. A method of claim 1, wherein the level of expression is compared to a Tox Mean and/or Non-Tox Mean value in Tables 5A-5WWW.
- 62. A method of claim 61, wherein the level of expression is normalized prior to comparison.
- 63. A method of claim 62, wherein the tissue or cell sample is a liver tissue or liver cell sample.
- 64. A computer system comprising:
- (a) a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising substantially all of the genes in Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF, 5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV; and
 - (b) a user interface to view the information.
- An array comprising probes which individually specifically hybridize to substantially all of the genes in Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF,

5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV.

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(57) Abstract: The present invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in liver tissues or cells exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The invention includes a database of genes characterized by liver toxin-induced differential expression that is designed for use with microarrays and other solid-phase probes.

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	cumentation searched (classification system follower 02/19, 27	d by class	ification symbols)	
Documentati	on searched other than minimum documentation to the	he extent	that such documents are include	d in the fields searched
Electronic de	ata base consulted during the international search (na	ume of dat	a base and, where practicable, s	search terms used)
	UMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where a			Relevant to claim No.
X	US 6,218,122 B1 (FRIEND et al.) 17 April 2001 (17.04.20	01), see column 1, lines 50-	1-6, 12-19 and 53-56
Y	61; column 7, lines 5-15, column 9, lines 15-19; c column 11, lines 35-45; column 13, lines 49-56; column 19-26.	olumn 10 olumn 21,	, lines 40-46 and lines 57-64; lines 52-56 and column 23,	7 and 20
Y	US 2001/0049139 A1 (LAGASSE et al.) 06 December 2001 (06.12.2001), see paragraphs 7 and 20 0032 and 0042.			
Further	documents are listed in the continuation of Box C.		See patent family annex.	
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24 June 2003 (24.06.2003) Name and mailing address of the ISA/US Author zed officer				
Mai Con P.O Alex	All this patters of the ISA/US 1 Stop PCT, Attn: ISA/US minissioner for Patents 1 Box 1450 candria, Virginia 22313-1450 1 (703)305-3230	Author Cheyn Telepho	D Ey One No. 703-308-0196	ges to

Form PCT/ISA/210 (second sheet) (July 1998)



International application No.

PCT/US03/03194

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)			
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:			
Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:			
2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:			
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).			
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)			
This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet			
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 			
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, 12-20 and 53-56; carcinogenesisand acetominophen			
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.			

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, 12-20, and 53-56, drawn to a method of predicting at least one toxic effect of a compound.

Group II, claim(s) 8, 12-17, 20, and 53-56, drawn to a method of predicting the progression of a toxic effect of a compound.

Group III, claim(s) 9, 12-17, 21, and 53-56, drawn to a method of predicting the hepatotoxicity of a compound.

Group IV, claim(s) 10, 12-17, and 53-56, drawn to a method of identifying an agent that modulates the onset or progression of a toxic response.

Group V claim(s) 11, 12-17, 22, and 53-56, drawn to a method of predicting the cellular pathways that a compound modulates in a cell.

Group VI, claim(s) 23-29, drawn to a set of at least two probes.

Group VII, claim(s) 30-34 and 50-52, drawn to a solid support comprising at least two probes.

Group VIII, claim(s) 35-49 and 64, drawn to a computer system with a database containing information identifying the expression level in a tissue or cell.

Group IX, claim(s) 57-63, drawn to a method of identifying an agent that modulates at least one activity of a protein encoded by a gene.

Group X, claim(s) 65, drawn to an array comprising probes which individually specifically hybridize to all of the genes in specified tables.

.2, they lack the same or corresponding special technical features for the following reasons:

Group I is directed to a method of predicting at least one toxic effect of a compound.

Group II is directed to a method of predicting the progression of a toxic effect of a compound.

Group III is directed to a method of predicting the hepatotoxicity of a compound.

Group IV is directed to a method of identifying an agent that modulates the onset or progression of a toxic response.

Group V is directed to a method of predicting the cellular pathways that a compound modulates in a cell.

Group VI is directed to a set of at least two probes.

Group VII is directed to a solid support comprising at least two probes.

Group VIII is directed to a computer system with a database containing information identifying the expression level in a tissue or cell.

Group IX is directed to a method of identifying an agent that modulates at least one activity of a protein encoded by a gene.

Group X is directed to an array comprising probes which individually specifically hybridize to all of the genes in specified tables.

Form PCT/ISA/210 (second sheet) (July 1998)

PCT/US03/031

Clearly, these 10 Groups lack the same or corresponding special technical features. Thus, Groups I-X are directed to different special technical features and thus support this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

Specific to Groups I-V, VIII, and IX, the claims of these groups include a series of generic technical features directed to diseases (claim 20) and toxins (claim 22), The technical group containing diseases have 8 species. The technical group containing toxins have 30 species. These species within each technical feature is distinct characterized by its functional properties, thus, each is its own special technical feature.

The first Group has been identified as Group I having species of carcinogenesis and acetominophen.

Election of a species of the disease and toxin is required for Groups I-V, VIII and IX. For each additional species for each Group, the fee for each additional Group is \$210.00 and each additional specie is \$210.

Specific to Groups VI, VII, and X, these inventions are directed to at least two sequences (4295 SEQ ID NOs) listed in specified tables and each SEQ ID Nos: has its own special technical features. Therefore, if Group VI, VII, or X is the elected Group, an additional fee of \$210.00 is required for each Group and \$210 for each pair of SEQ ID Nos: from 1-4295 (2148 pairs).

The total for search reports on the inventions of Group I-X and all the species is \$1,705,830.

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